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## **MACADAM: A user-friendly MetAboliC pAthways DAtabase for complex Microbial community function Analysis**

Malo Le Boulch, Patrice Dehais, Sylvie Combes, Géraldine Pascal

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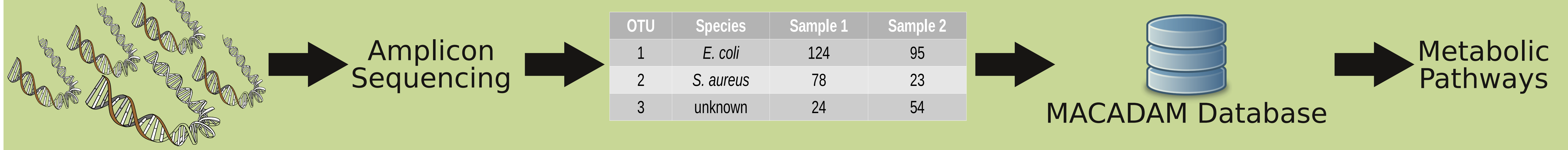
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# MACADAM: A user-friendly MetAboliC pAthways DAtabase for complex Microbial community function Analysis

Malo Le Boulch<sup>1</sup>, Patrice Dehais<sup>1</sup>, Sylvie Combes<sup>1</sup>, Geraldine Pascal<sup>1</sup>

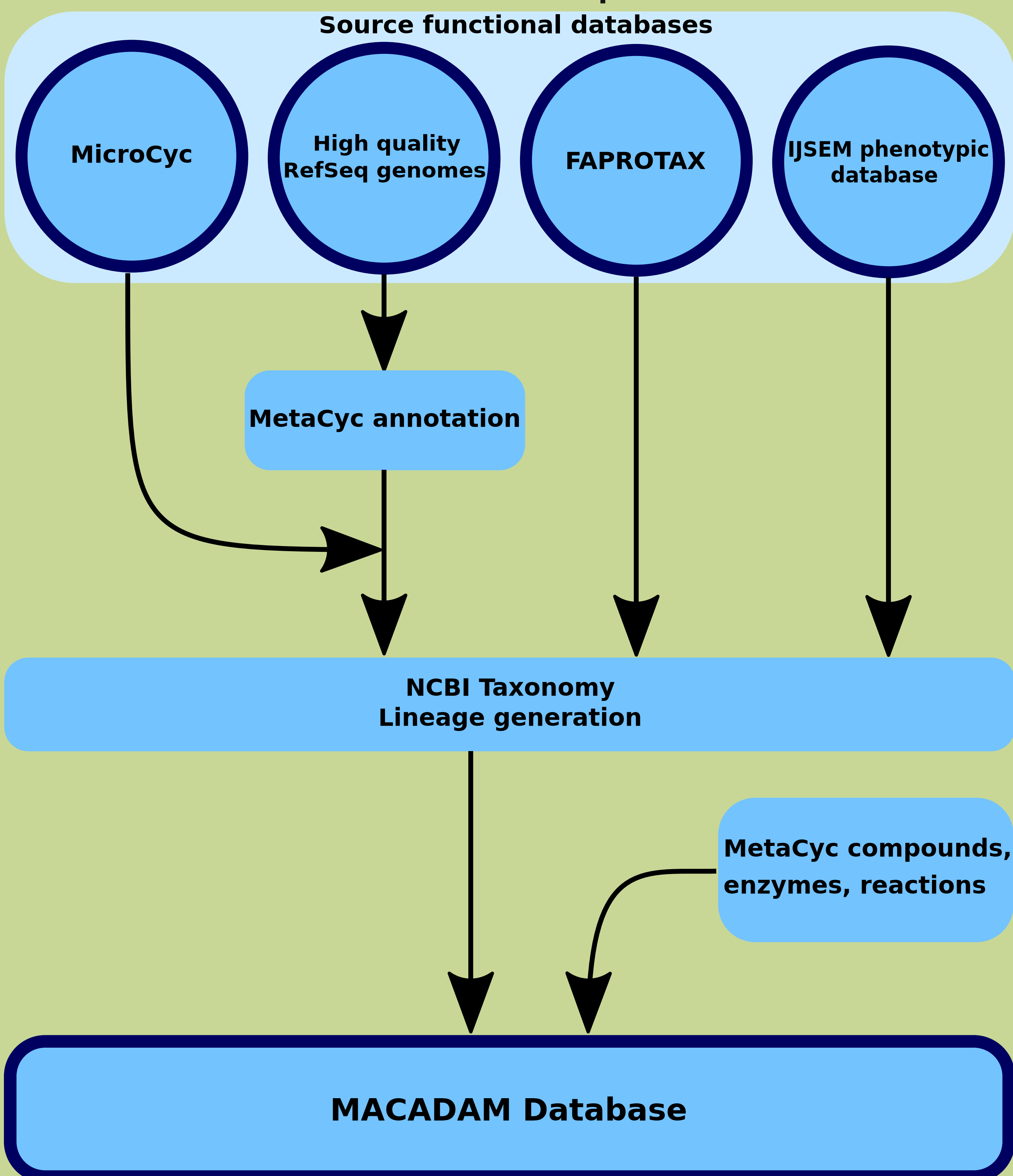
<sup>1</sup> GenPhySE, Université de Toulouse, INRA, ENVT, Castanet Tolosan, France

## How to access functional data from amplicon sequencing?



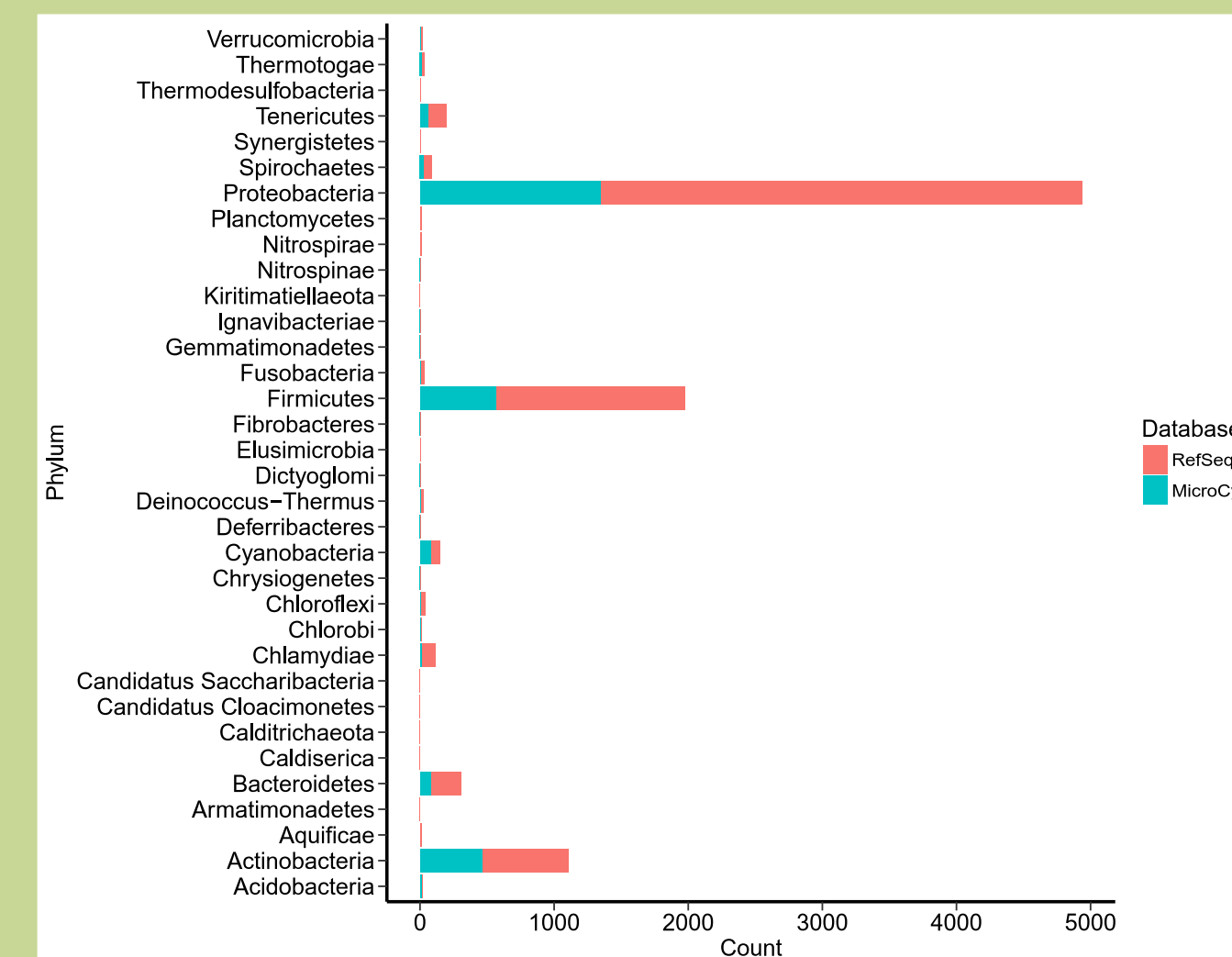
Our aim is to provide a **database** linking **taxonomic information** to **functional information**.  
**MACADAM Database** is designed to obtain functional information when only taxonomic information is available.

## Database composition



## MACADAM statistics

Unique species	8849
Unique pathways	1198
Unique functional annotations	98
Compounds	2313
Enzymes	7620
Average pathways per organism	182 [1-422]
Average pathway score	0.81

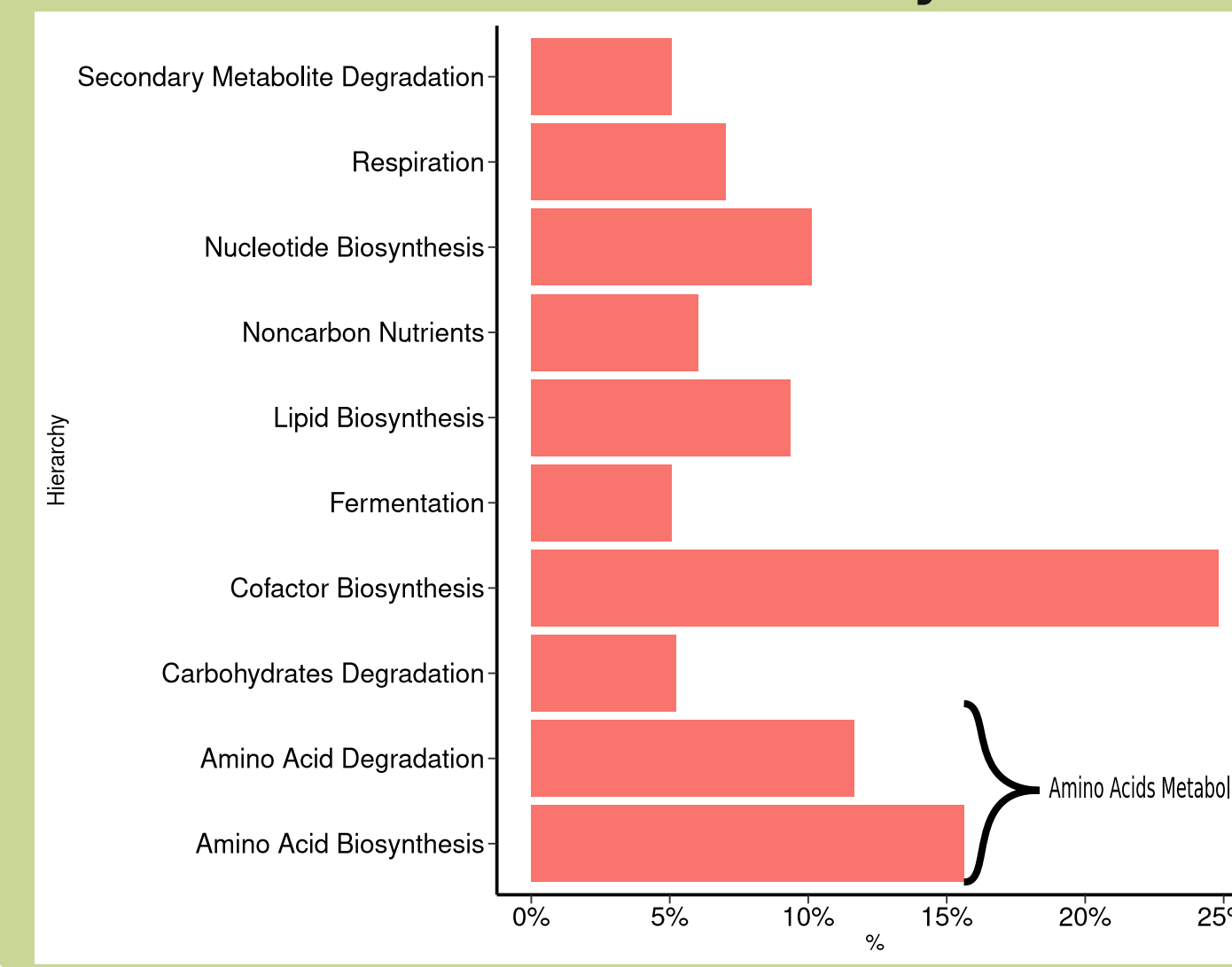


### MACADAM taxonomic diversity

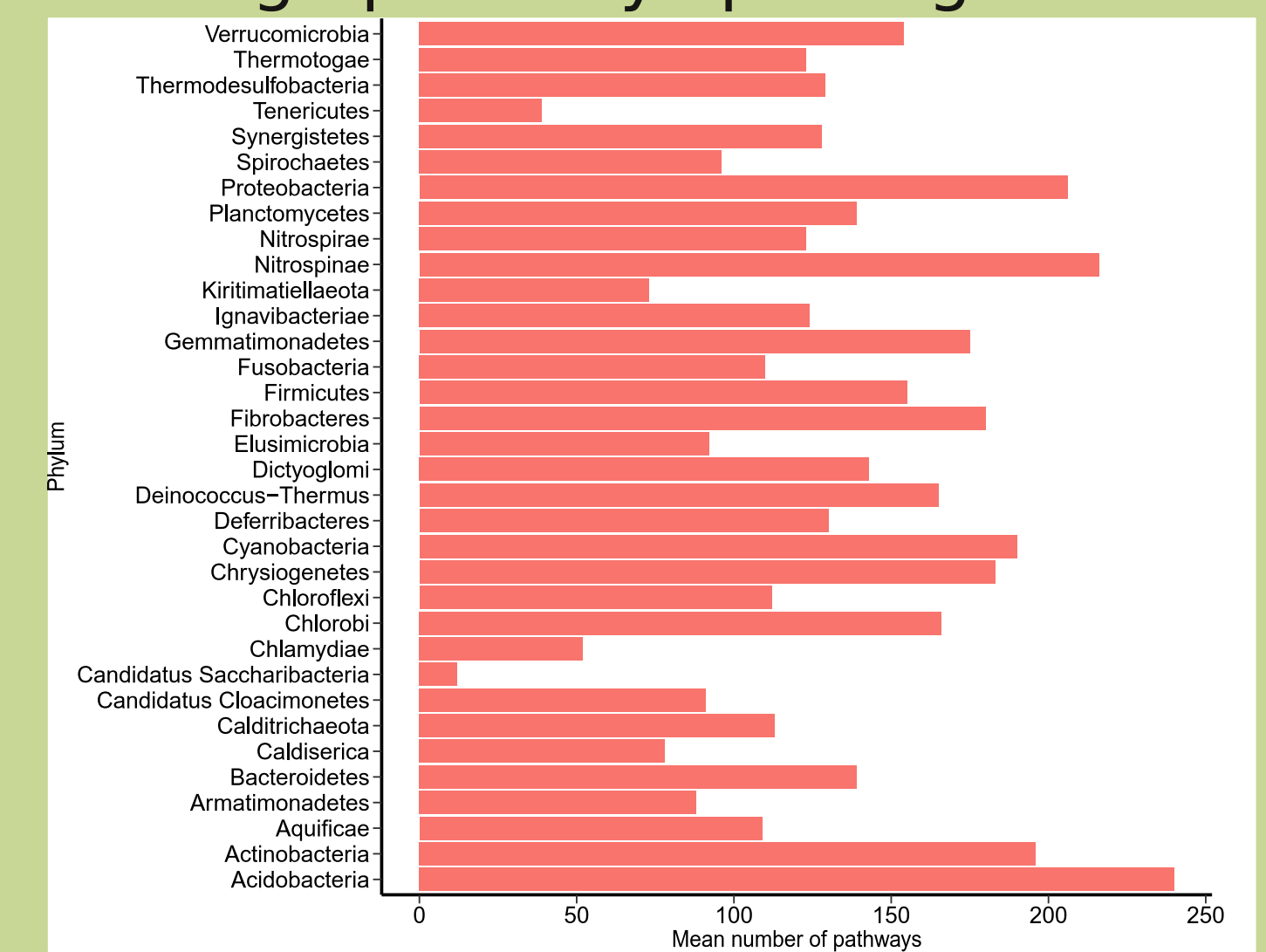
Presence of **34 different phyla**:  
All 29 LSPN phyla are present.  
The other 5 are recent proposals by the scientific community.

Overrepresentation of *Proteobacteria*,  
*Firmicutes* and *Actinobacteria*.

### Functional diversity



### Average pathways per organism



## Database characteristics

Databases	Strengths	Technologies
Functional: MetaCyc MicroCyc FAPROTAX IJSEM Pheno DB Taxonomic: NCBI Taxonomy	Interoperable Standardized taxonomy Unique completeness score Quality information Query by pathways, metabolites, enzymes and reactions	Python scripts SQLite Python CGI on Apache server

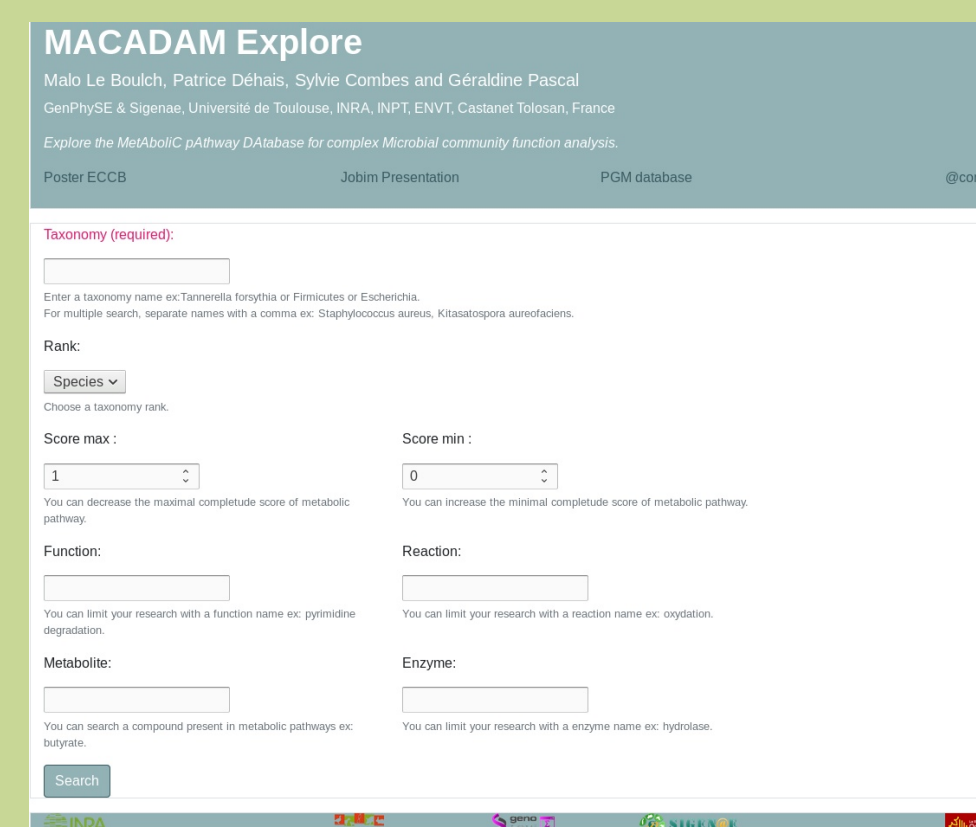
## Conclusions

MACADAM is a functional database combining information from multiple sources and linking them to taxonomical information.

A web interface (MACADAM Explore) is available for easy exploration.

This database is made to be used as part of a functional inference tool.

## MACADAM Explore



<http://macadam.toulouse.inra.fr/>



Results for a request on *Staphylococcus aureus* on urea pathways.

Pathway	Present in	Median of score	Median of frequency	Present in match
pyruvate fermentation to acetate VIII	45/215	1	2.33	Lactobacillus
pyruvate fermentation to butanoate	13/215	1	1	Lactobacillus
succinate fermentation to butanoate	13/215	0.12	0.12	Lactobacillus
mixed acid fermentation	8/215	0.5	0.75	Lactobacillus
heterolactic fermentation	8/215	0.89	1.5	Lactobacillus
pyruvate fermentation to lactate	14/215	1	2	Lactobacillus
pyruvate fermentation to propionate II	8/215	0.57	1.14	Lactobacillus
pyruvate fermentation to (R)-acetoin I	2/215	0.5	0.5	Lactobacillus
pyruvate fermentation to (R)-acetoin II	13/215	1	1	Lactobacillus
pyruvate fermentation to (S)-acetoin	33/215	0.67	0.87	Lactobacillus
pyruvate fermentation to acetoin III	2/215	0.5	0.5	Lactobacillus
pyruvate fermentation to acetone	28/215	0.2	0.2	Lactobacillus
pyruvate fermentation to ethanol I	5/215	1	1.5	Lactobacillus
pyruvate fermentation to ethanol II	28/215	1	1	Lactobacillus

MACADAM Explore is able to infer functional information for species with no functional information.  
Example for *Lactobacillus cerevisiae*.

