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

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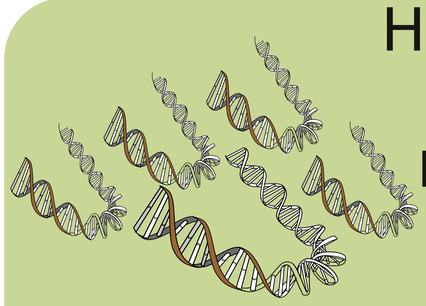
How to access functional data from amplicon sequencing?



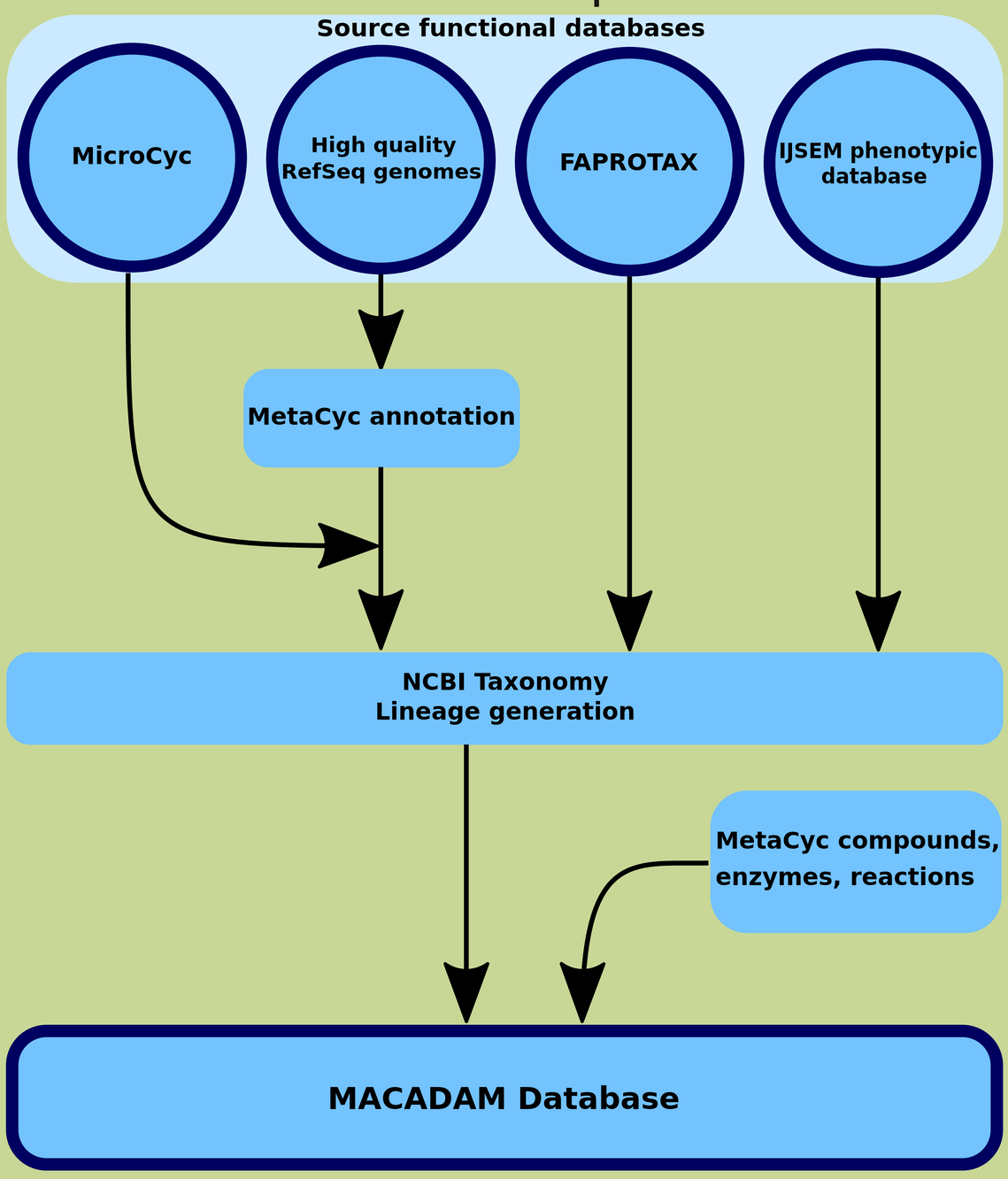
Amplicon Sequencing →

OTU	Species	Sample 1	Sample 2
1	*E. coli*	124	95
2	*S. aureus*	78	23
3	unknown	24	54

→ MACADAM Database → Metabolic Pathways

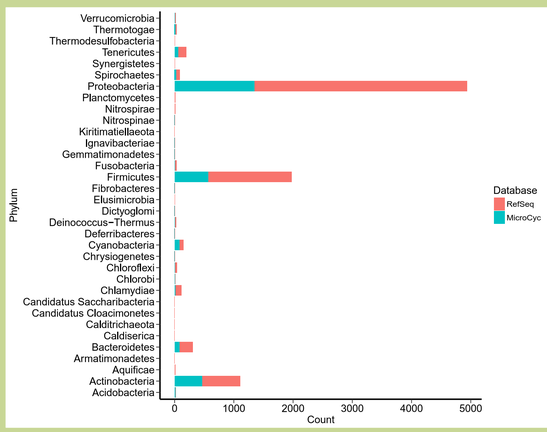
Our aim is to provide a **database** linking **taxonomic information** to **functional information**.
MACADAM Database is designed to obtain functional information when only taxonomic information is available.

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

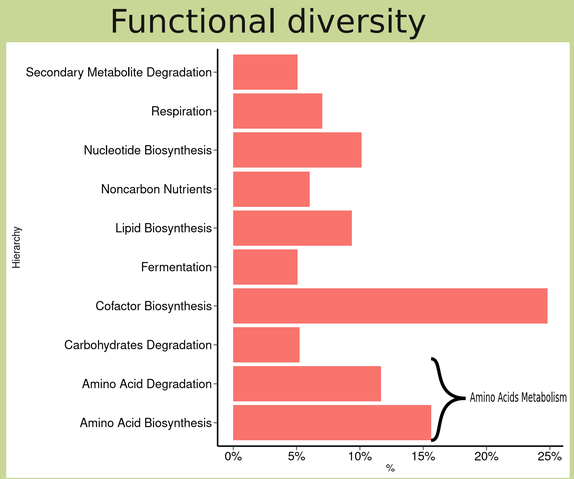


MACADAM taxonomic diversity

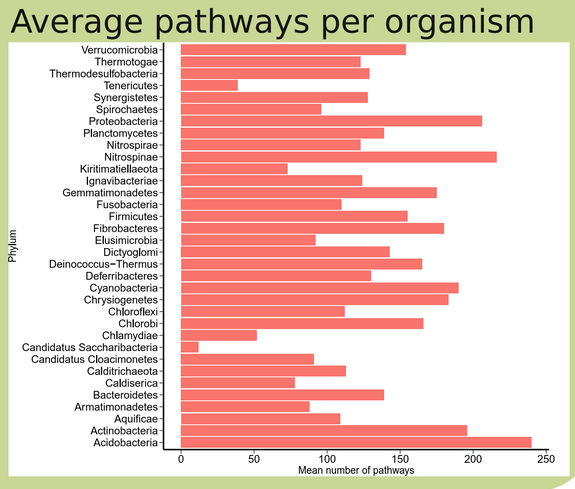
Presence of **34 different phyla**:
All 29 LSPN phyla are present.
The other 5 are recent proposals by the scientific community.

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

Functional diversity



Average pathways per organism



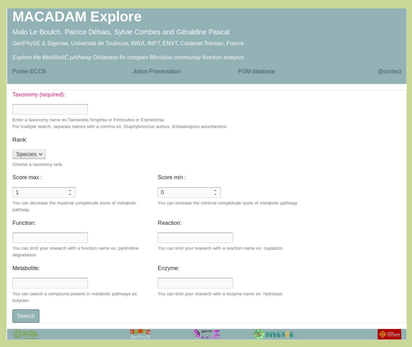
Database charateristics

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.

##TaxID:1280					
##Taxonomy: Staphylococcus aureus					
##Matching Point of the Database: 1280					
##Matching Point Taxonomy: Staphylococcus aureus					
#Metacyc:					
#Pathway	Present in	Median of score	Median of frequency	Present in match	Hierarchy
urea degradation I	7/156	0.5	1.5	Staphylococcus aureus	Degradation.AMINE-DEG.Urea-Degradation.PWY-5703.
urea degradation II	156/156	1	3	Staphylococcus aureus	Degradation.AMINE-DEG.Urea-Degradation.PWY-5704.
urea cycle	144/156	0.8	1	Staphylococcus aureus	Degradation.Noncarbon-Nutrients.NITROGEN-DEG.PWY-4984.

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

##TaxID:1704076				
##Taxonomy: Lactobacillus cerevisiae				
##Matching Point of the Database: 1578				
##Matching Point Taxonomy: Lactobacillus				
#Metacyc:				
#Pathway	Present in	Median of score	Median of frequency	Present in match
pyruvate fermentation to acetate **II**	45/215	1	2,33	Lactobacillus
pyruvate fermentation to acetate **VIII**	11/215	1	1	Lactobacillus
pyruvate fermentation to butanoate	10/215	0,29	0,29	Lactobacillus
succinate fermentation to butanoate	13/215	0,12	0,12	Lactobacillus
mixed acid fermentation	82/215	0,5	0,75	Lactobacillus
heterolactic fermentation	96/215	0,89	1,5	Lactobacillus
pyruvate fermentation to lactate	145/215	1	2	Lactobacillus
pyruvate fermentation to propanoate **I**	8/215	0,57	1,14	Lactobacillus
pyruvate fermentation to (R)-acetoin **I**	22/215	0,5	0,5	Lactobacillus
pyruvate fermentation to (R)-acetoin **II**	180/215	1	1	Lactobacillus
pyruvate fermentation to (S)-acetoin	33/215	0,67	0,67	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**	52/215	1	1,5	Lactobacillus
pyruvate fermentation to ethanol **II**	26/215	1	1	Lactobacillus

References: Tatusova, T., Ciufo, S., Fedorov, B., et al. (2014) RefSeq microbial genomes database: new representation and annotation strategy, Nucleic Acids Res., 42, D553-559.
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