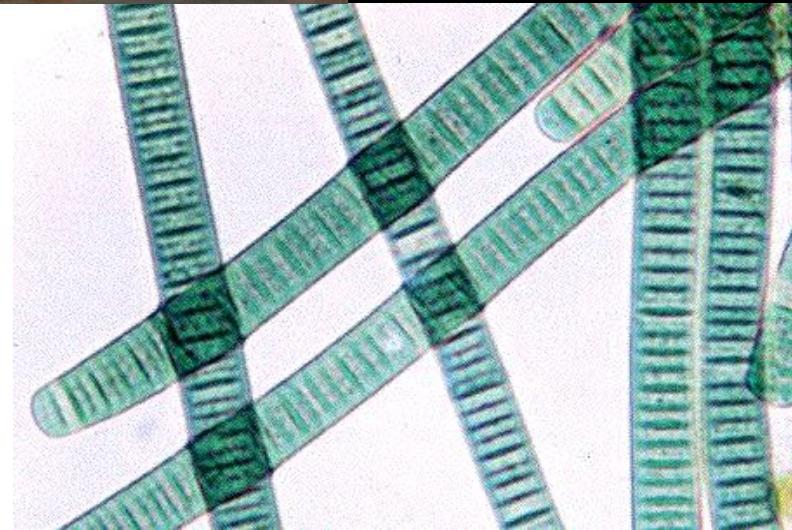


Tale of two sections in gut - Distribution of gut microbiota across foregut and cecum

Arpan Kumar Basak
Evolutionary Physiology Team
Institute of Environmental Sciences,
Jagiellonian University

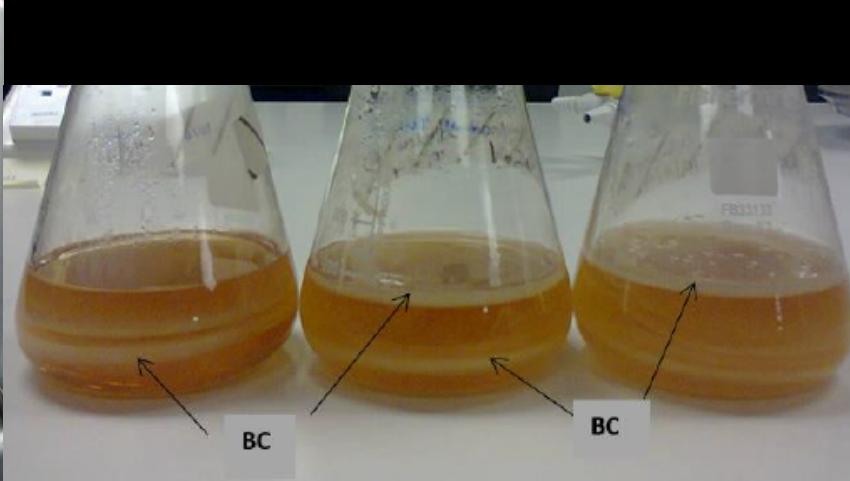
Visweswaraya Technological University

Graduation in Engineering - Biotechnology



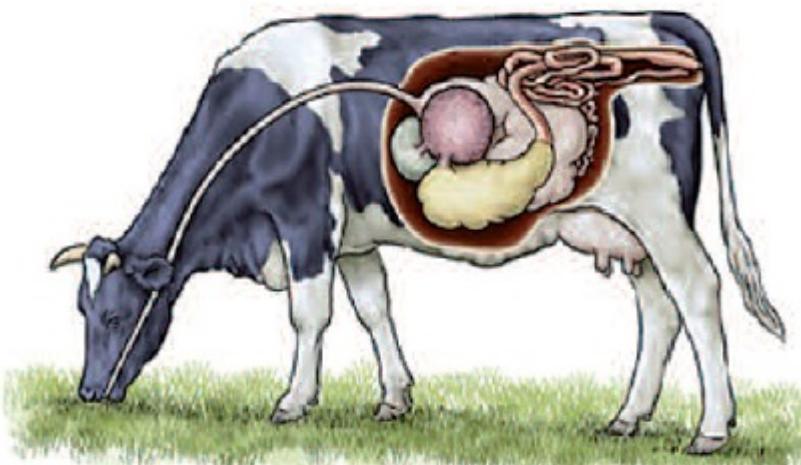
National Institute of Technology

Masters in Engineering - Biotechnology

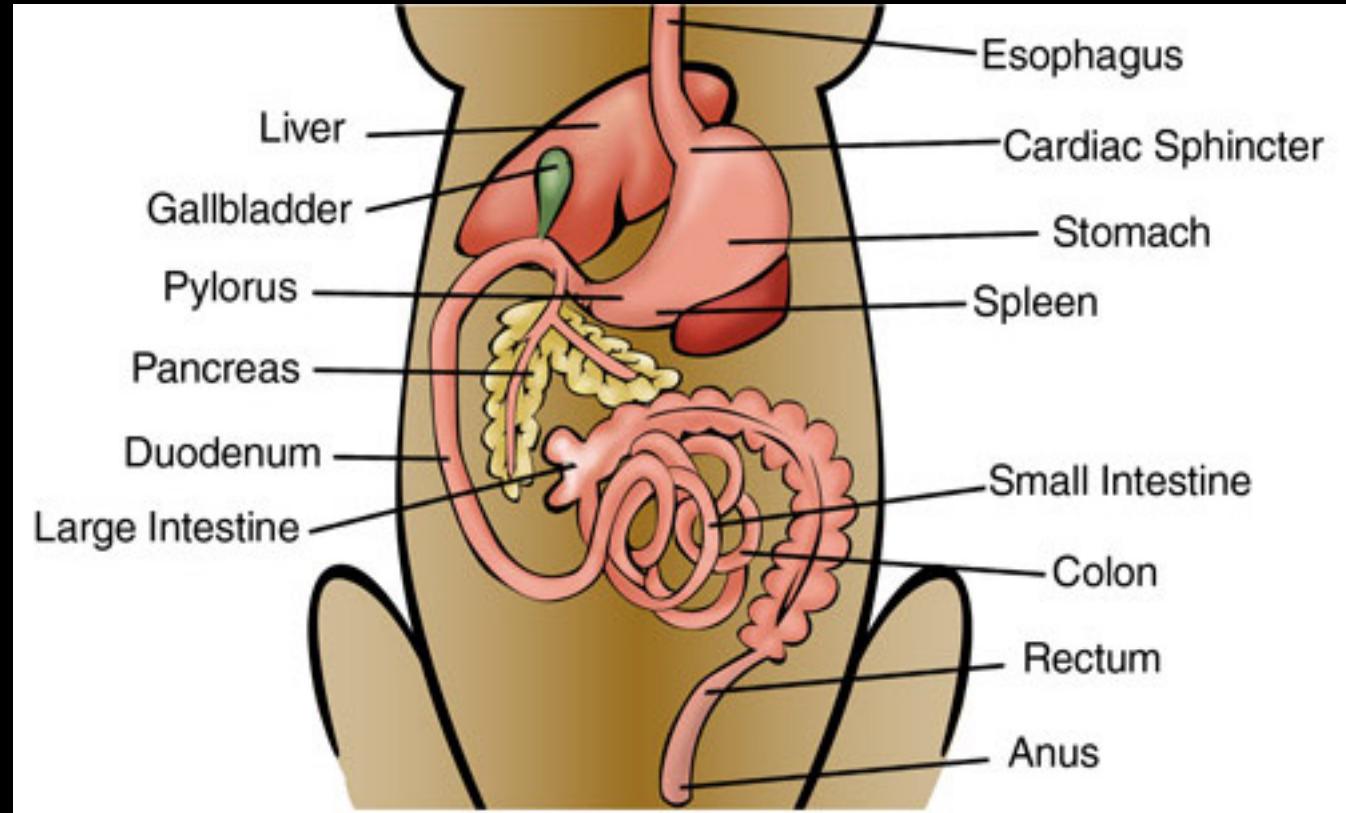


Central Mechanical Engineering Research Institute

Intern in Thermal Engineering – Delignification strategies
for complex biomass

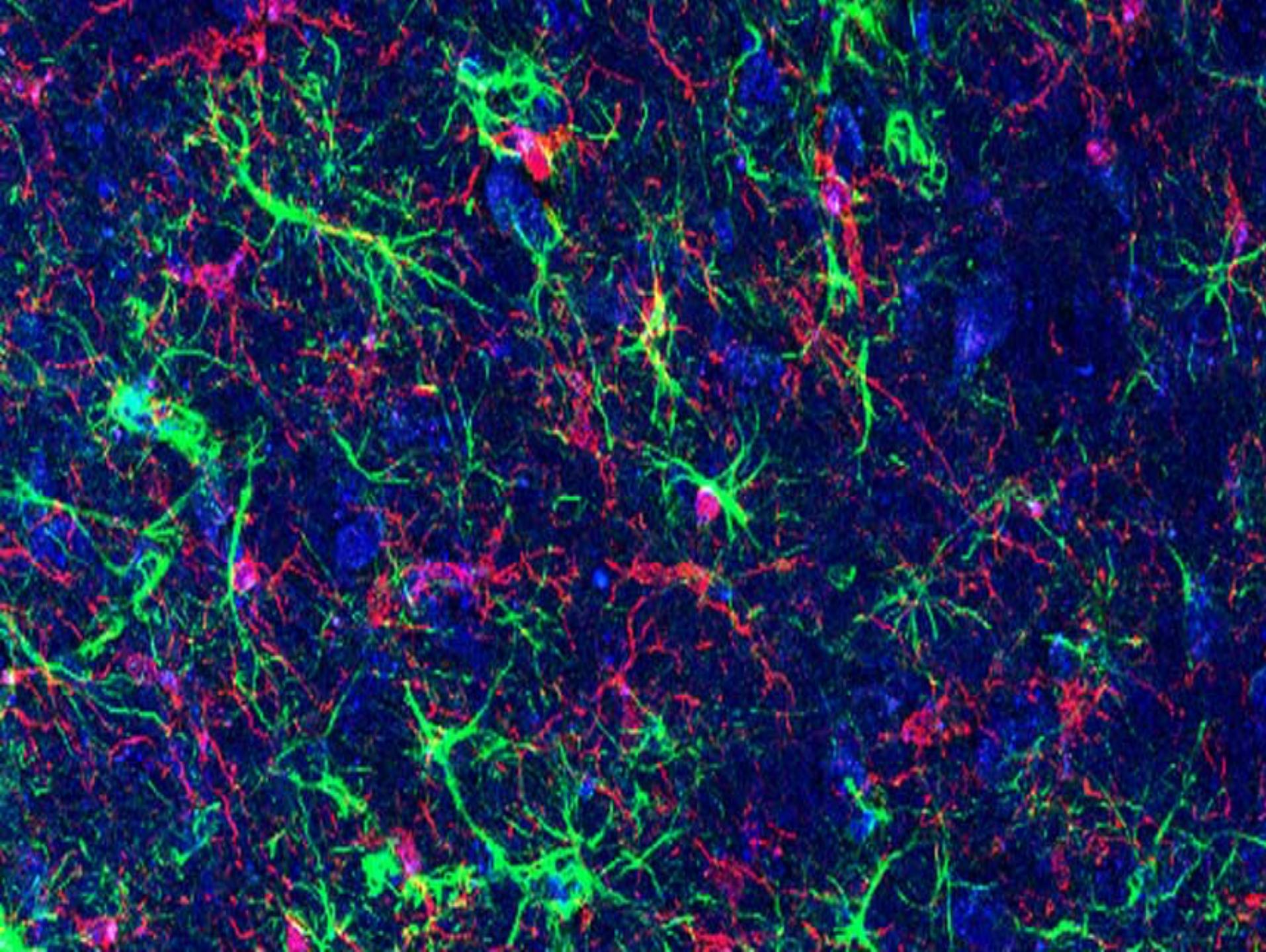


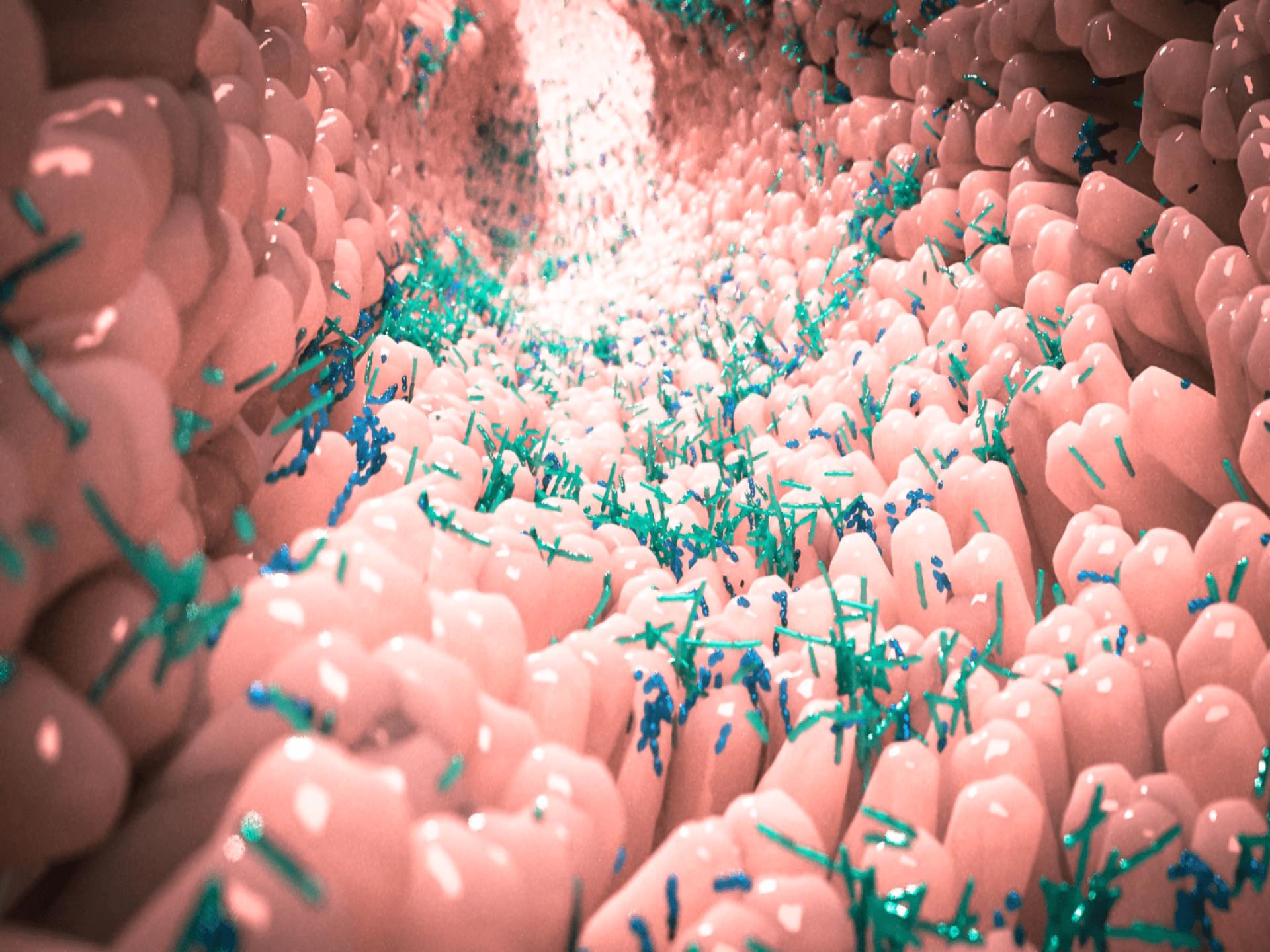
Gut as a bio-reactor



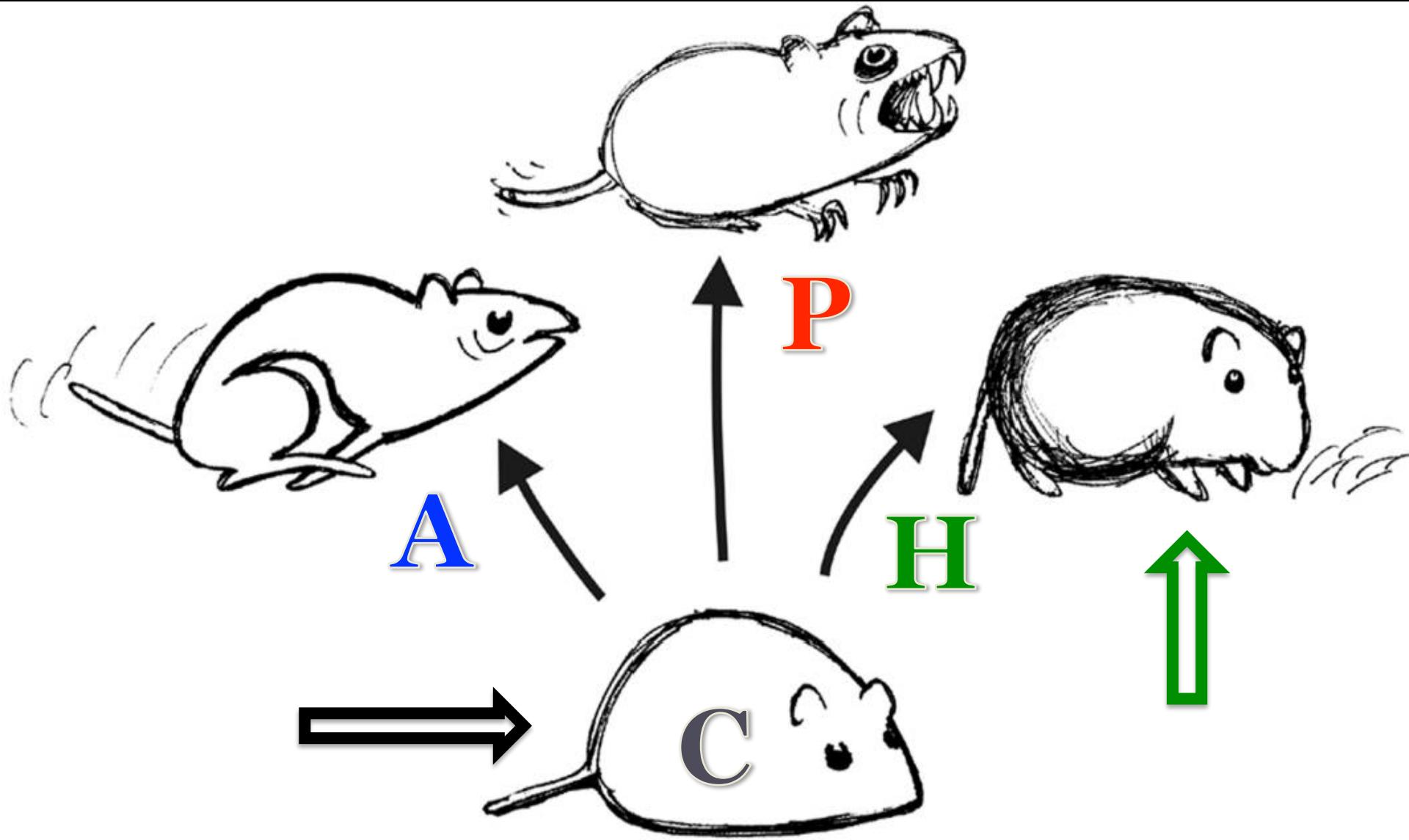








Adaptive Radiation model

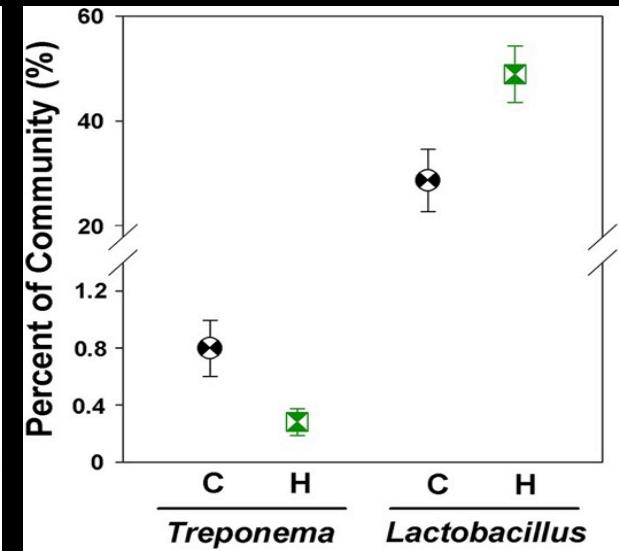
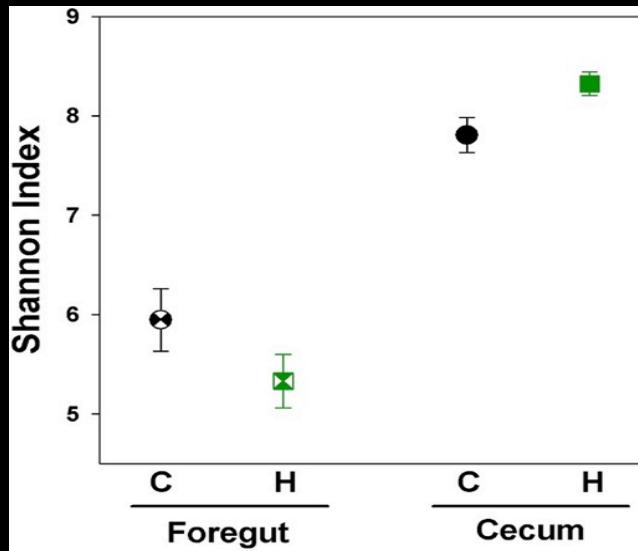
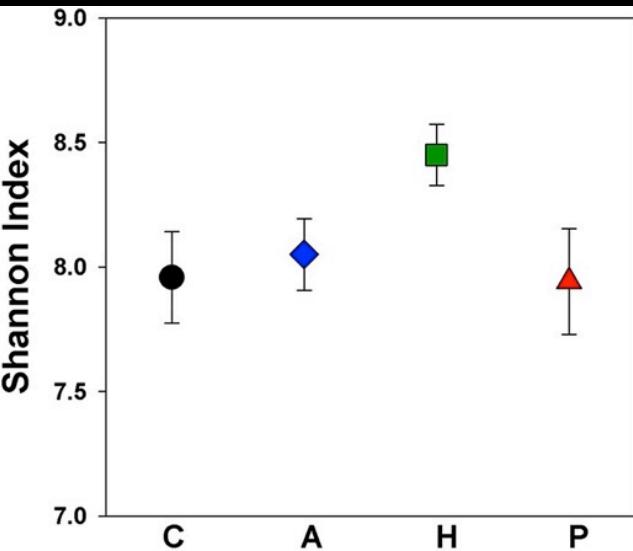


Background

- How does Herbivores digest complex fibre?
- What complex mechanism makes them develop the ability of enhanced digestibility?
- Do they have relatively more abundant fibre digesting gut -microbiota?
- How is this symbiotic relation maintained - from the point of host-microbe interaction?

Previous studies

- H lines are born fibre digesters
- Cecum is a natural fermentation tank
- Lactobacillus populates the H-Line gut



Objectives

- Community structure of microbes in gut sections
- Diversity within bacterial community
- Mean relative abundance of gut-microbes across gut-sections
- Obtain significant microbial genus on gut-sections

Predictions

- There will be less differences in microbial community within sections
- Dramatic differences between sections foregut and cecum
- Fiber digesting bacterial genus will be more in cecum

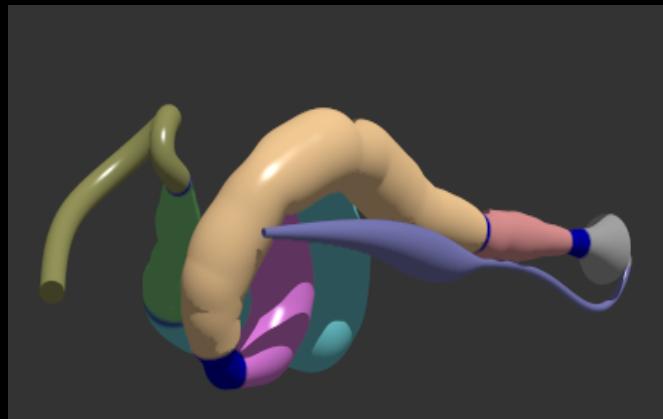
Methods in Microbial culture

- ✓ Classical
 - ✓ Microbial Plating
 - ✓ Microscopy and staining techniques
 - ✓ Shot-gun sequencing
- ✓ Next Generation Sequencing
 - ✓ Genetic marker followed by sequencing



16 Animals

Foregut



2 Sub-sections

Cecum



3 Sub-sections

Methodology

- Sample Collection
- 16s Ribosomal RNA Sequencing

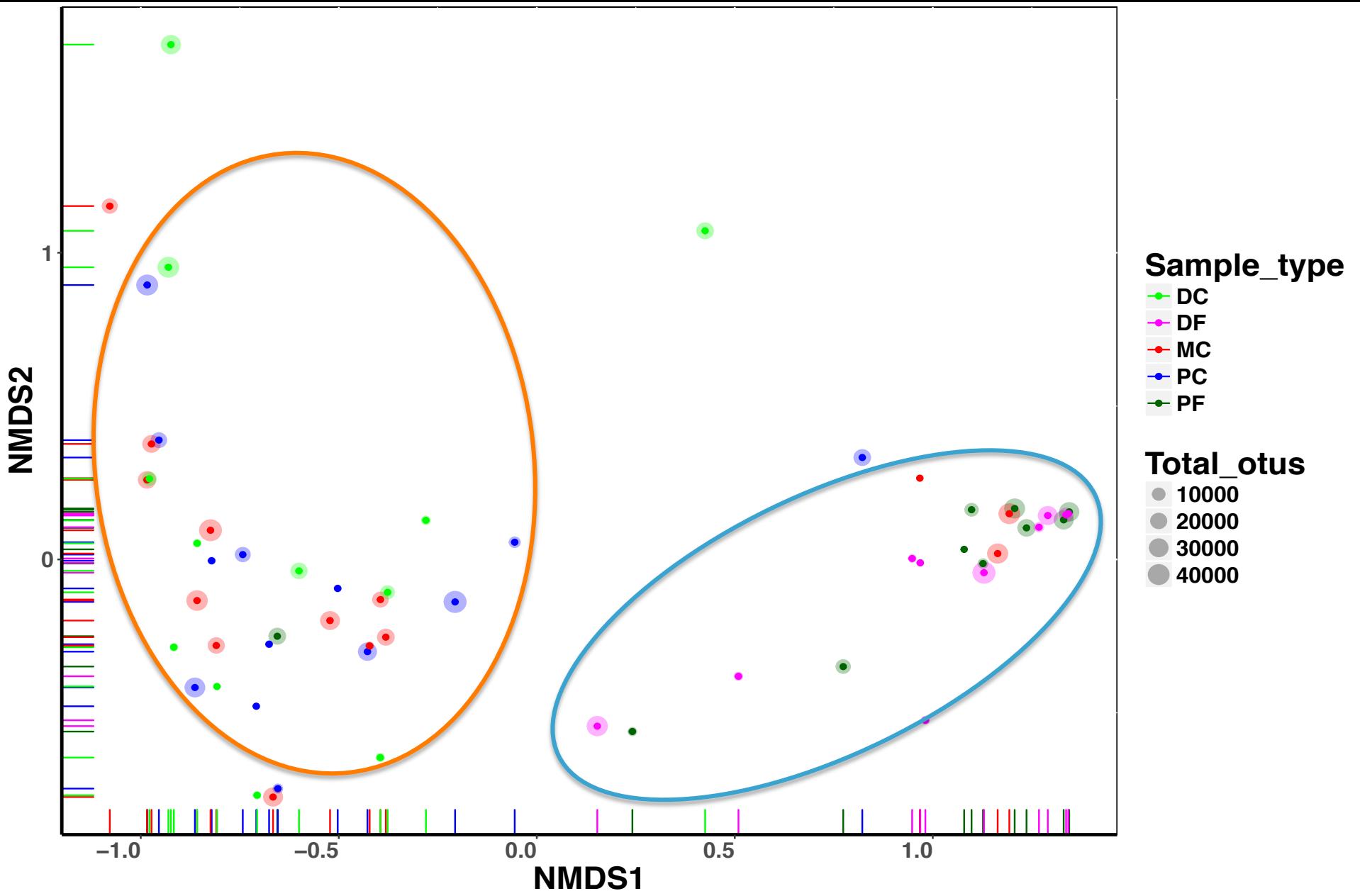


DC - Distal Cecum
DF - Distal Foregut
MC - Mid Cecum
PC - Proximal Cecum
PF - Proximal Foregut

Community structure

- Bray Curtis and Weighted UniFrac Distances
- NMDS (Non-metric Multi-Dimensional Scaling)

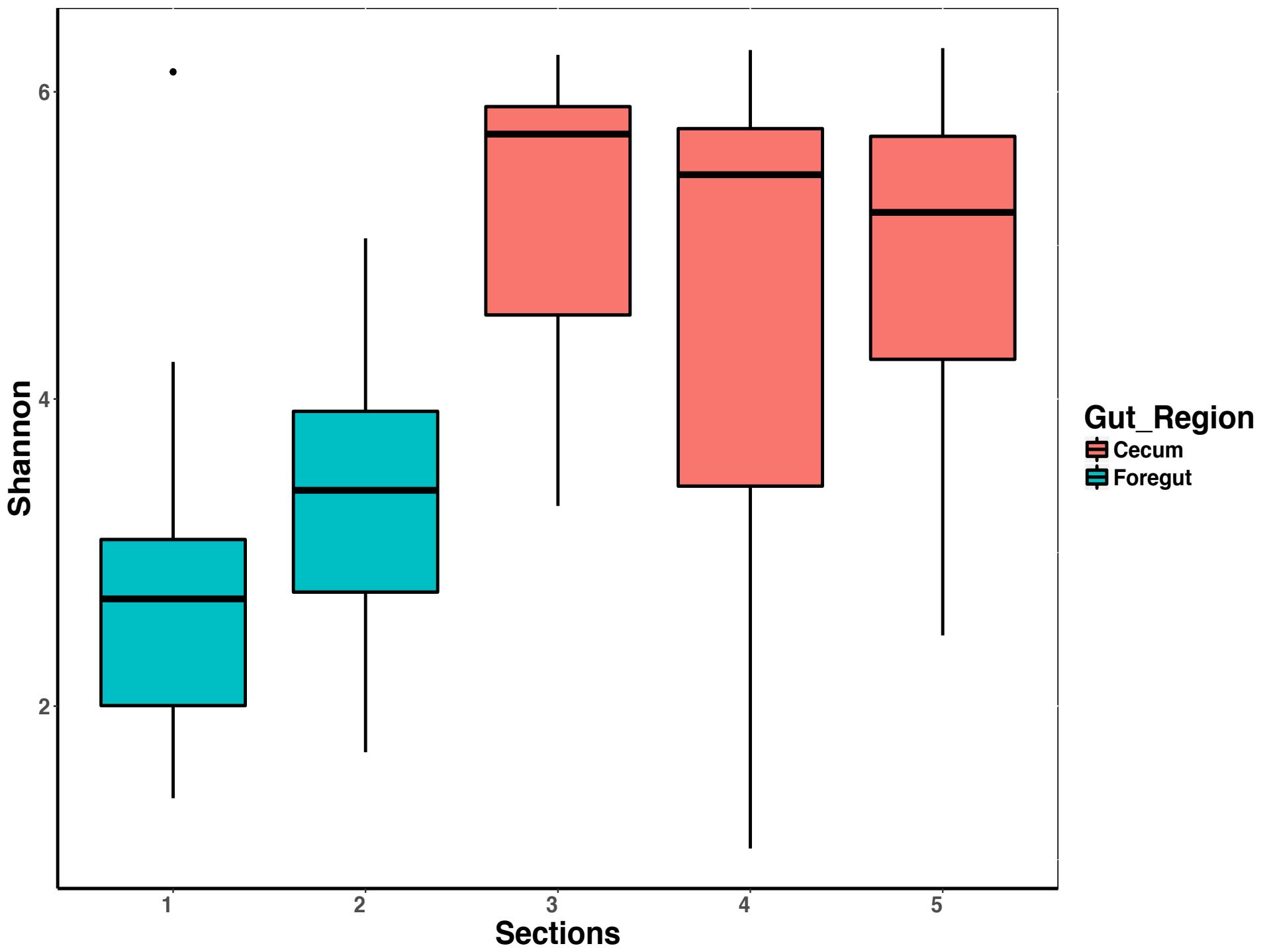
Community structure



Diversity within sections

➤ Pairwise wilcoxon test

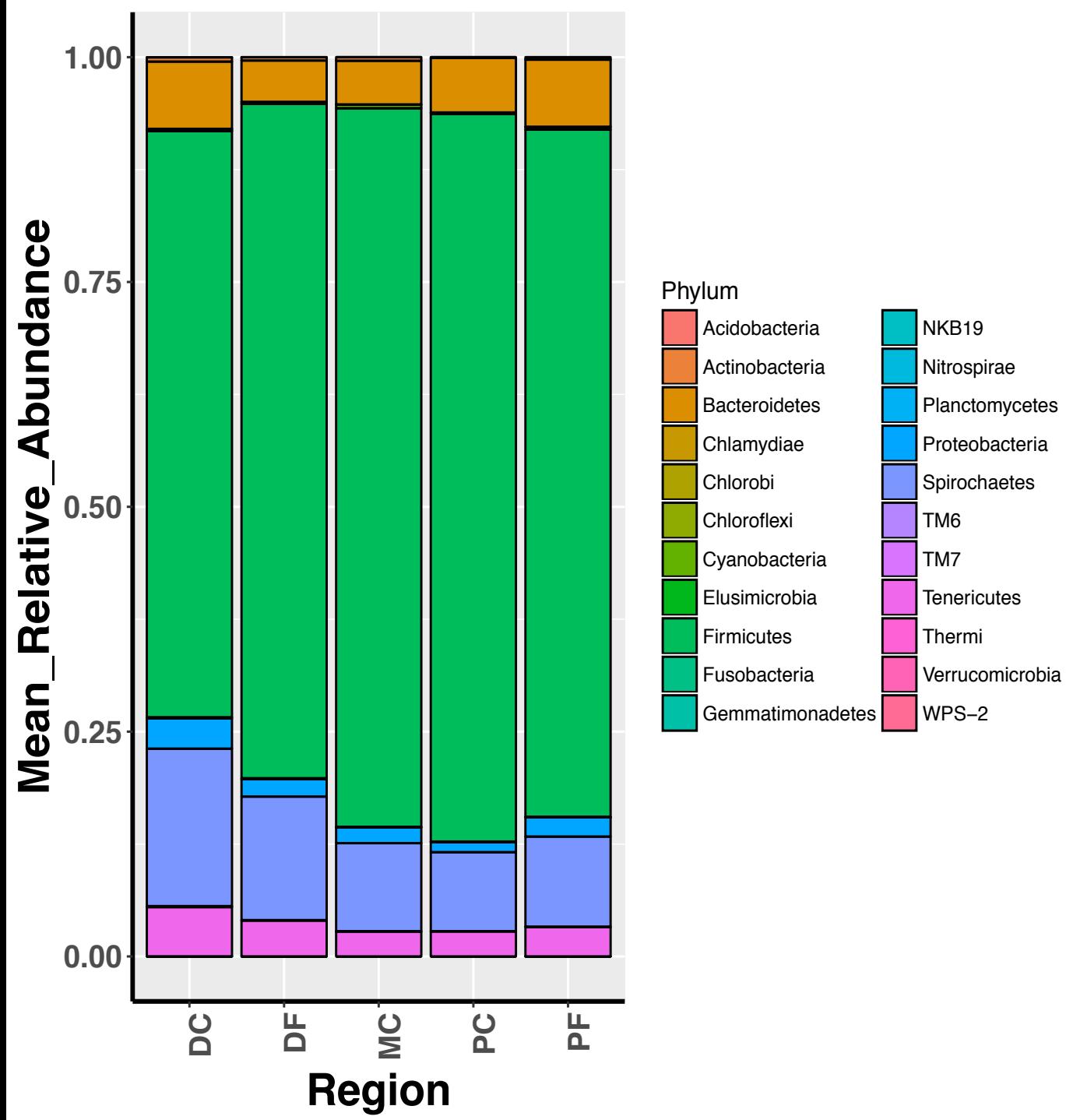
- Within foregut - Not Significant ($p > 0.05$)
- Within Cecum - Not Significant ($p > 0.05$)
- Between Foregut and Cecum - Significant ($p < 0.05$)

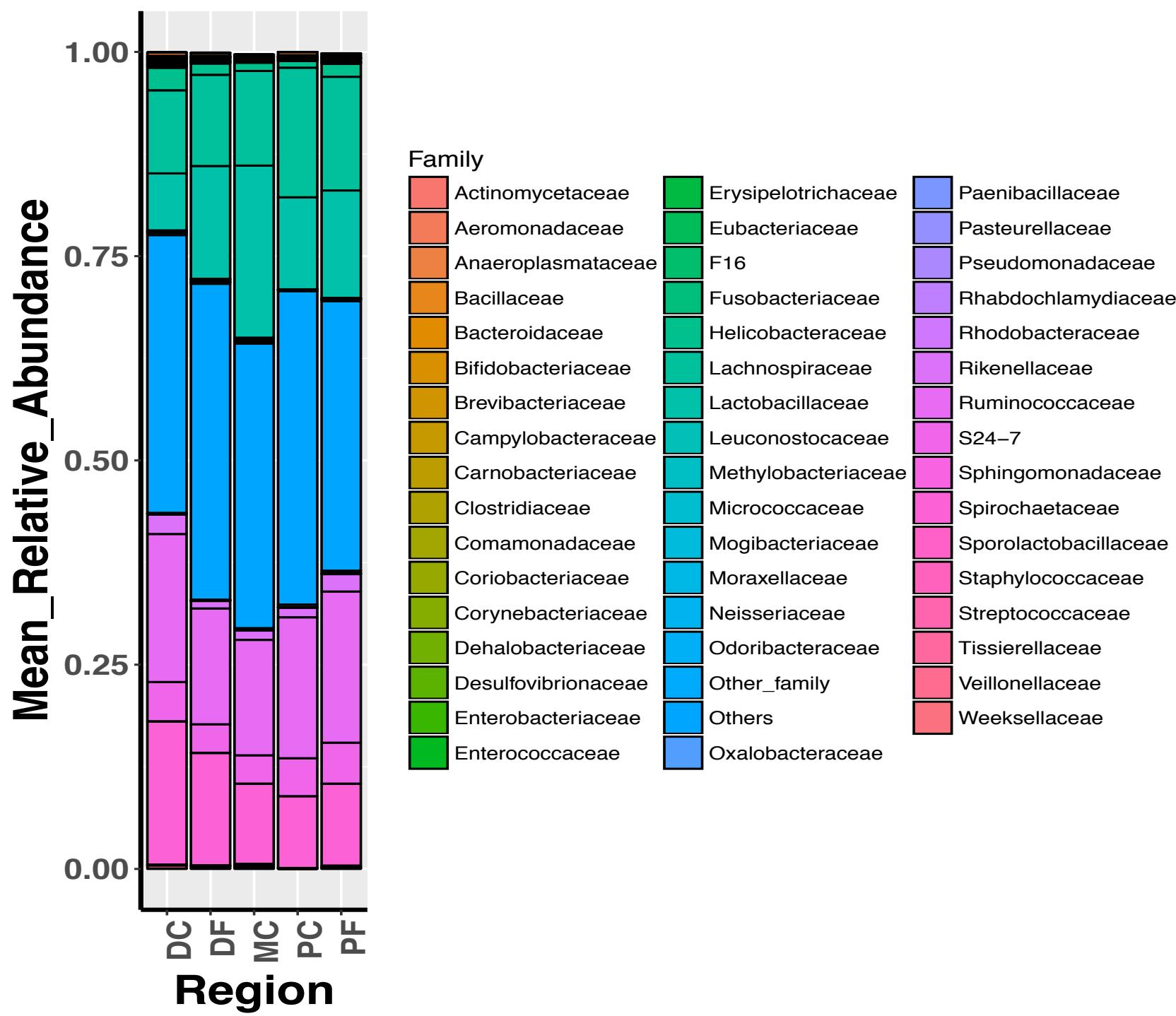


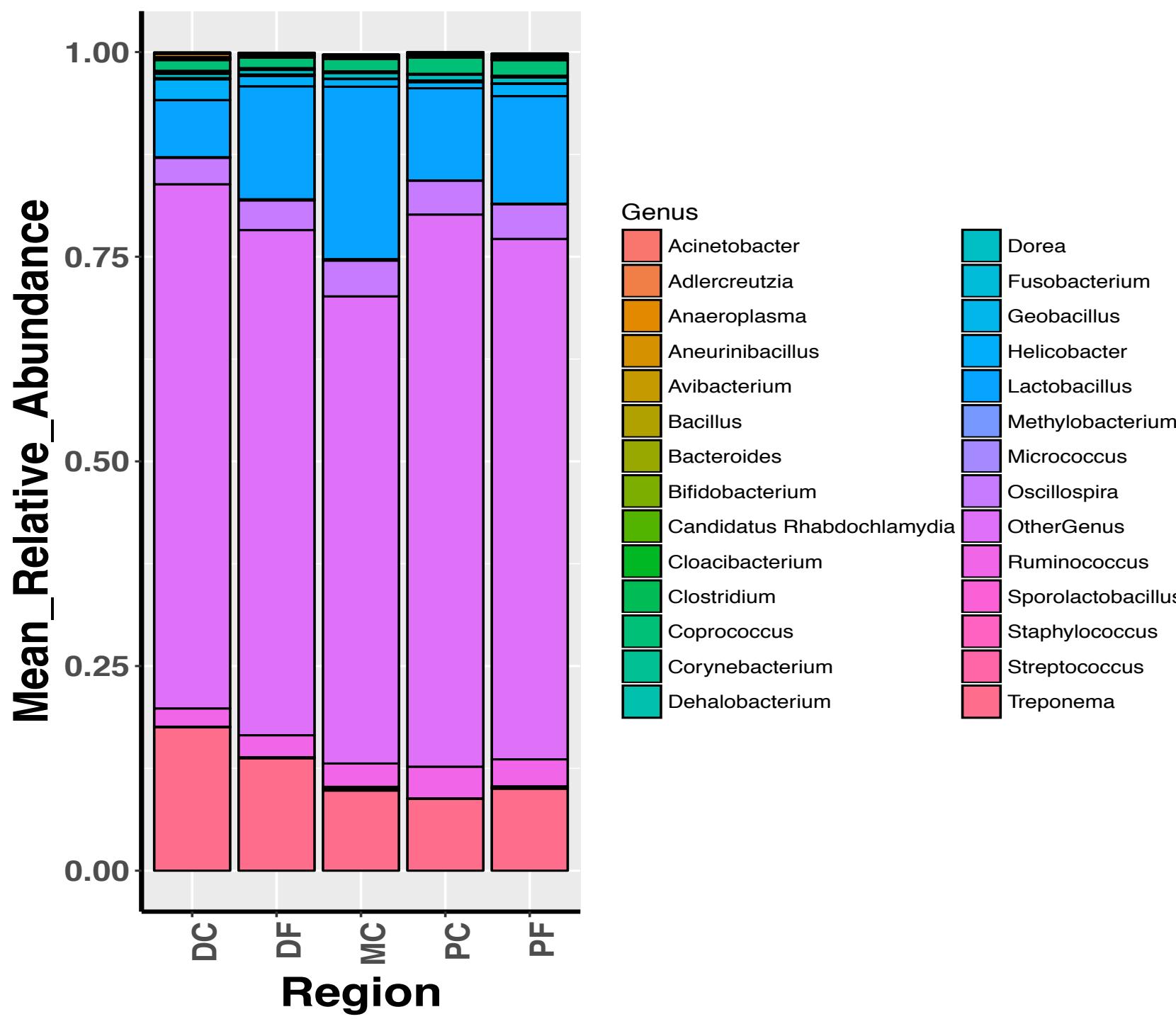
Abundance of microbes

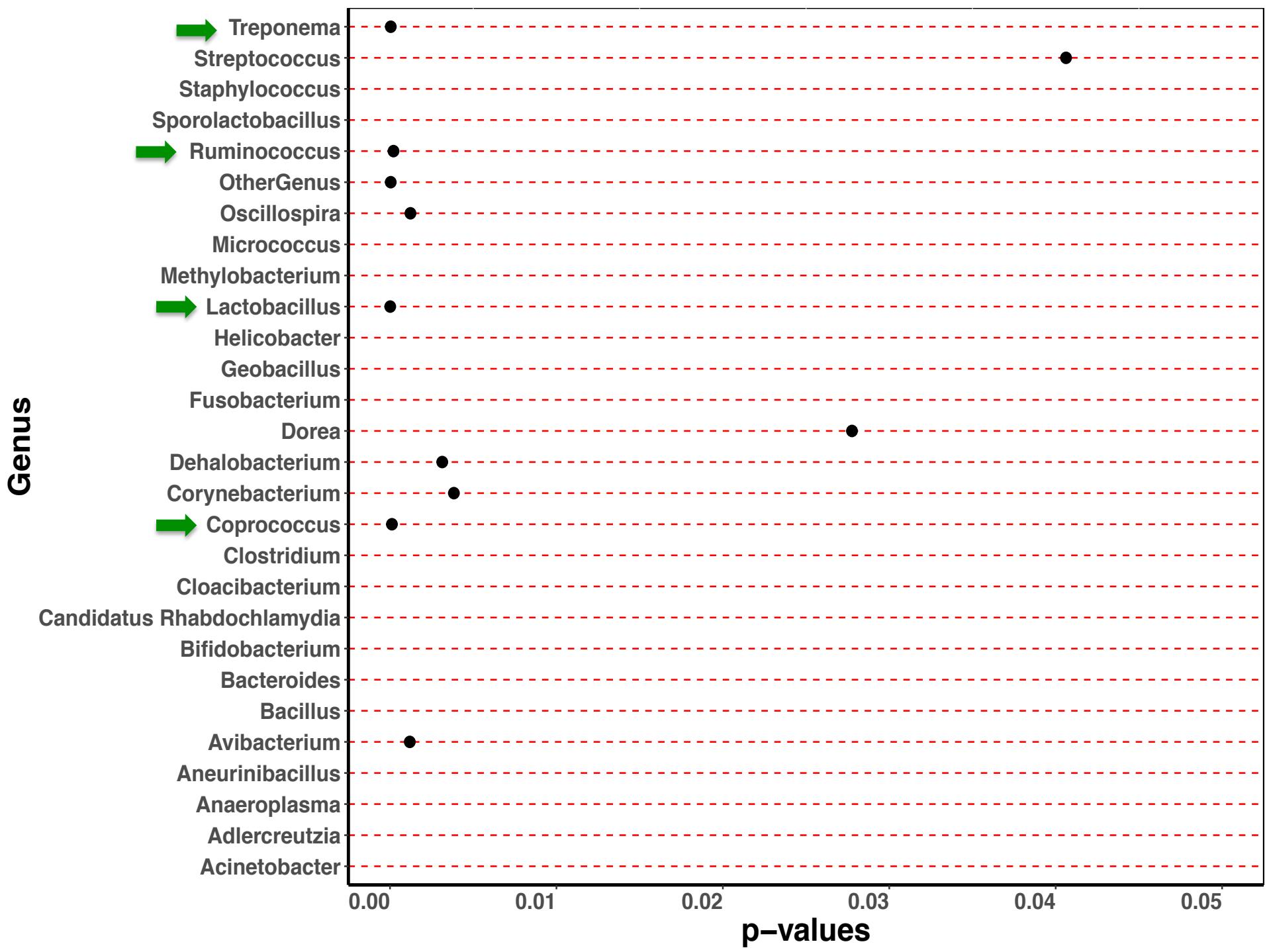
- Mean relative abundance compared across sections of gut
- Kruskal Wallis Test
 - Distribution was not normal

DC - Distal Cecum
DF - Distal Foregut
MC - Mid Cecum
PC - Proximal Cecum
PF - Proximal Foregut

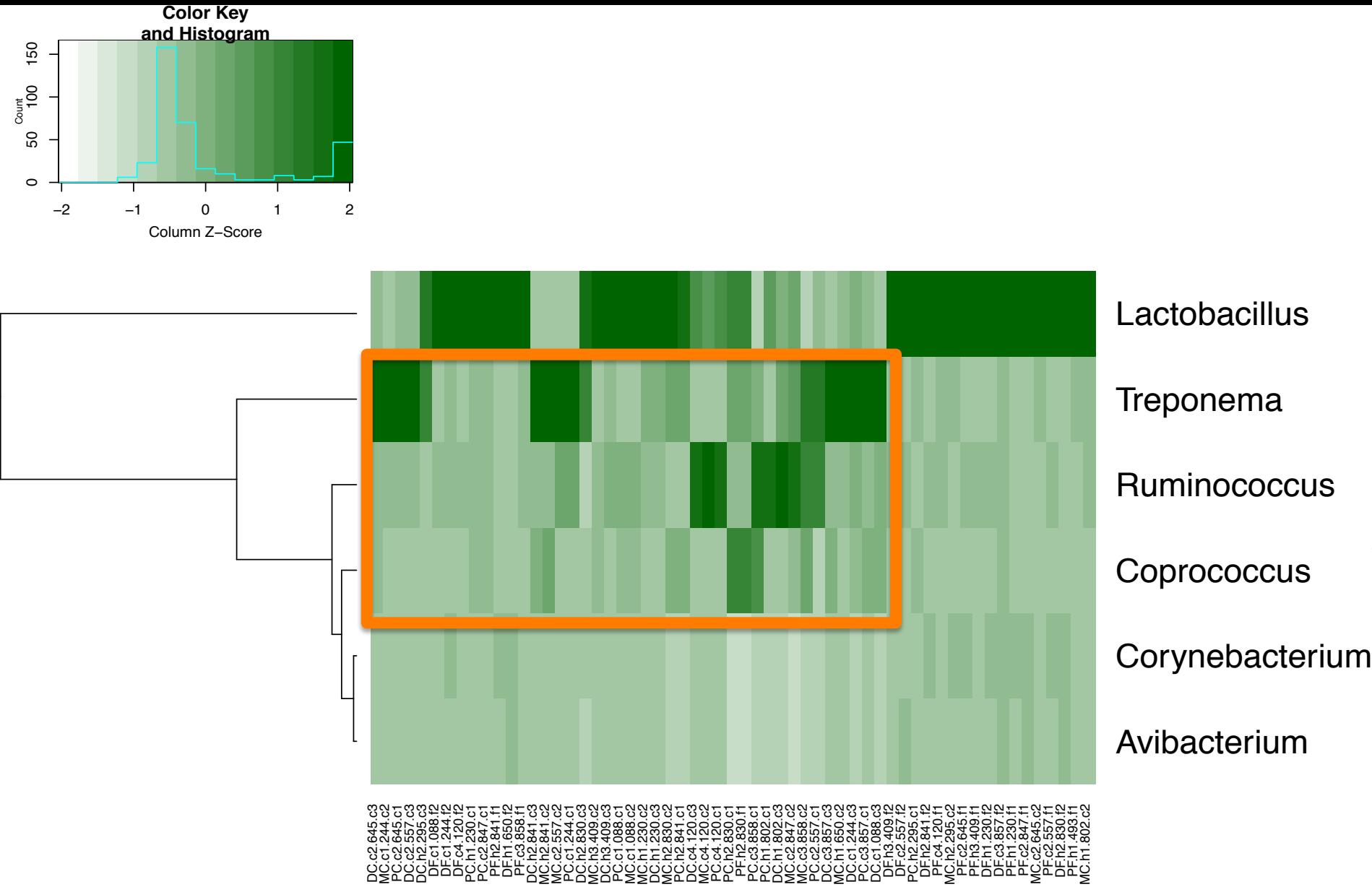








Heatmap



Ruminococcus

Relative Abundance

0.100

0.075

0.050

0.025

0.000

1

2

Sections

Gut_Region

- Cecum
- Foregut



Treponema

Relative Abundance

0.6

0.4

0.2

0.0

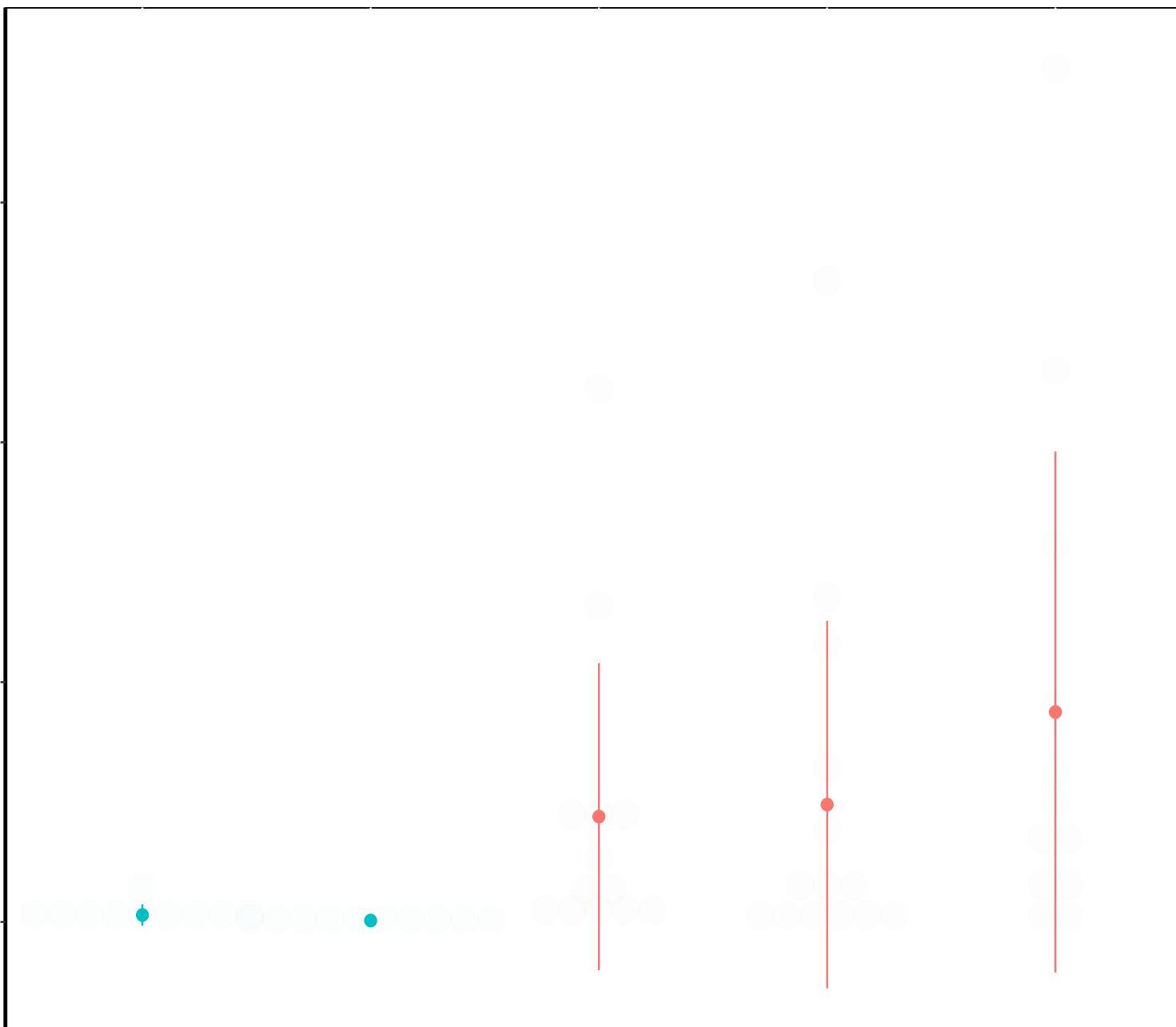
1

2

Sections

Gut_Region

- Cecum
- Foregut



Coprococcus

Relative Abundance

0.08

0.06

0.04

0.02

0.00

1

2

Sections

Gut_Region

- Cecum
- Foregut



Further research

- How bacterial community in the gut shapes a physiological trait in a complex organism?
 - Enhanced digestibility in herbivore
 - Gut-microbes ~ Liver + Brain + Pancreas + Immunity + ...
- How the host-organism selectively cultures efficient microbes in gut?
 - Is it genetic or environmental influx?
 - How the concept of HOLOBIONT (host-microbe interaction) significantly develop the trait of “Herbivore”

Conclusion

- Micro-organisms are dispersed across our gut
- Environment of specific region of host organism shape specific microbial community
- Specific microbes play important role in fiber digestion.

Find the presentation and documents on
https://github.com/arpankbasak/ZFE_UJ

Thank you for your attention!

