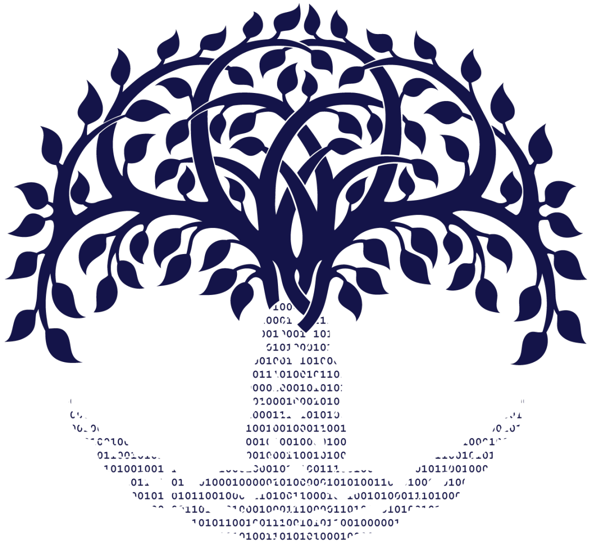
DTU



DTU Health Technology
Bioinformatics

Human microbiome

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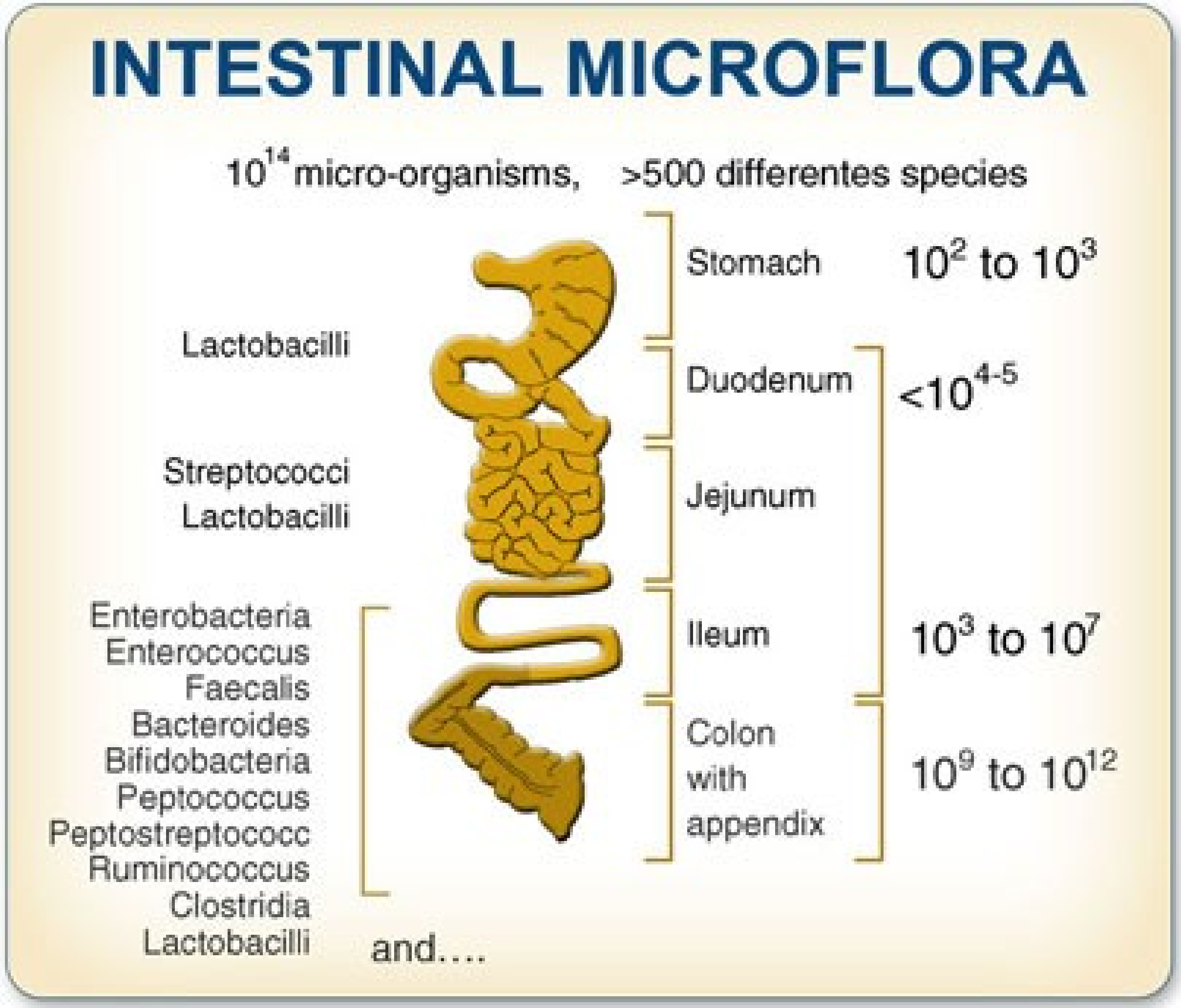
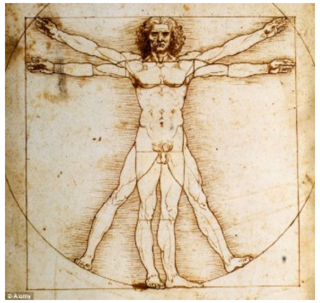
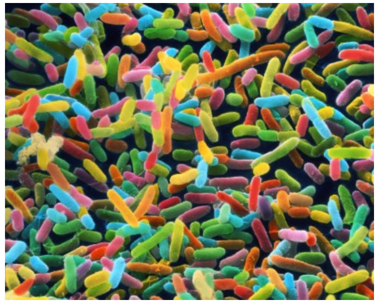
Human microbiome



Human microbiome in numbers



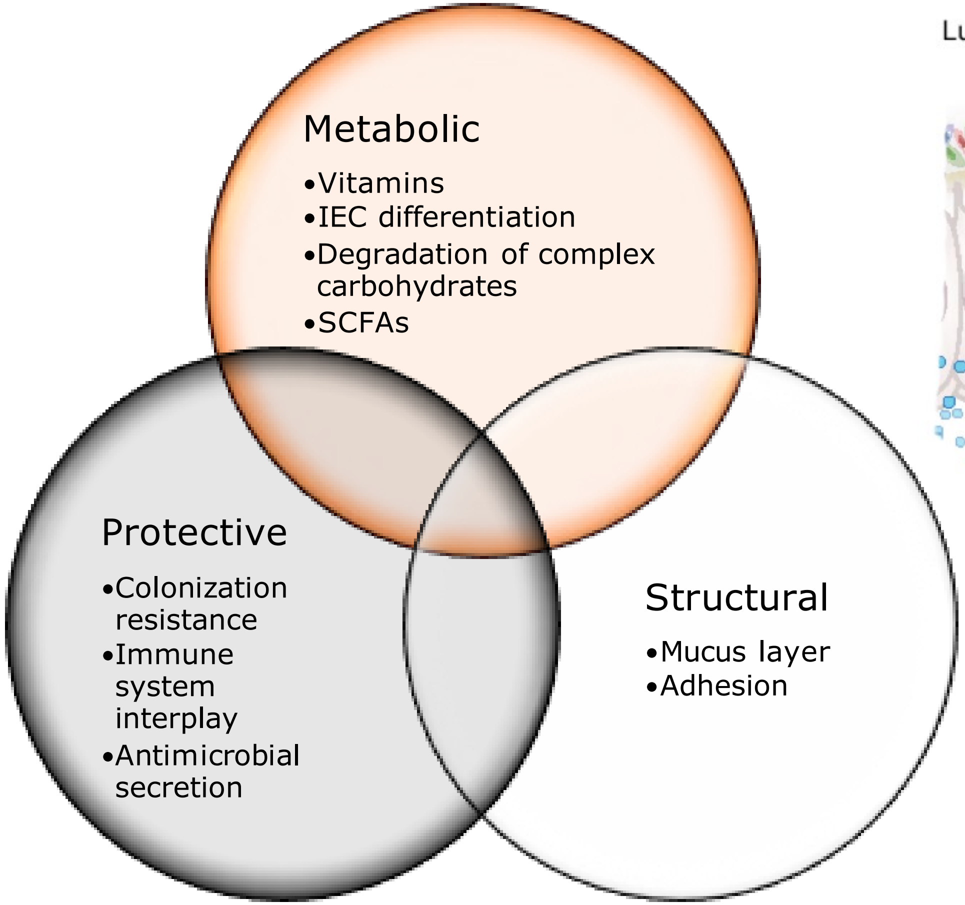
vs.



	Human (isolated)	Microbiota
weight	~ 50-100 kg	~ 2 kg
species	1	1000-5000
cells	~ 10^{12}	10^{13} - 10^{14}
genes	25.000	>4.000.000

IGC catalogue (non-redundant genes found in gut microbes): >9.800.000 genes

Human microbiome: Functions



Metabolic

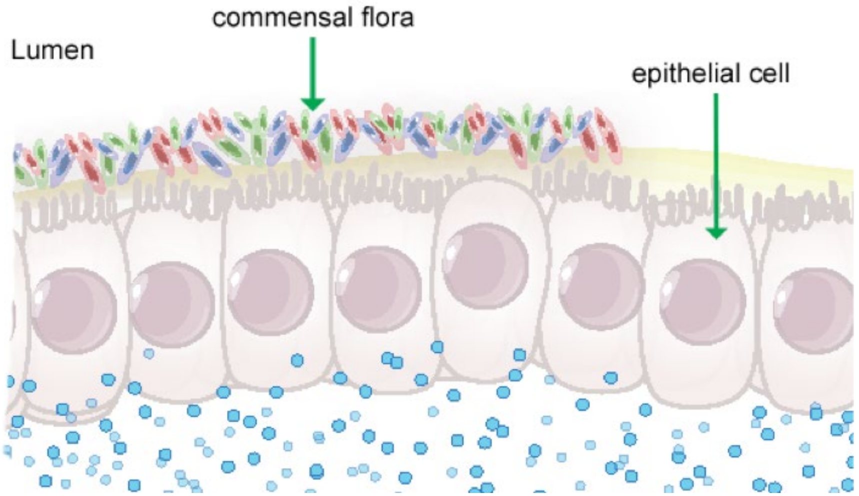
- Vitamins
- IEC differentiation
- Degradation of complex carbohydrates
- SCFAs

Protective

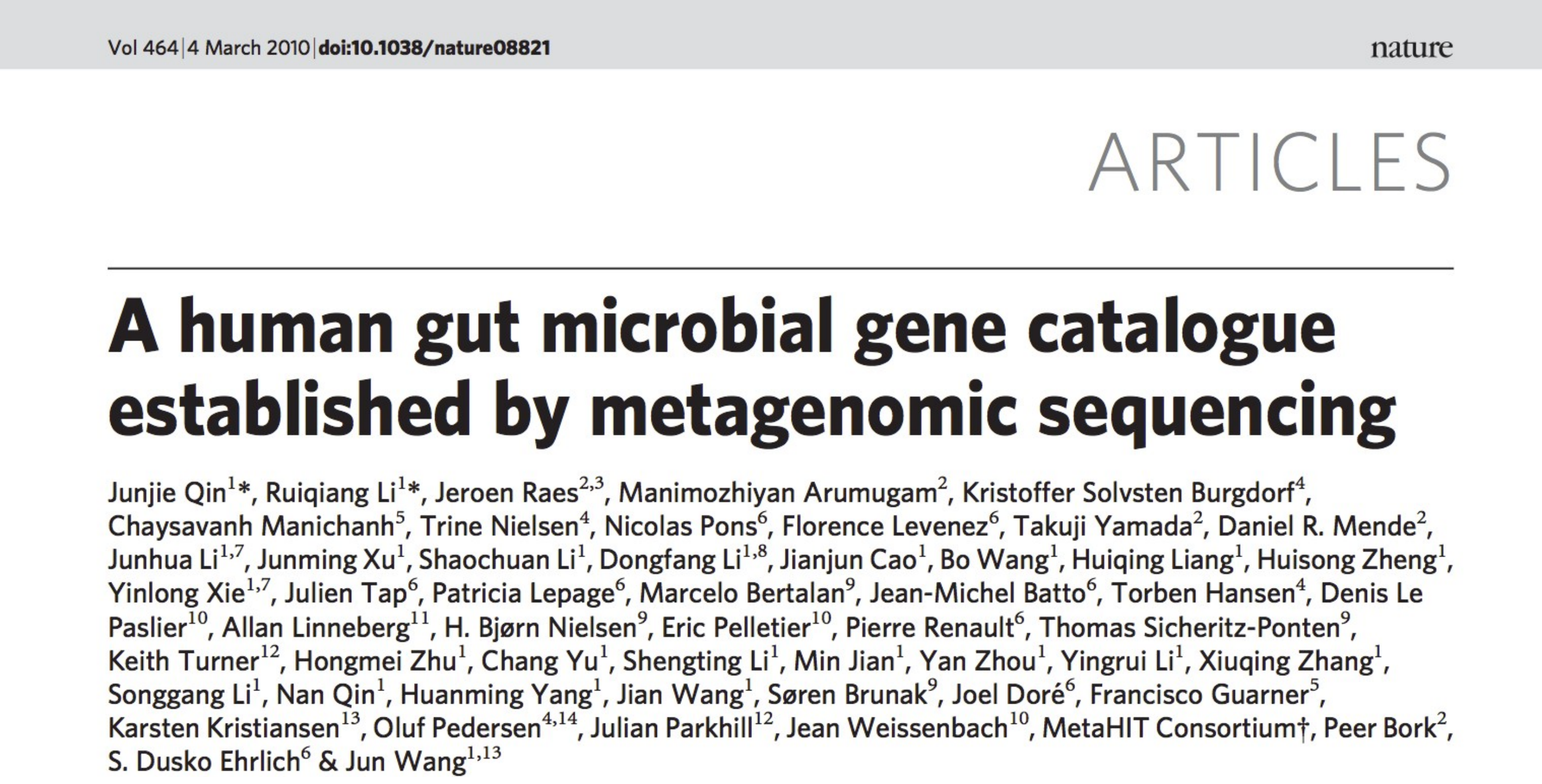
- Colonization resistance
- Immune system interplay
- Antimicrobial secretion

Structural

- Mucus layer
- Adhesion



Human gut microbial gene catalogue



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ARTICLES

A human gut microbial gene catalogue established by metagenomic sequencing

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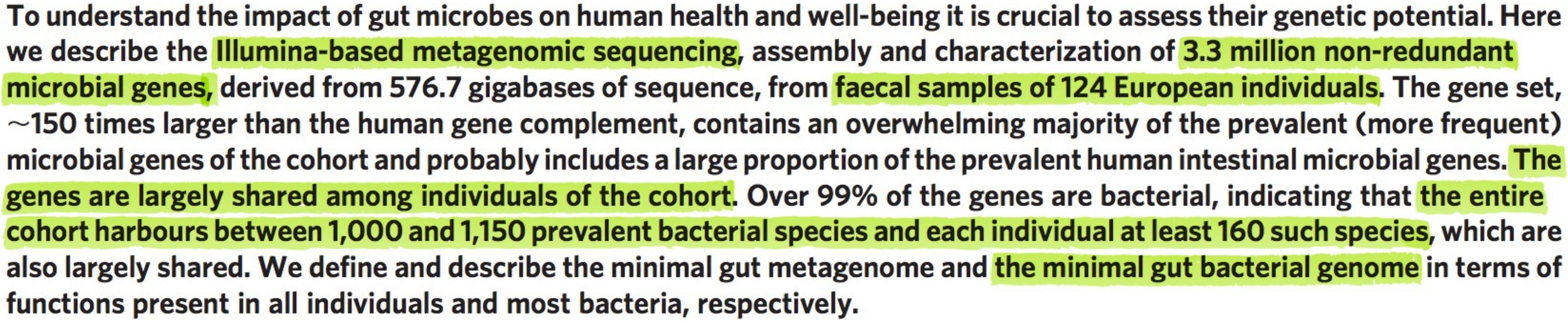
Human gut microbial gene catalogue



To understand the impact of gut microbes on human health and well-being it is crucial to assess their genetic potential. Here we describe the Illumina-based metagenomic sequencing, assembly and characterization of 3.3 million non-redundant microbial genes, derived from 576.7 gigabases of sequence, from faecal samples of 124 European individuals. The gene set, ~150 times larger than the human gene complement, contains an overwhelming majority of the prevalent (more frequent) microbial genes of the cohort and probably includes a large proportion of the prevalent human intestinal microbial genes. The genes are largely shared among individuals of the cohort. Over 99% of the genes are bacterial, indicating that the entire cohort harbours between 1,000 and 1,150 prevalent bacterial species and each individual at least 160 such species, which are also largely shared. We define and describe the minimal gut metagenome and the minimal gut bacterial genome in terms of functions present in all individuals and most bacteria, respectively.

- Sequence (Illumina) based metagenomic study
- 3.3 million microbial genes
- 124 samples from a European cohort
- Large overlap between the individuals
- ~ 1000 – 1.150 prevalent bacterial species
- ~160 prevalent species per individual
- Minimal gut bacterial genome and metagenome

Human gut microbial gene catalogue

Aim/hypothesis:

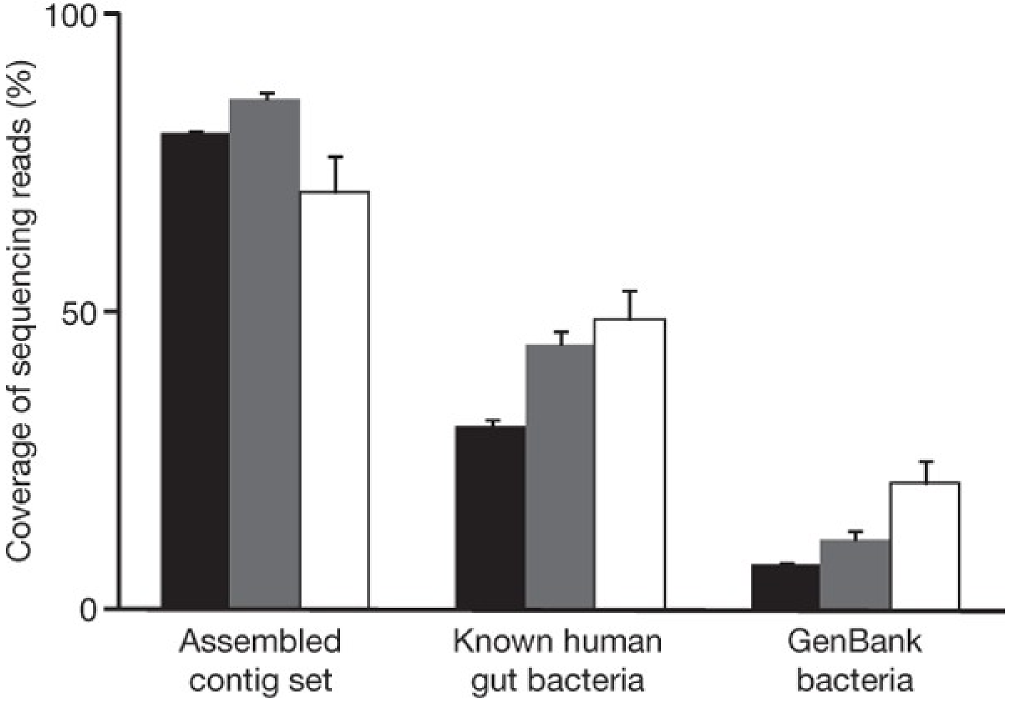
“To get a broader overview of the human gut microbial genes we used the Illumina Genome Analyser (GA) technology to carry out deep sequencing of total DNA from faecal samples of 124 European adults.”

Human gut microbial gene catalogue

- Sequence (Illumina) based metagenomic study
- 3.3 million microbial genes
- 124 samples from a European cohort
- Large overlap between the individuals (>86%)
- Large majority of prevalent intestinal microbial genes
  - over 70% of the metagenomic reads American and Japanese individuals can be mapped
  - about 80% of the microbial genes from 89 common gut reference genomes are present in our set.

Human gut microbial gene catalogue

- 80% of reads could be mapped to assembly at 90% identity
- Less than 50% of reads could be mapped to known gut bacteria
- Interestingly, the majority of reads from two other larger studies could also be mapped to assembly



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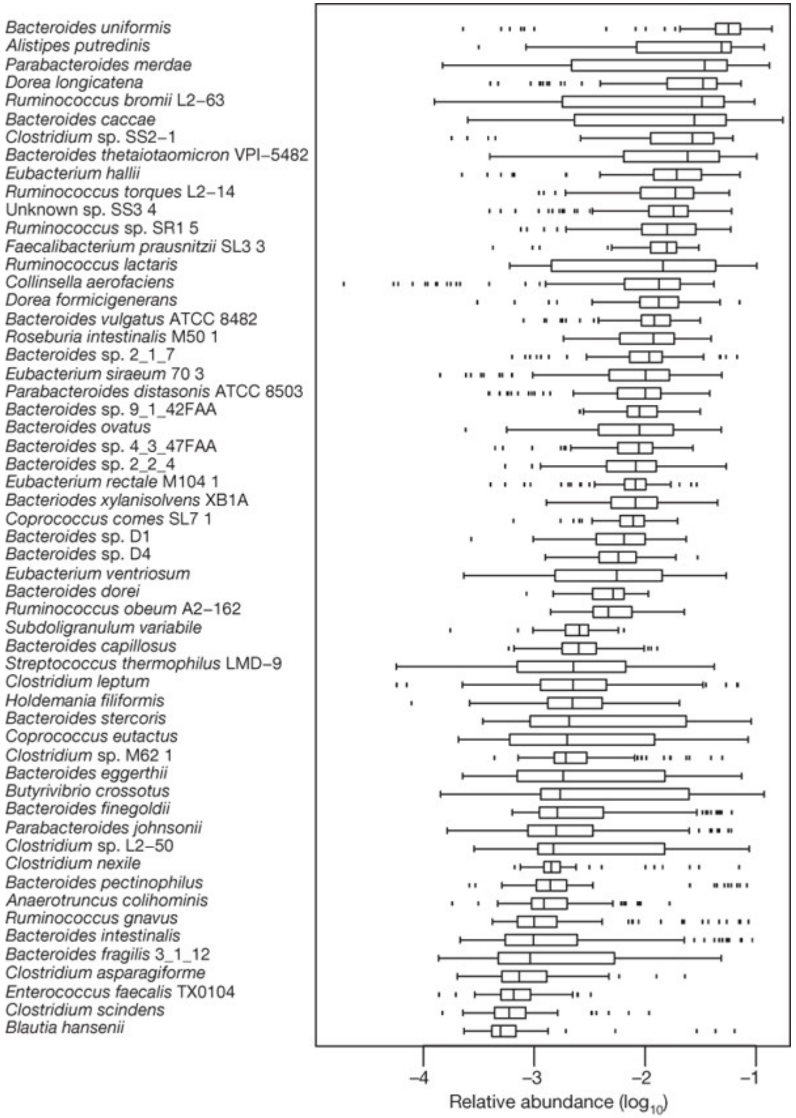
Human gut microbial gene catalogue



Relative abundance of 57 frequent microbial genomes among individuals in cohort

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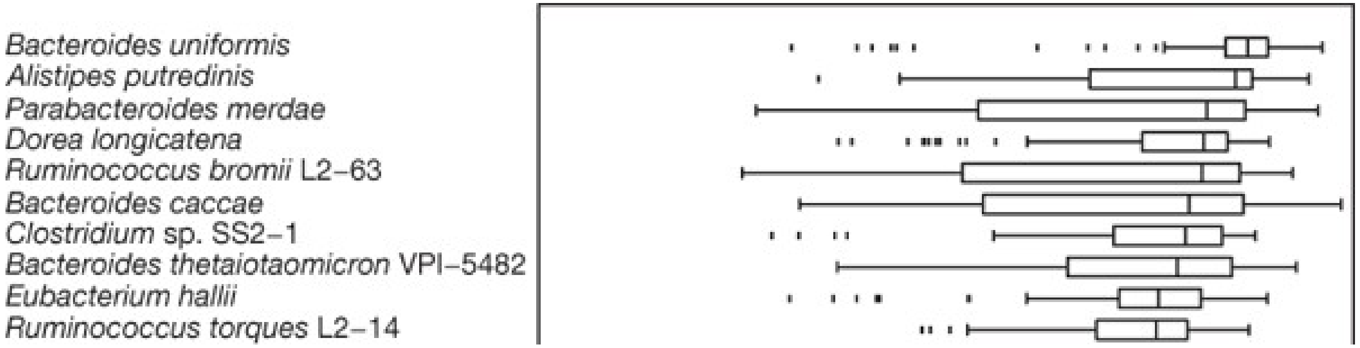
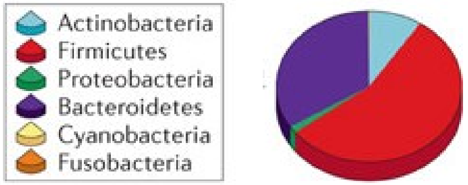
Human gut microbial gene catalogue





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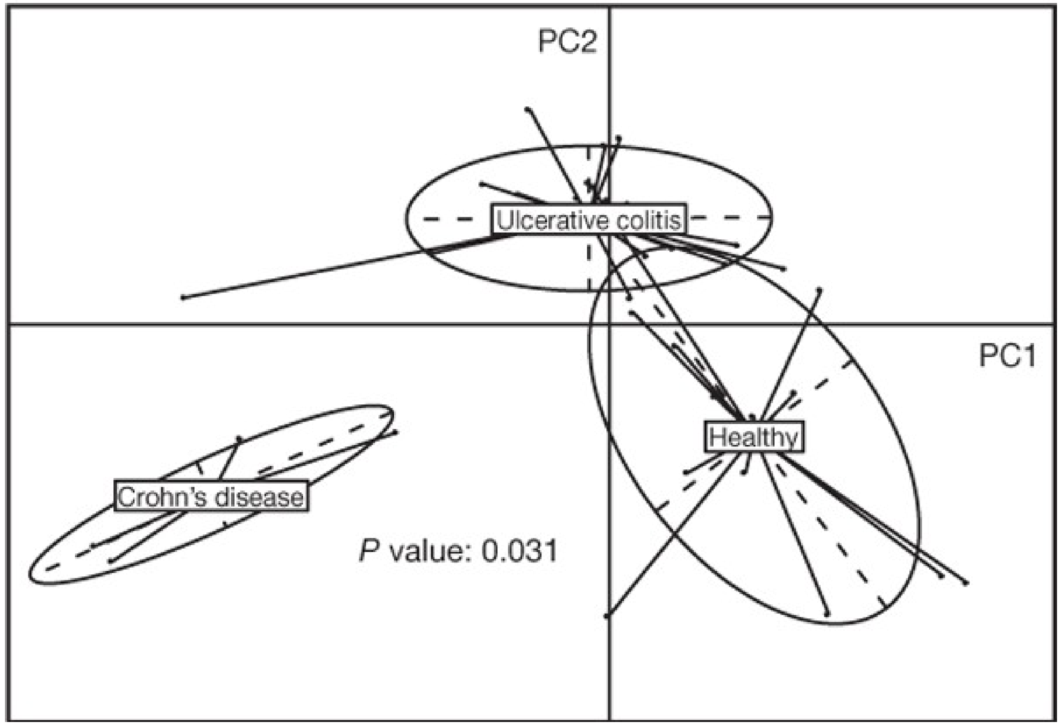
Human gut microbial gene catalogue

Bacterial species abundance: Differentiation of IBD patients and healthy individual



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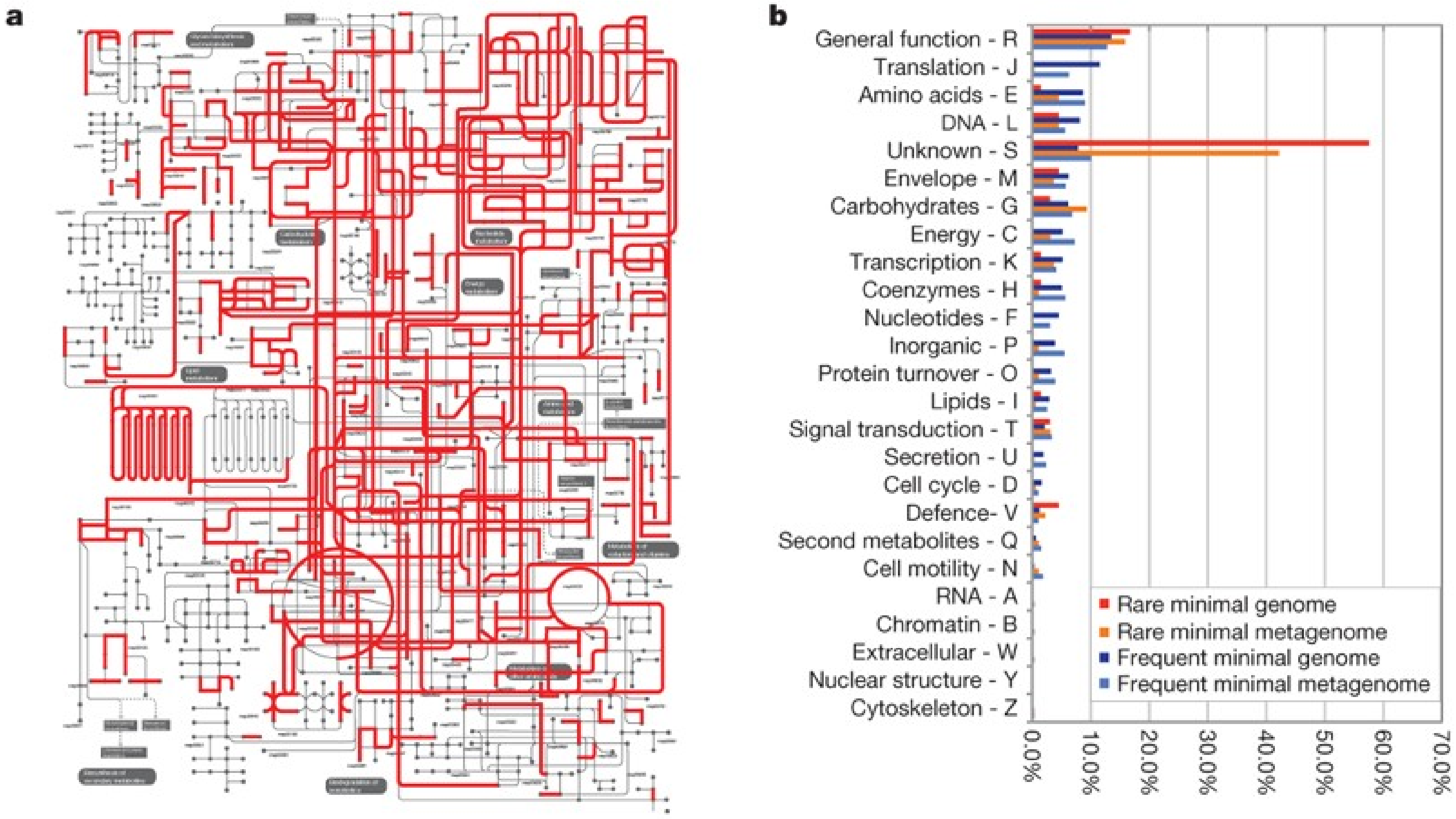
Human gut microbial gene catalogue

Minimal gut genome and metagenome

KEGG mapping indicates +6000 functions in the minimal gut microbiome



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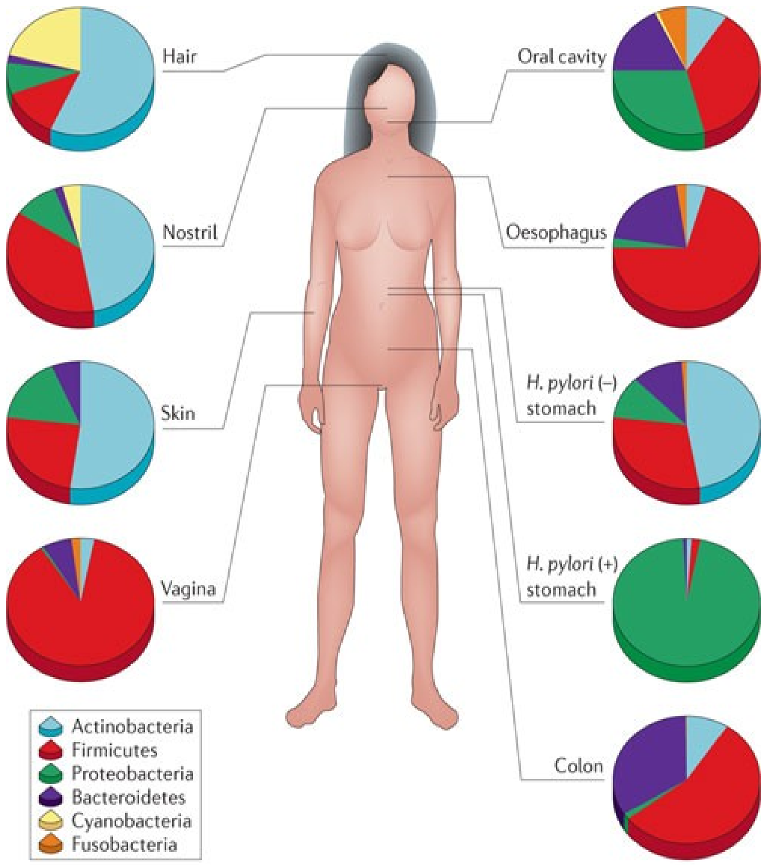
Human microbiome: overview

- **Substantial microbiome differences between anatomical sites**
- **Substantial microbiome differences individuals at each anatomical site**
- **Healthy microbiomes are longitudinally stable**



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Paper exercise time!