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# Contrasting Spatial Patterns and Ecological Attributes of Soil Bacterial Taxa across French National Territory



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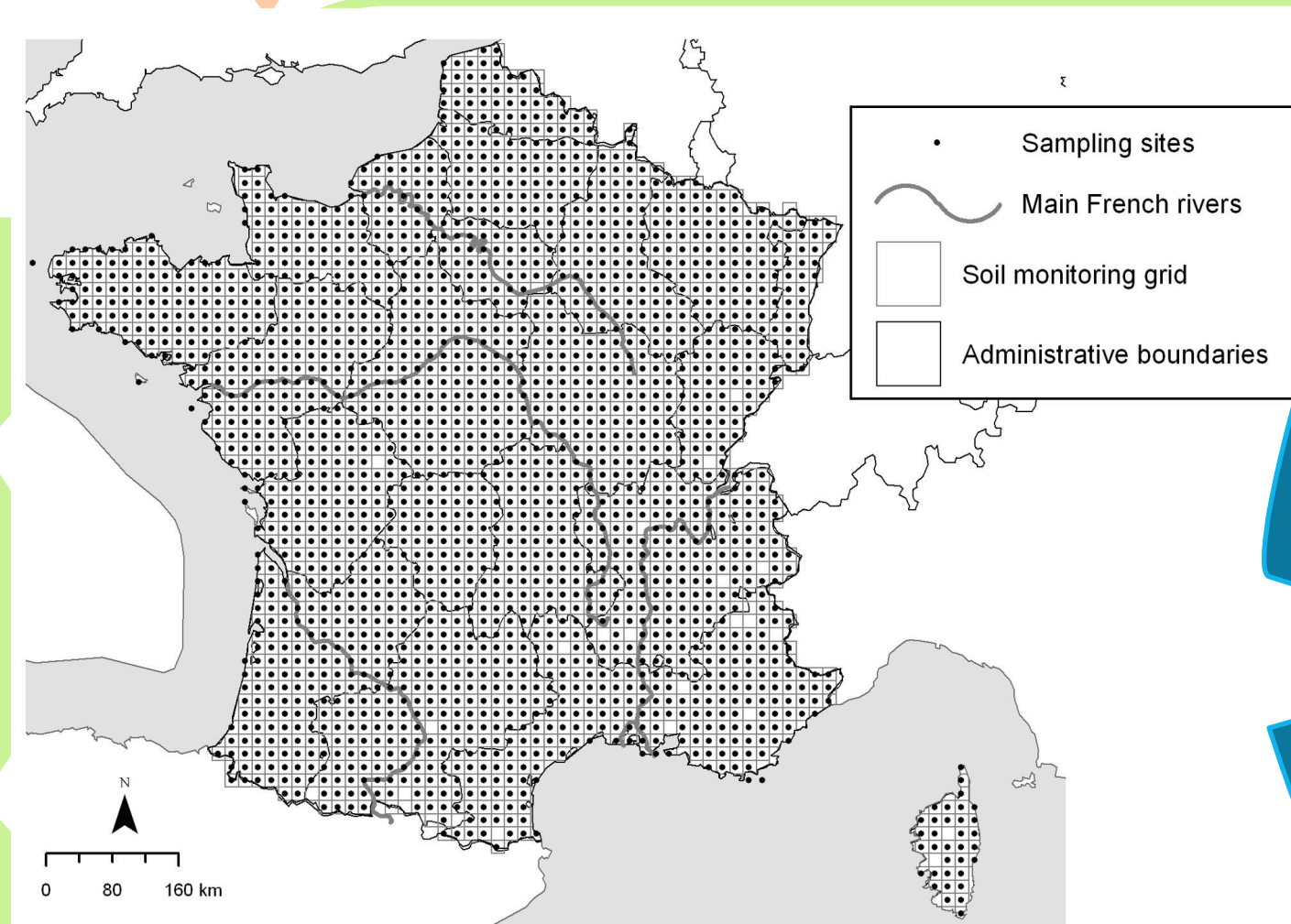
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Although soil bacteria have a key role in ecosystem services and are the most abundant organisms on Earth, the ecological processes and filters regulating their distribution at large scale remain poorly understood. Recent studies have clarified the influence of environmental filters on bacterial community diversity and concluded that soil pH, texture and C are the main drivers selecting an higher diversity. However, the filters constraining bacterial populations variations remain unclear. In consequence, our ability to understand the ecological attributes of soil bacteria and to predict microbial community response to environmental stress is therefore limited.

Based on the framework of the French Soil Quality Monitoring Network (RMQS, Réseau de Mesure de la Qualité des Sols), the objectives were to:

- Identify the bacterial and archaeal community composition at the scale of French National Territory
- Determine the spatial patterns of the main phyla at a large scale
- Rank the ecological processes and environmental filters most influencing the distribution of these phyla.



**RMQS = French Soil Quality Monitoring Network**  
16 km regular grid across the 550 000 km<sup>2</sup> territory  
2137 monitoring sites

### Environment characterization

- Climatic factors
- Spatial location
- Land management
- Soil physico-chemical properties

### Microbial community characterization

Pyrosequencing approach targeting 16S rRNA genes  
GnS-PIPE processing and taxonomic assignment

### Descriptive Statistics

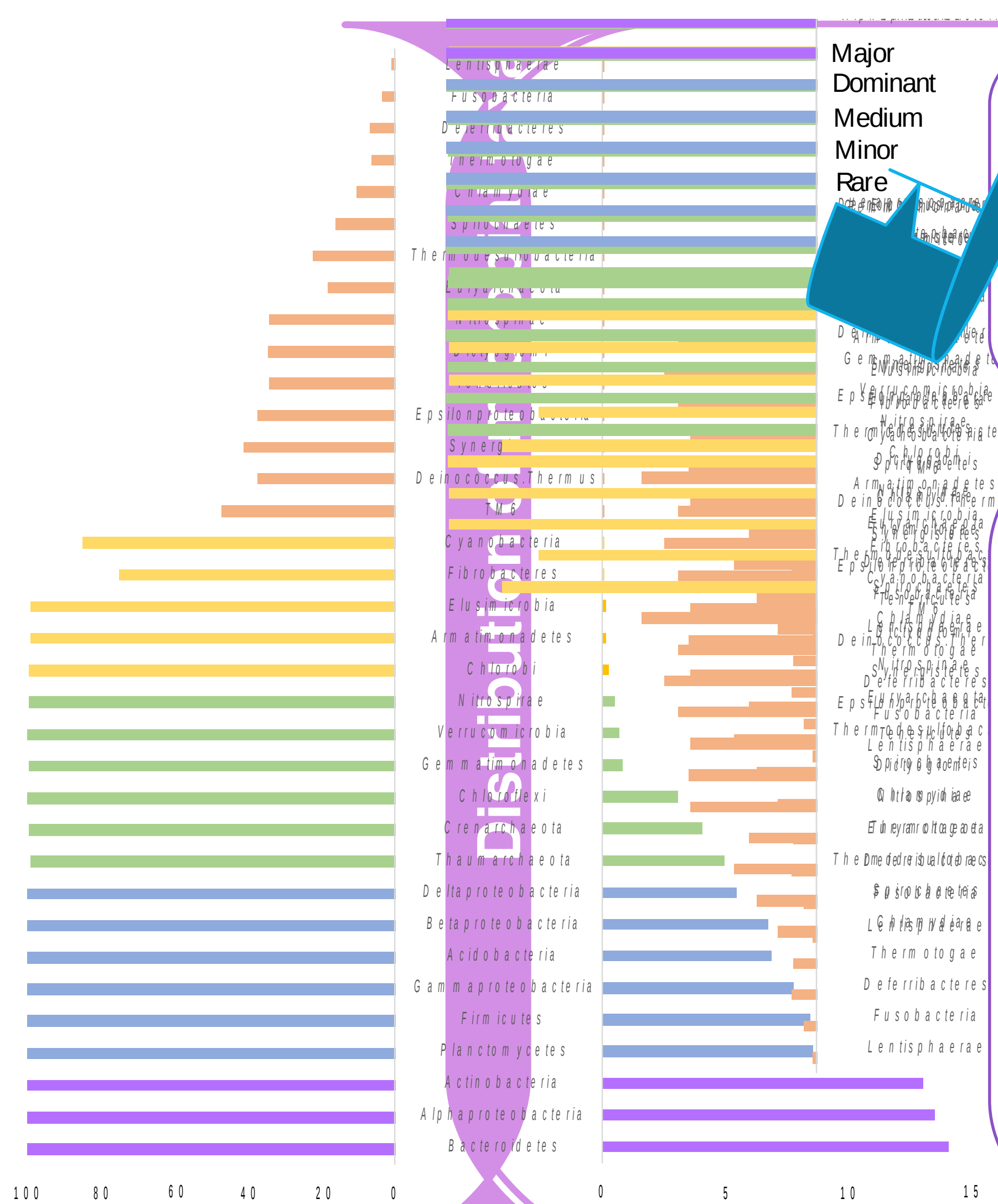
Occurrence  
Average relative abundance

### Geostatistical approach

Kriging and Mapping

### Variance partitioning

Ranking ecological processes  
Identifying environmental filters



### Descriptive Statistics

18 cosmopolitan phyla (in all sampling sites)  
15 rare phyla (<50% of sites)

12 phyla represented each more than 3% of

### Mapping

4 spatial patterns with different patch size (radius)

- Fine (~50km)

*Chloroflexi, Fibrobacteres,*

*Cyanobacteria*

- Medium (~100km)

*Bacteroidetes, Alphaproteobacteria,*

*Acidobacteria, Deltaproteobacteria,*

*Thaumarchaeota, Crenarchaeota*

- Coarse (~200km)

*Planctomycetes, Gemmatimonadetes,*

*Verrucomicrobia, Armatimonadetes*

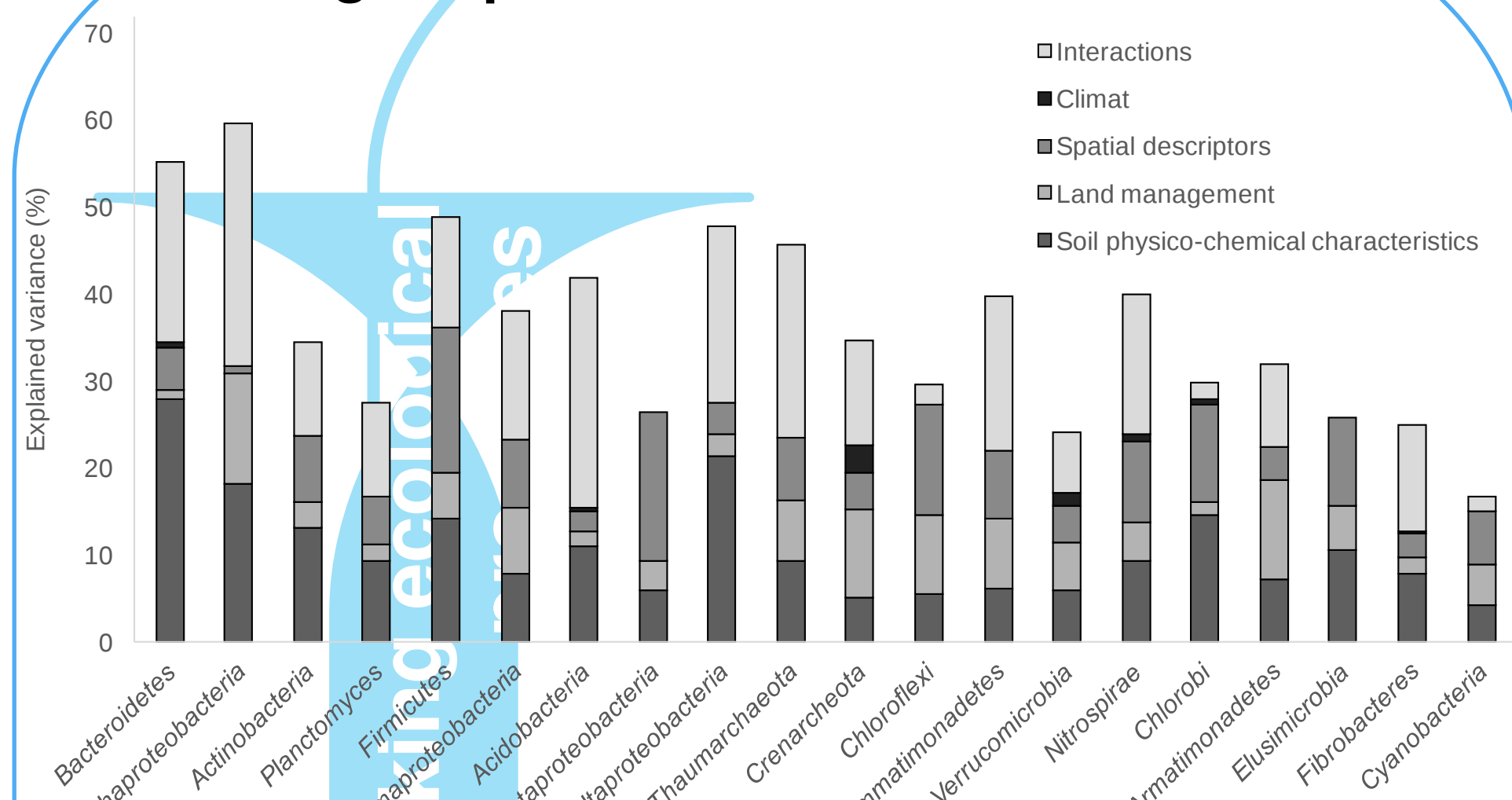
- Large (>200km)

*Actinobacteria, Firmicutes, Chlorobi,*

*Gammaproteobacteria, Nitrospirae,*

*Elusimicrobia*

### Ecological processes



Between 24% et 60% of total variance explained:

- Interactions □ 12.3 %
- Soil physico-chemical properties □ 10.7%
- Spatial descriptors □ 7.3%
- Land management □ 5.4 %
- Climatic factors □ 0.4 %

**Selection and dispersal limitation are the main drivers involved in the bacterial phyla determinism.**

### Contribution and effects of environmental filters

#### Soil physico-chemical properties

**pH and texture are the main filters**

#### Land management

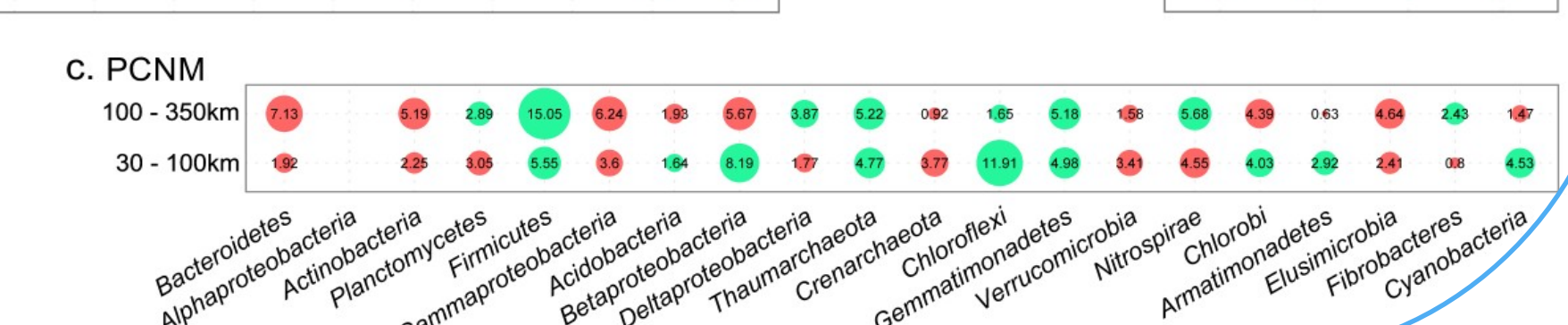
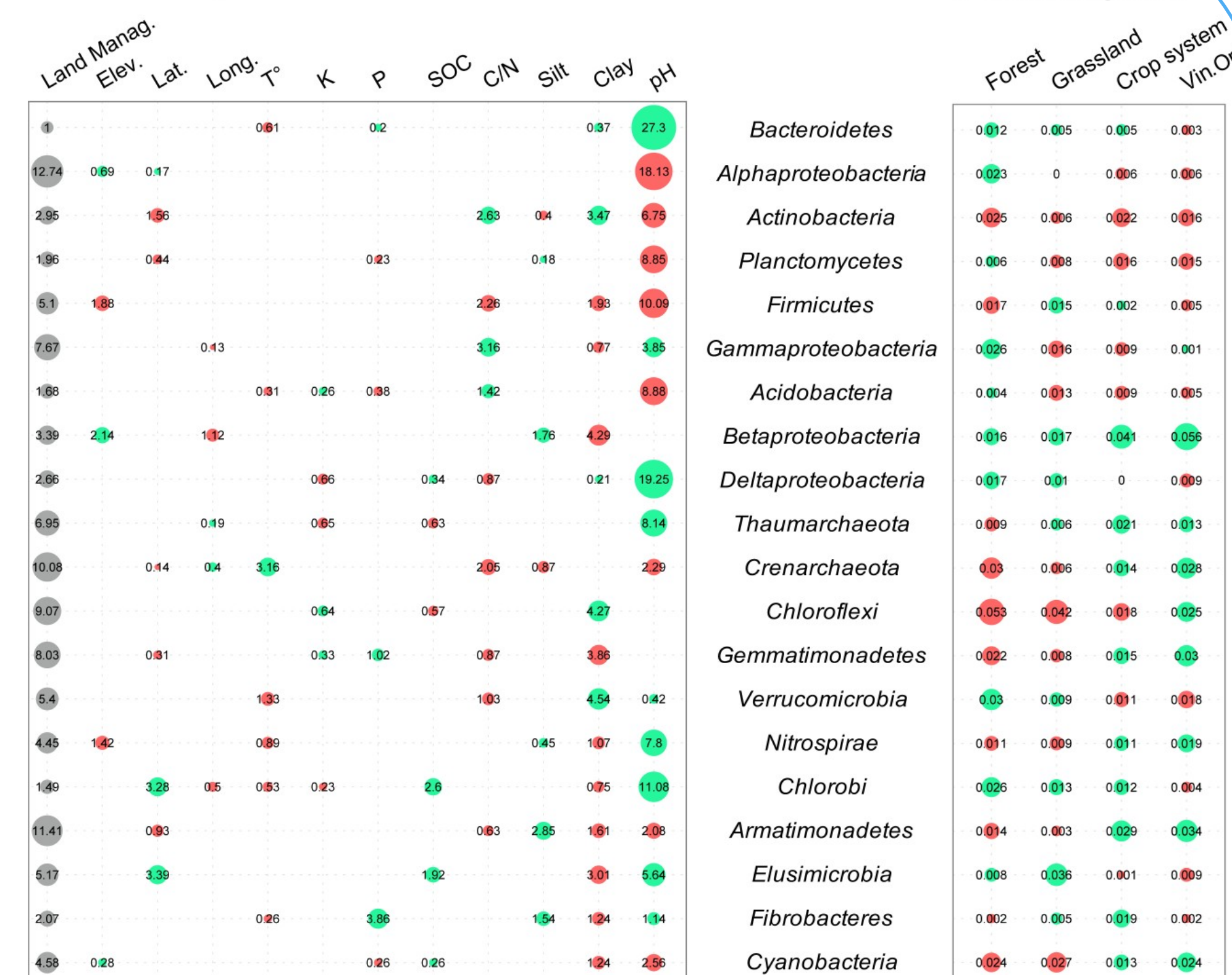
**3 different responses to the anthropization gradient**

- Positive relation *e.g. Betaproteob., Chloroflexi*
- No relation *e.g. Firmicutes, Fibrobacteres*
- Negative relation *e.g. Alphaproteob., Deltaproteob.*

#### Spatial descriptors

**Two scales of geographical filters**  
**Response depend on the phylum**

#### a. Environmental parameters



#### Anthropization gradient

