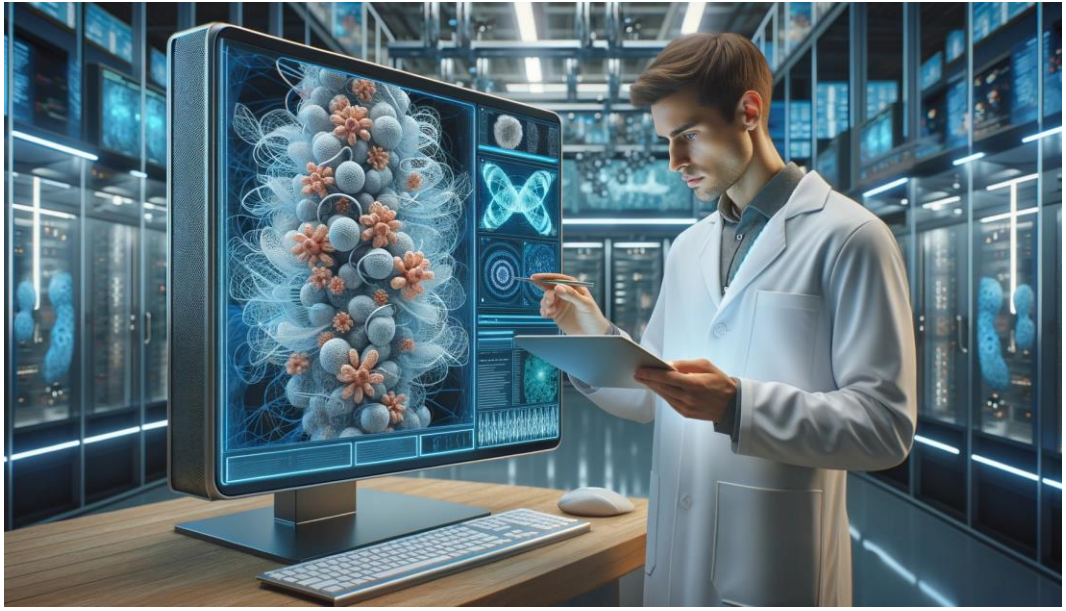
Profils métagénomiques et métabolomiques dans les MICI : comprendre les changements microbiens et métaboliques à partir d'une vaste cohorte profondément phénotypée

Marius Bredon

marius.bredon@sorbonne-universite.fr
CRSA, APHP, Sorbonne Université



IBD

Inflammatory Bowel Disease

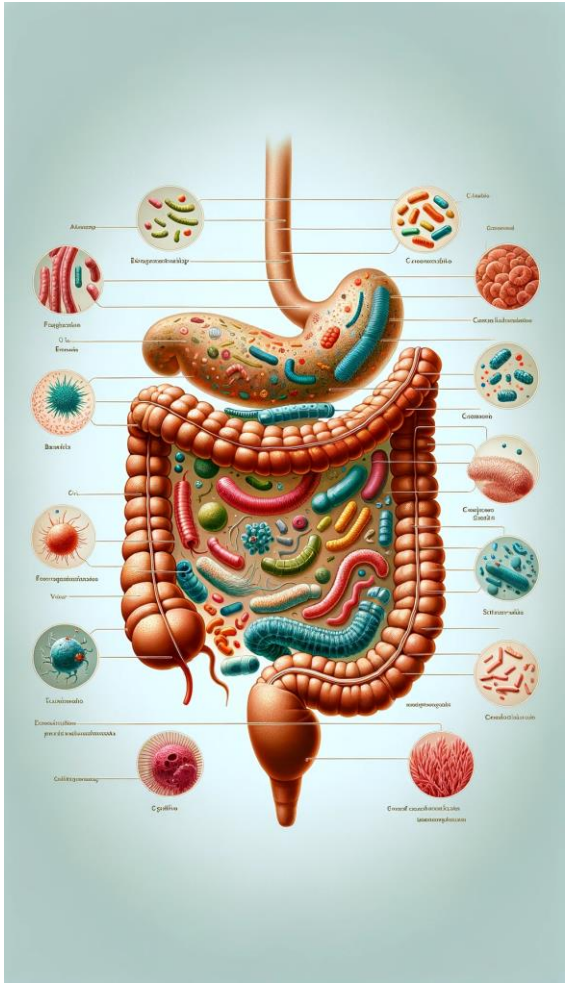
Principal types:

- Crohn's Disease (CD):

May affect any segment of the gastrointestinal tract

- Ulcerative Colitis (UC):

Colon and rectum



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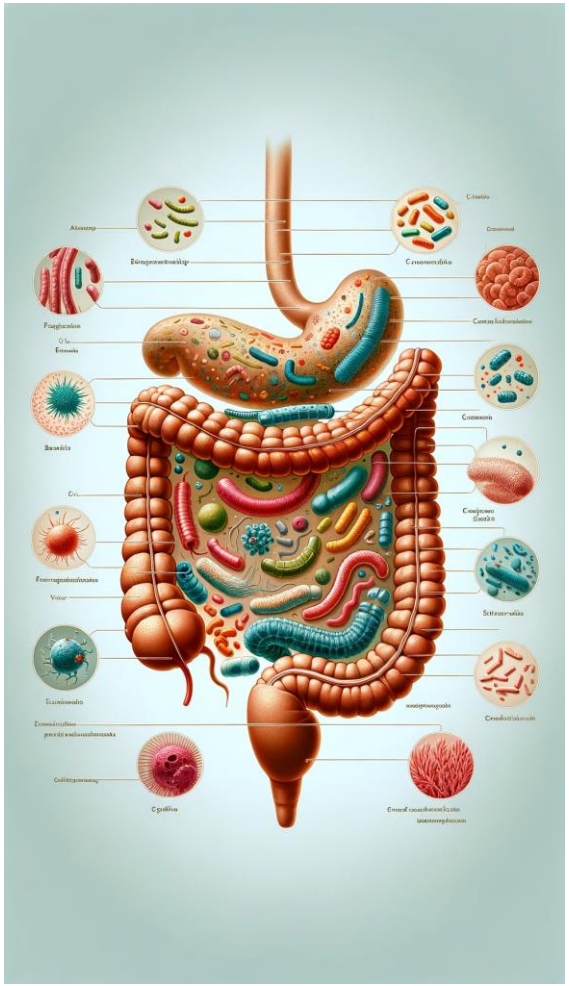
↓

Alterations in gut microbiota composition and functionality

↘ microbial diversity
↘ tryptophan & butyrate-producing bacteria
↗ pathobionts



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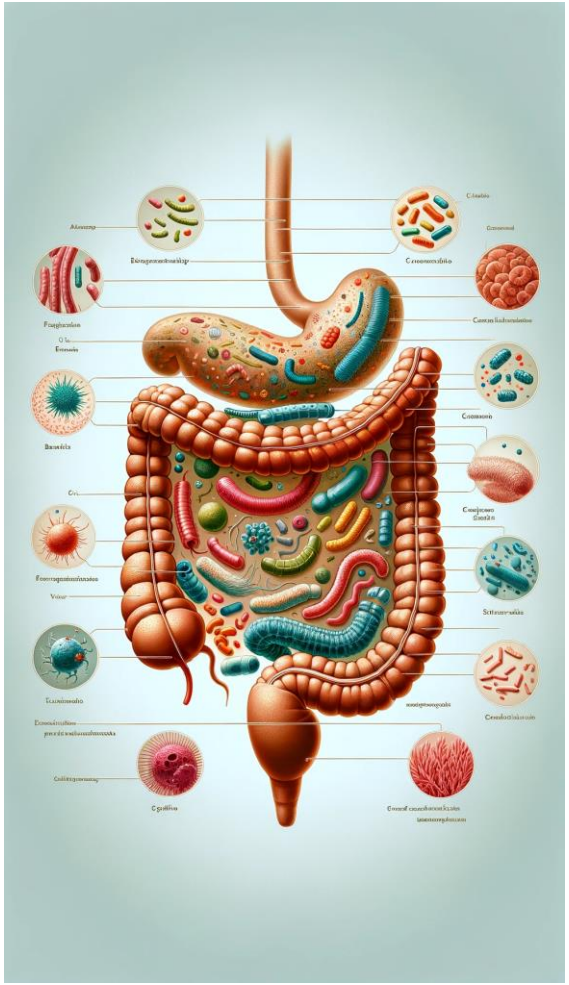
Large studies analyzing both gut microbiota and metabolomics data are scarce



Metagenomic and metabolomic profiles in IBD: understanding microbial and metabolic shifts from a large deeply phenotyped cohort

Shotgun metagenomic sequencing of 764 faecal samples:

447 Crohns

262 UC

55 Healthy

Bioinformatics analysis:

Trimmomatic, KneadData, Metaphlan, HUMAnN3…

Biostatistical analyses:

Phyloseq, Vegan, MaAsLin2, energy, VSURF…

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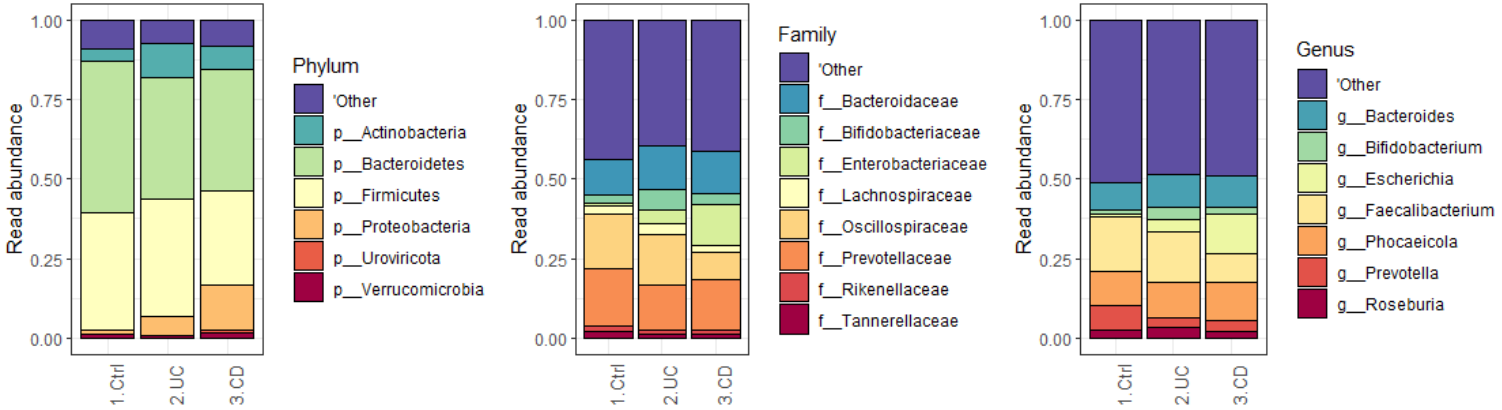
+ Metabolomics data encompassing 294 different molecules

Generalities

Taxonomic profiles



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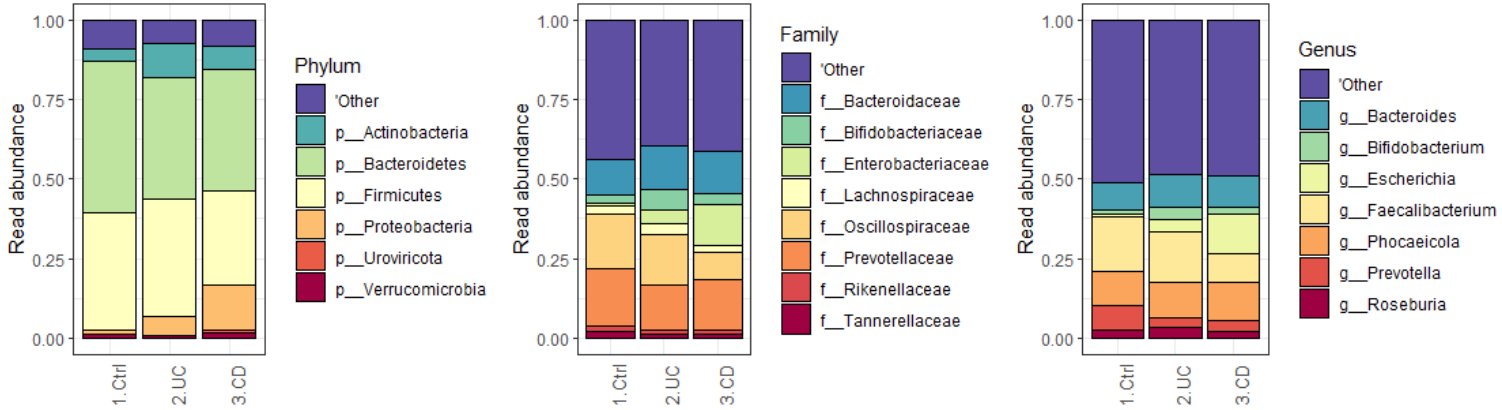
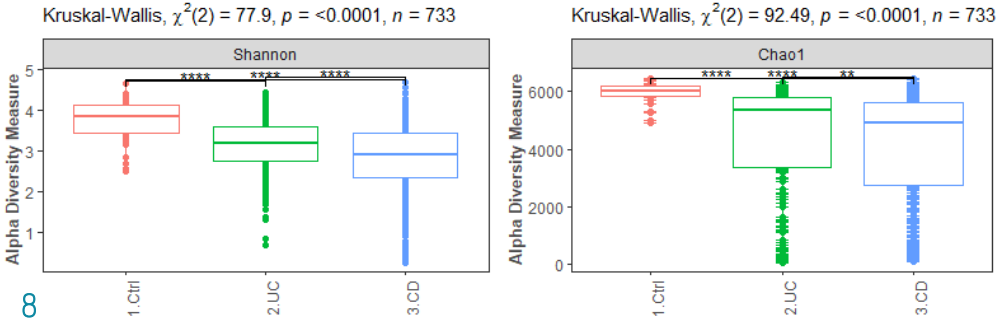
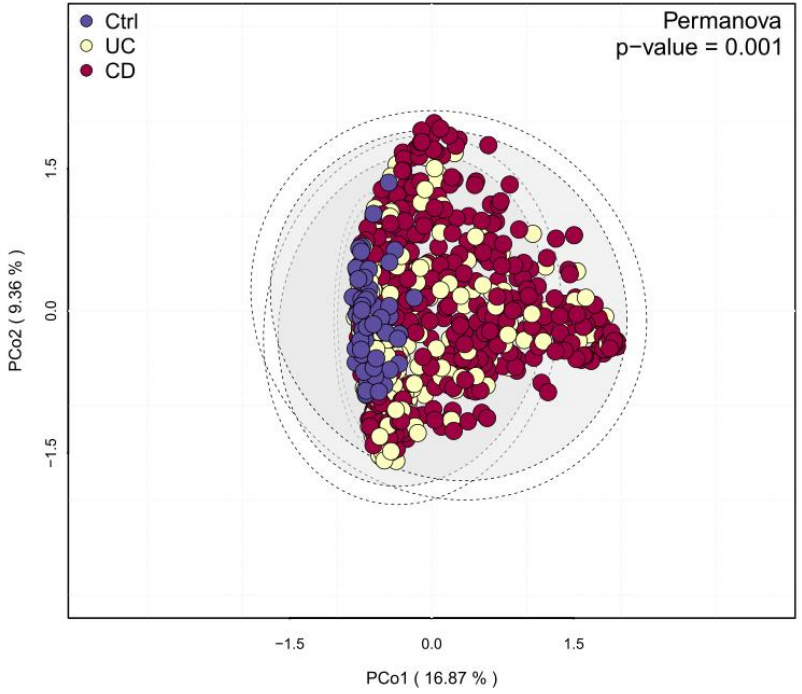


Alpha diversity



Beta Diversity

Taxonomy



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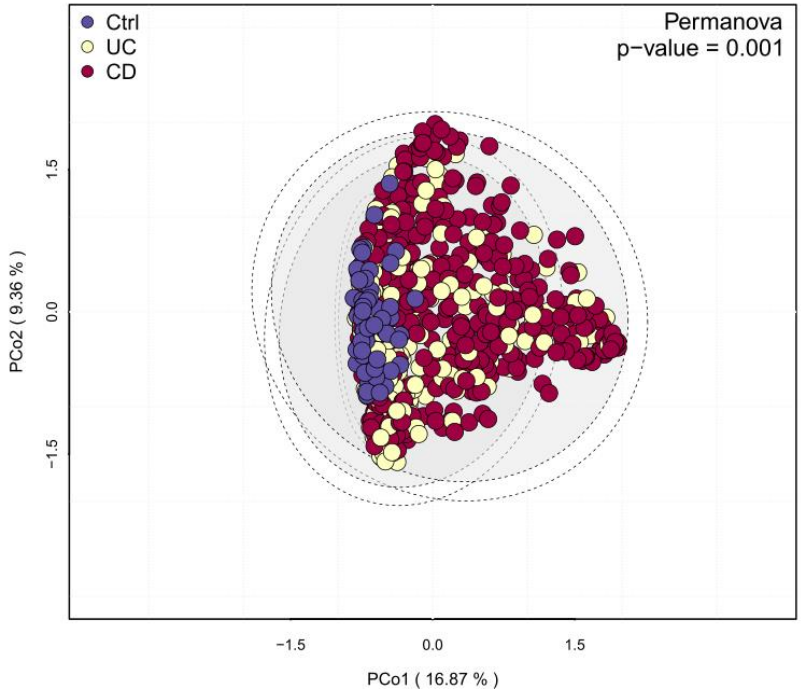

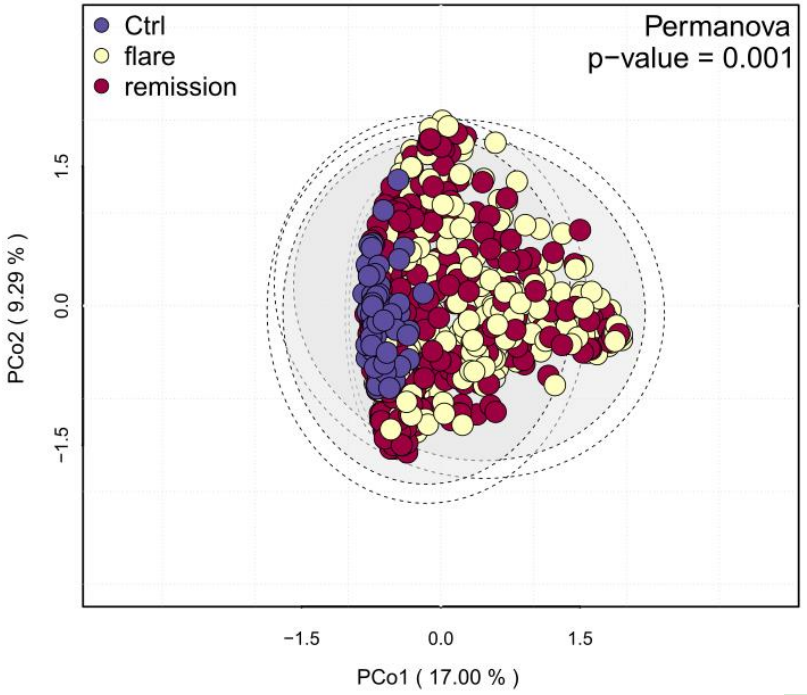

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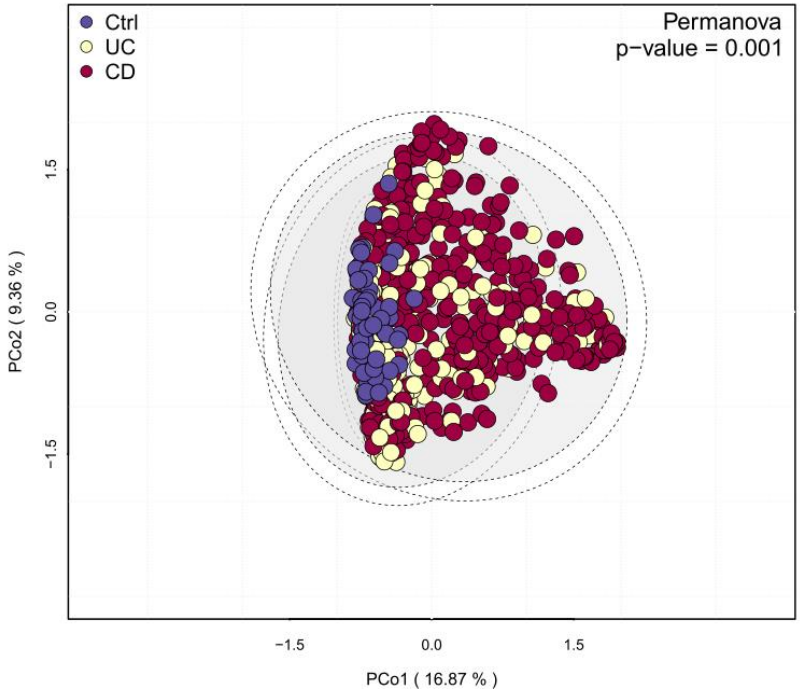
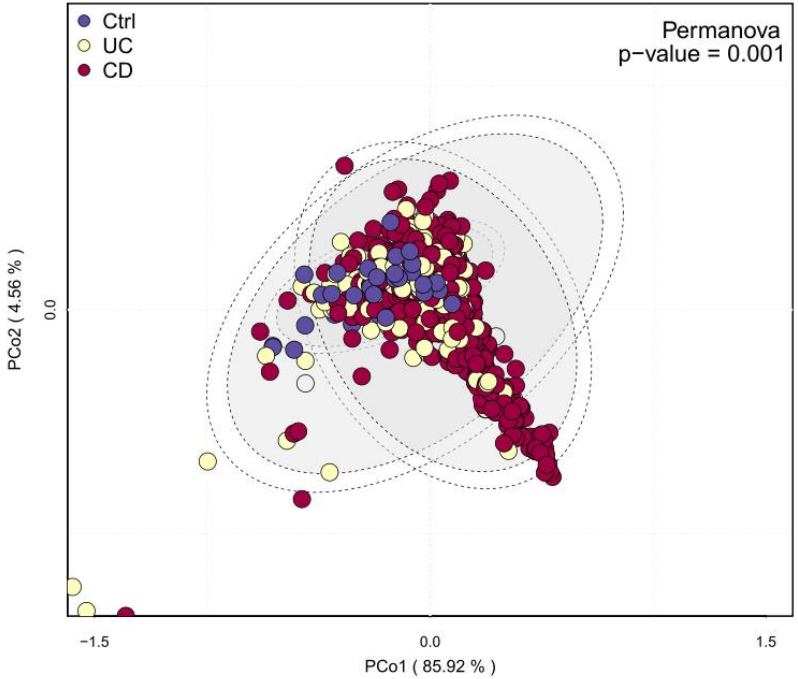
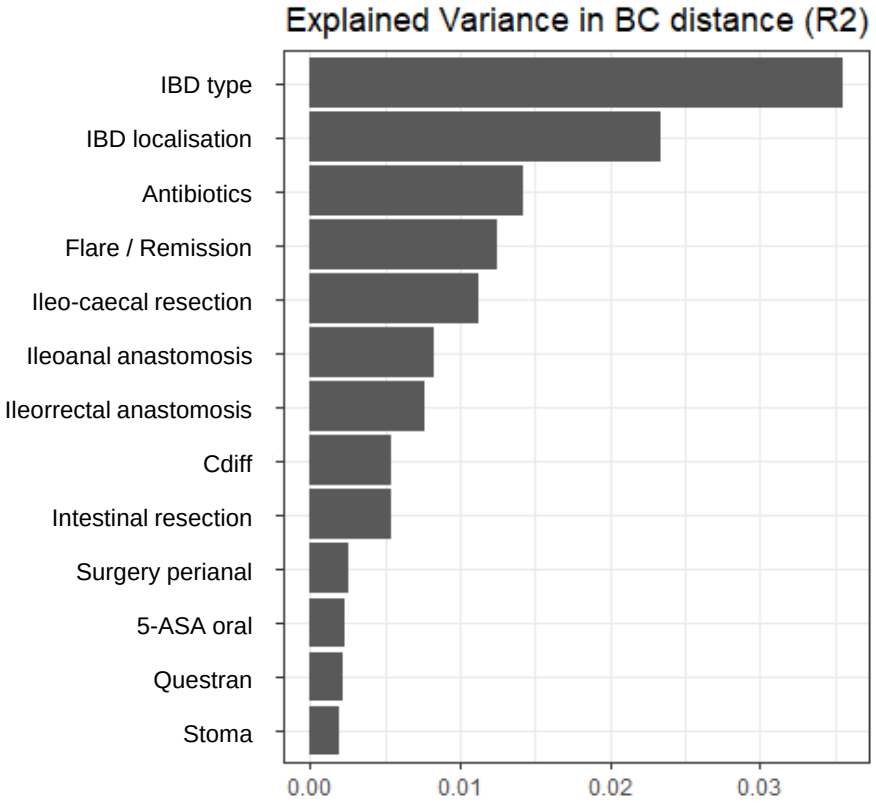


Pathways

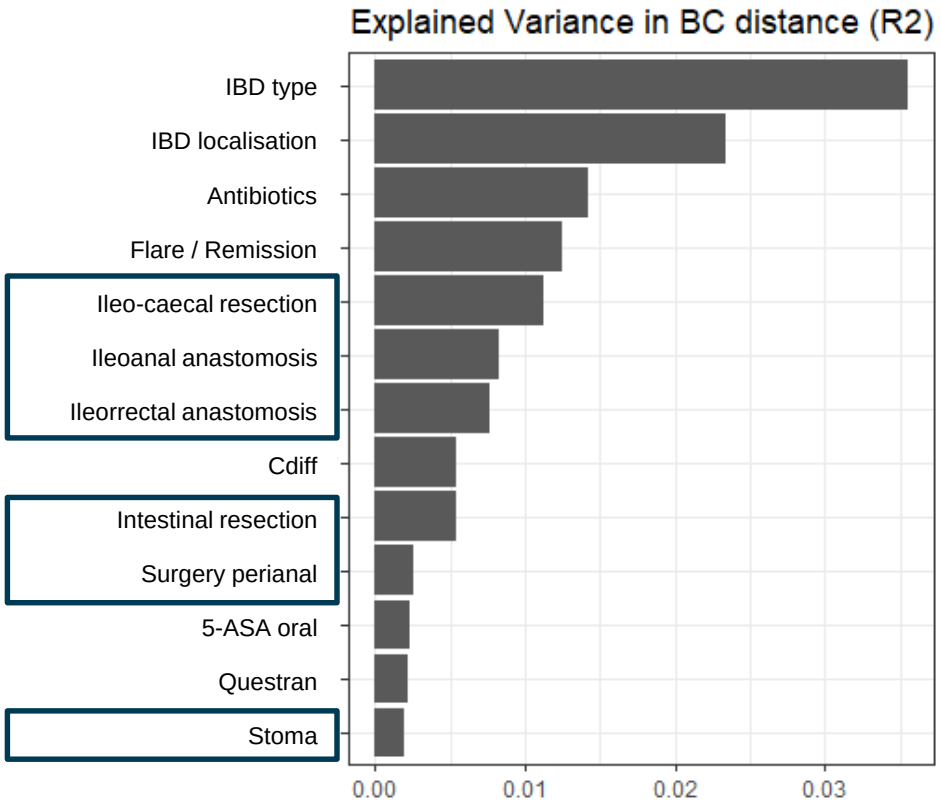


Explained Variance



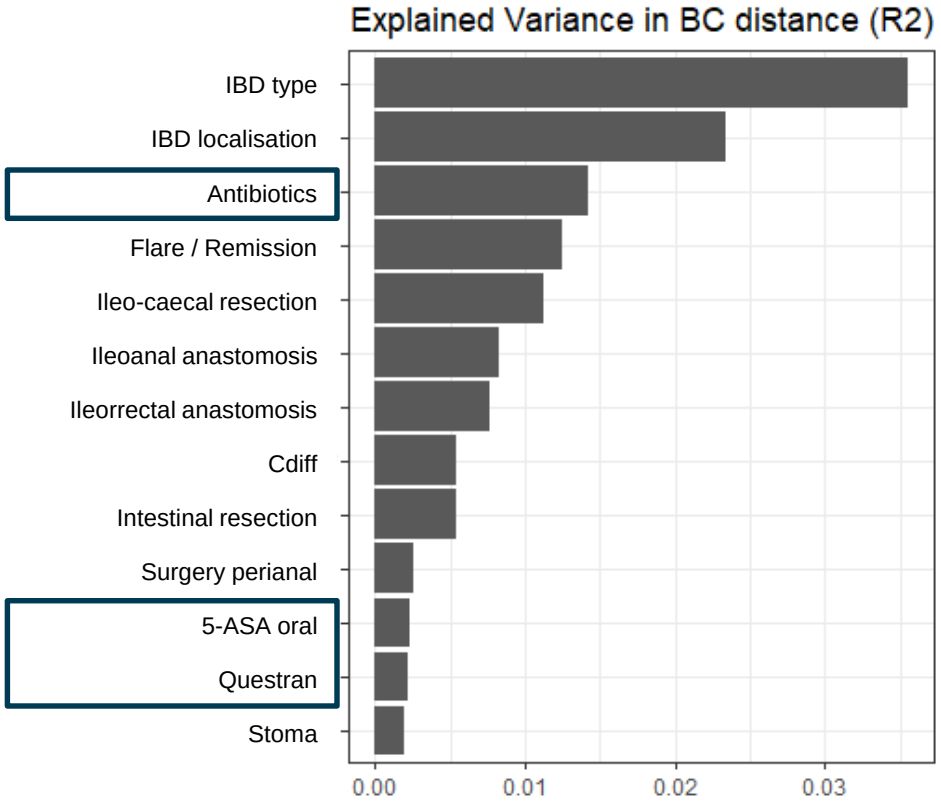
Explained Variance

Surgery

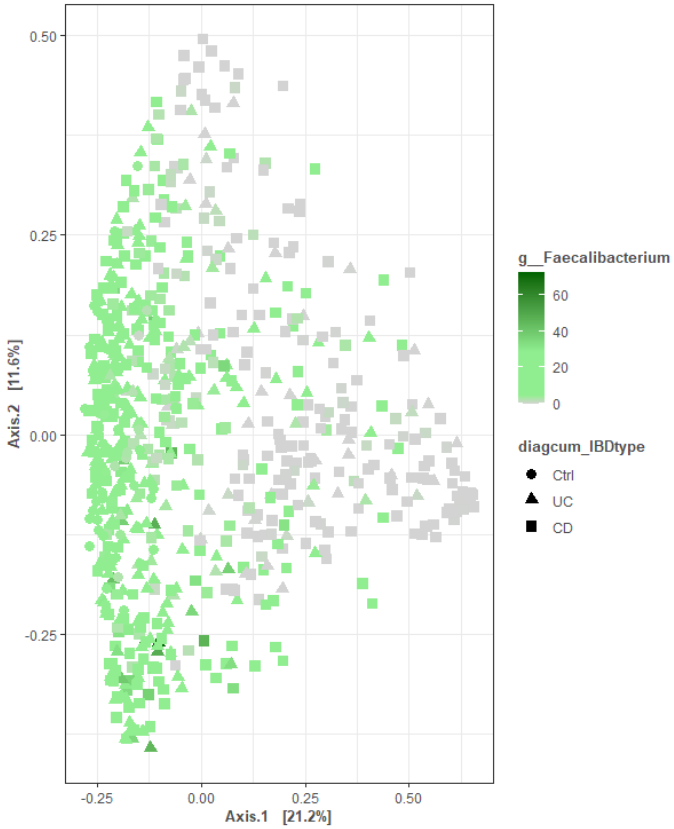


Explained Variance

Treatment



Faecalibacterium prausnitzii



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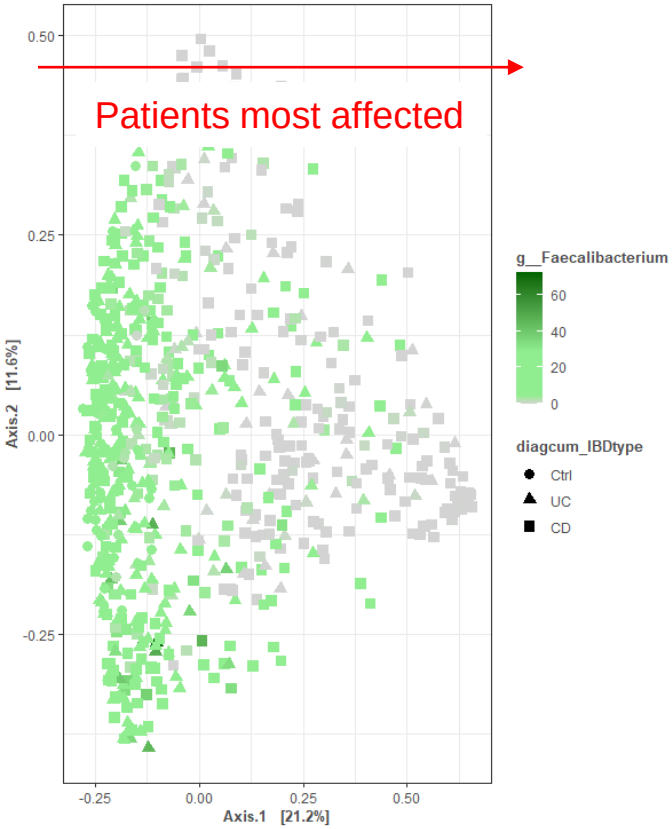
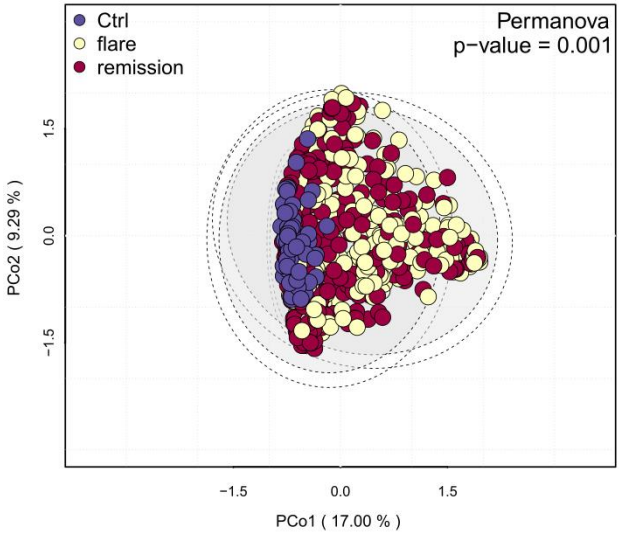
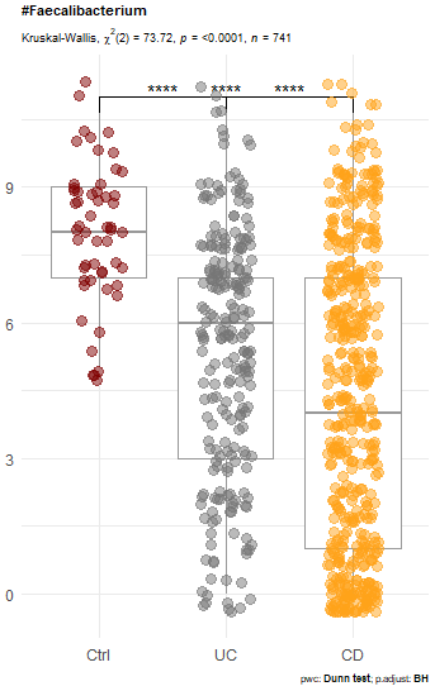
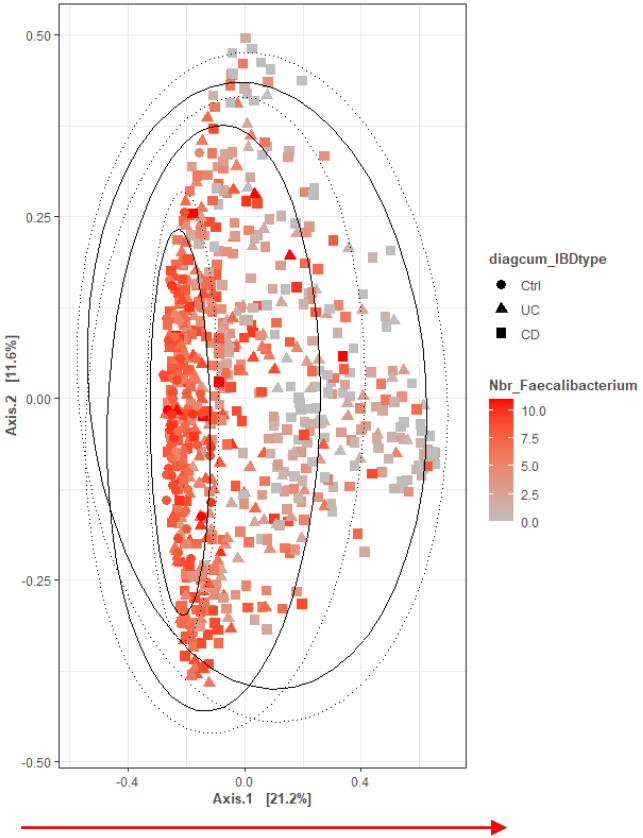




Faecalibacterium strains

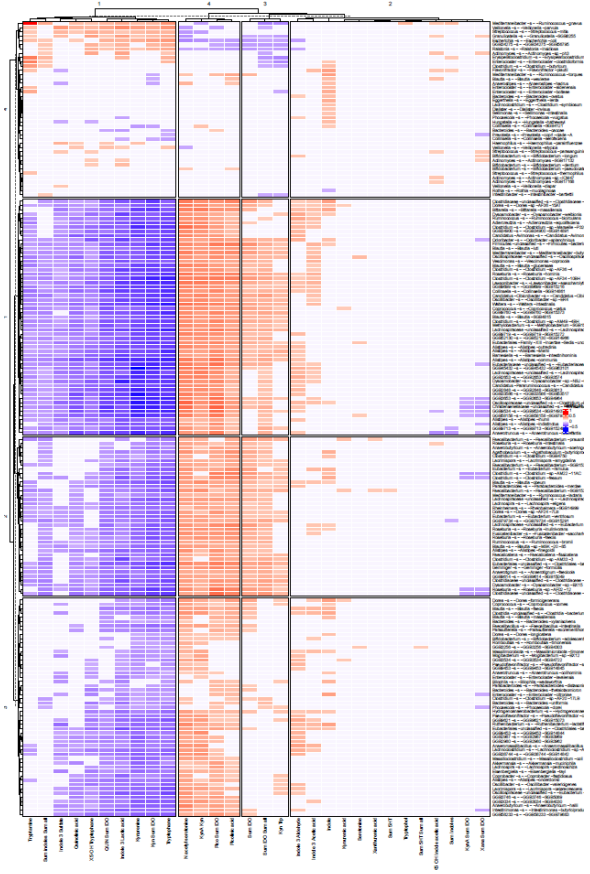




Patients most affected

Metabolite correlations

Feces *FDR =0,001*



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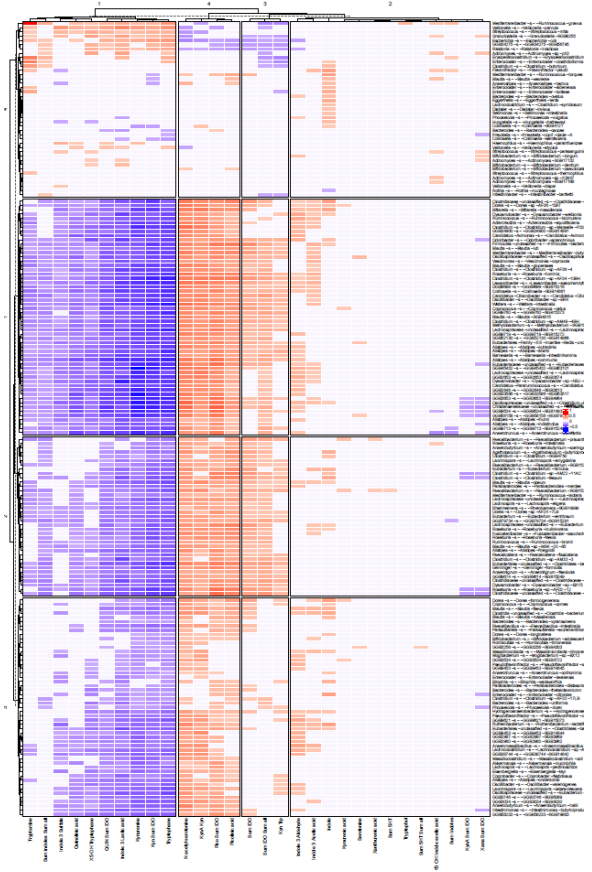
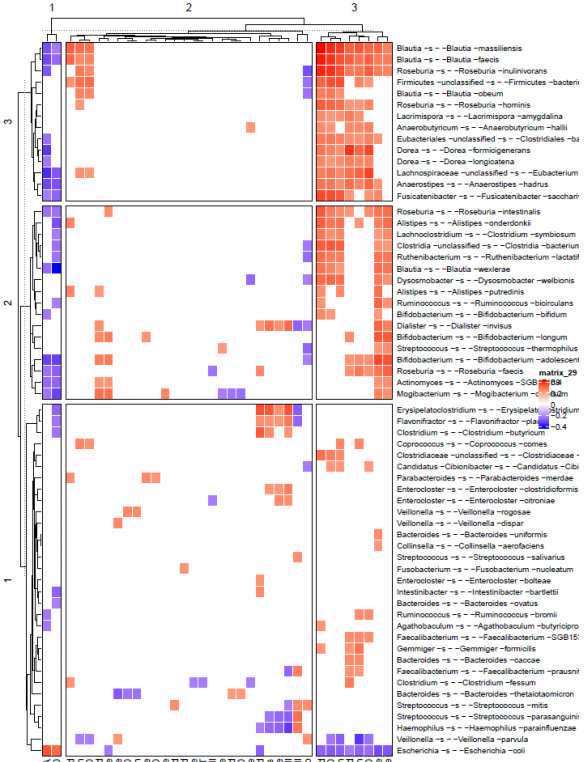
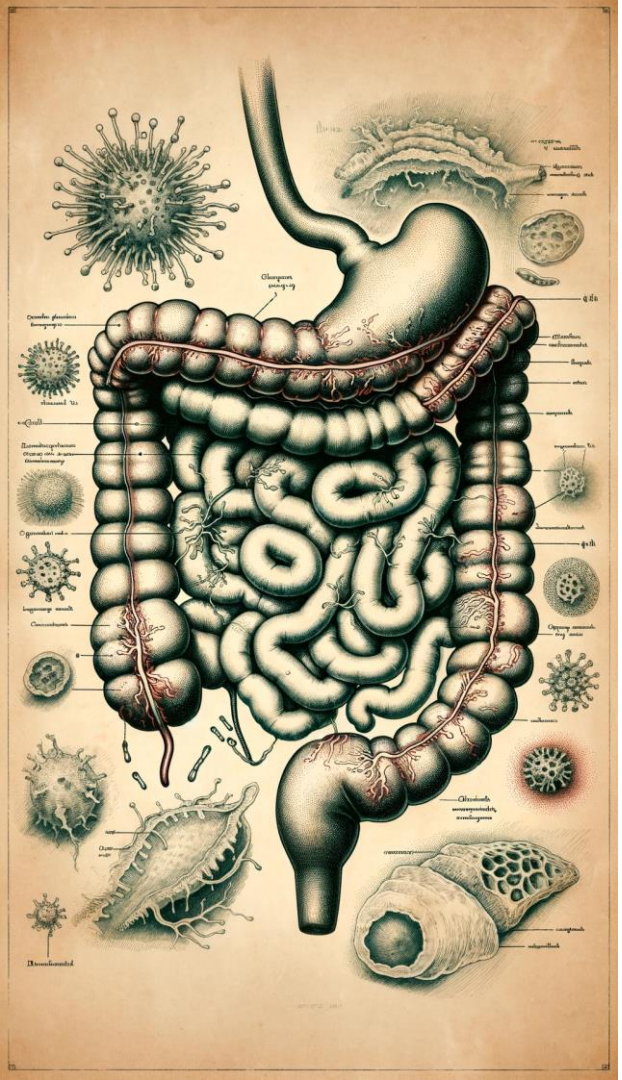


Serum *FDR = 0,25*





Conclusion:

- The most important drivers of microbiota composition were the disease location, treatment, disease activity (flare vs remission) and history of surgery

- The decrease in microbiota diversity was stronger in CD than in UC

- In parallel to a decreased amount of *Faecalibacterium* in IBD, there is also a decrease in the diversity of *Faecalibacterium* strains

- There are many correlations between metabolites and microbial abundance

Thank you for your attention!

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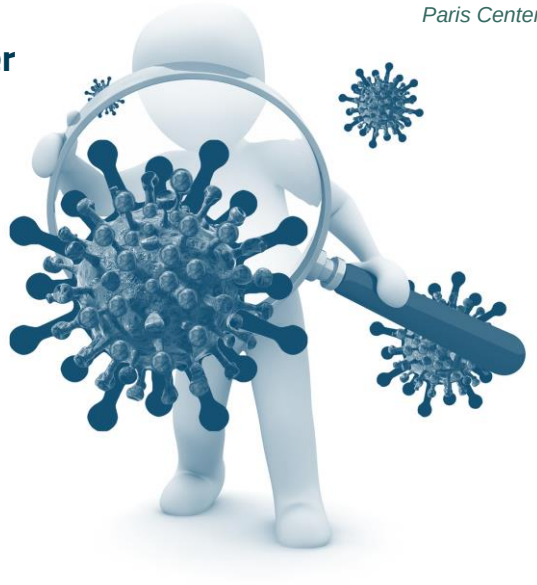

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