



***a platform for quantitative metagenomic
profiling of complex ecosystems***

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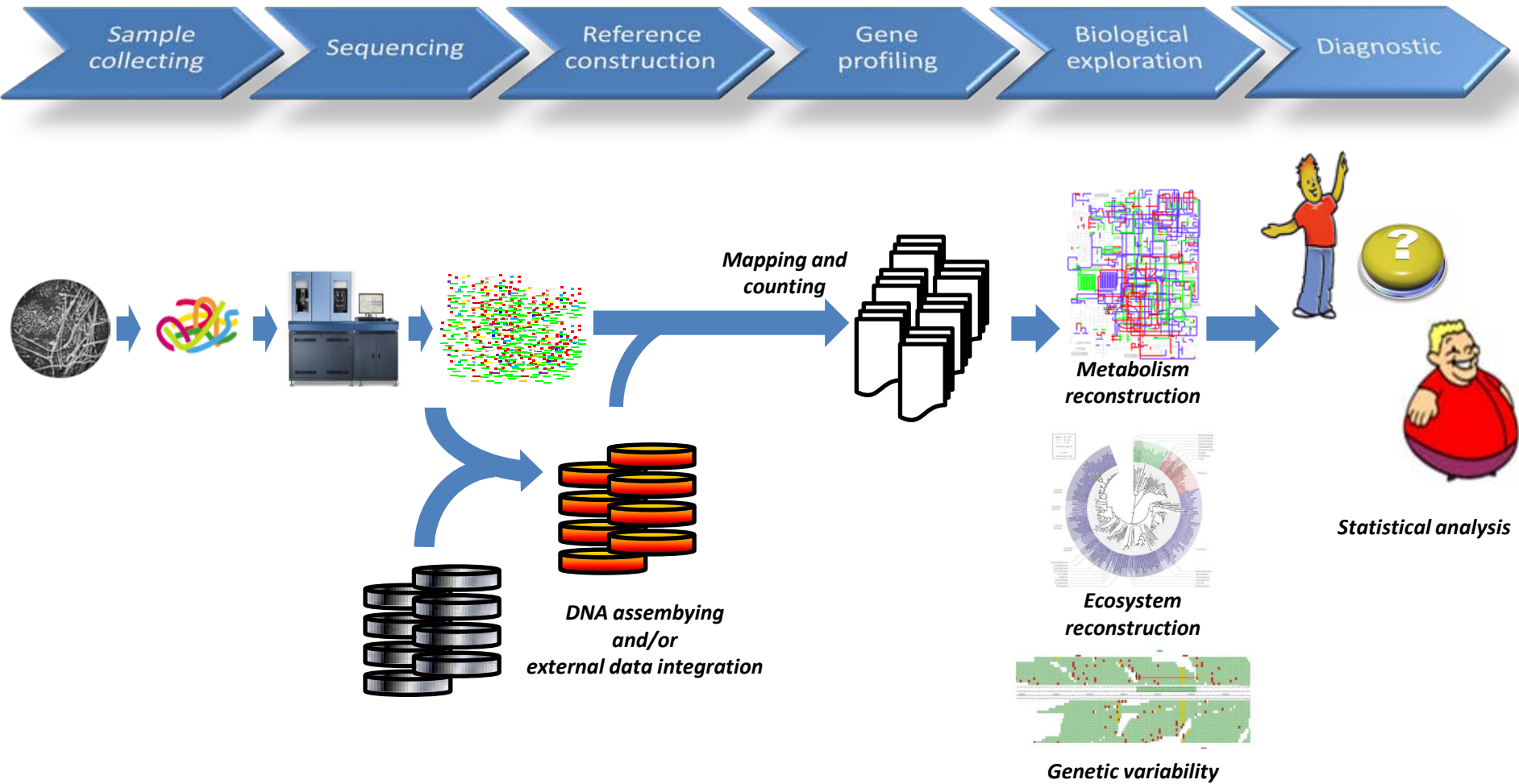


*Micalis - MetaQuant Platform
Jouy-en-Josas*

Poster 19



What is quantitative metagenomic ?



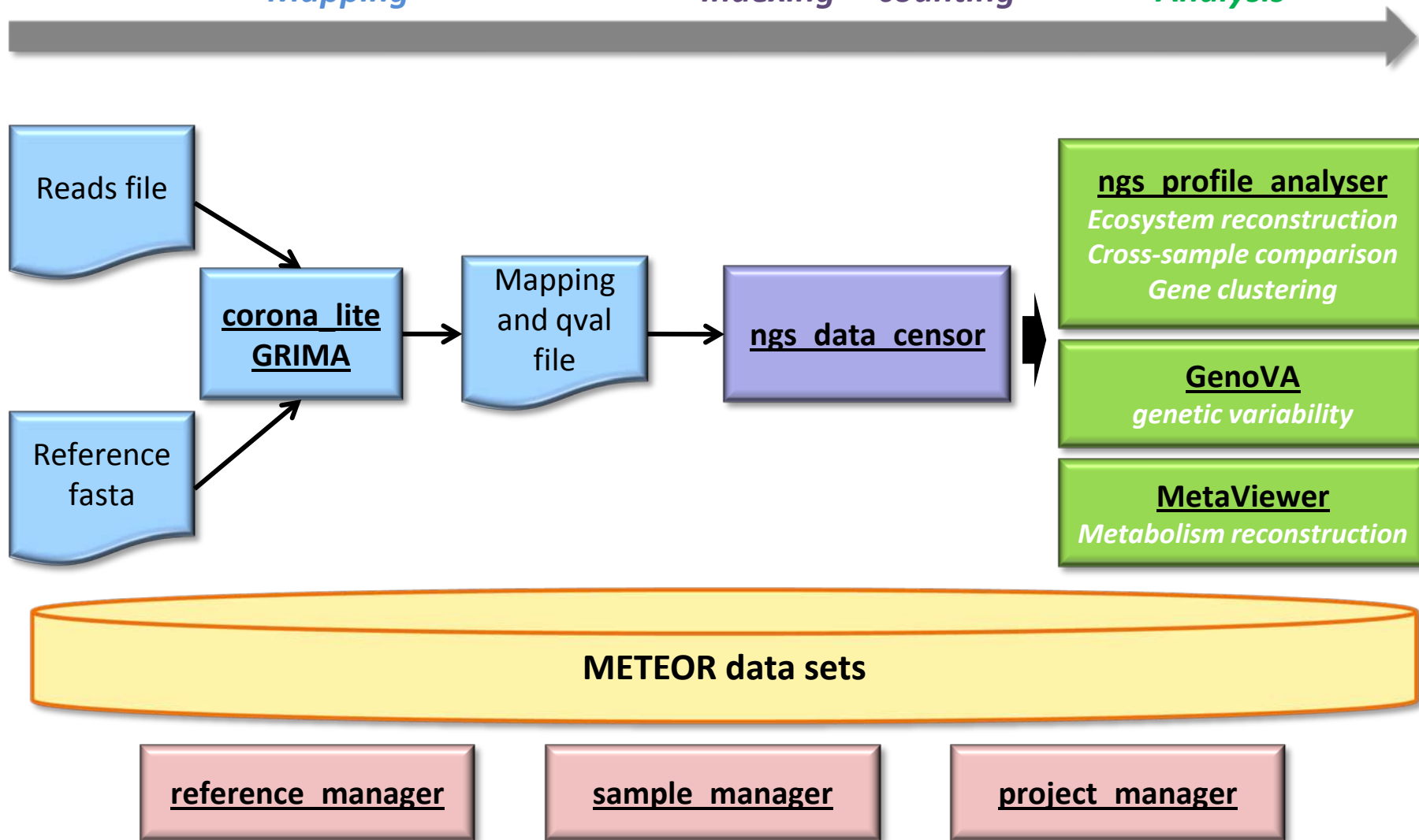


METagenomic ExploratOR

Mapping

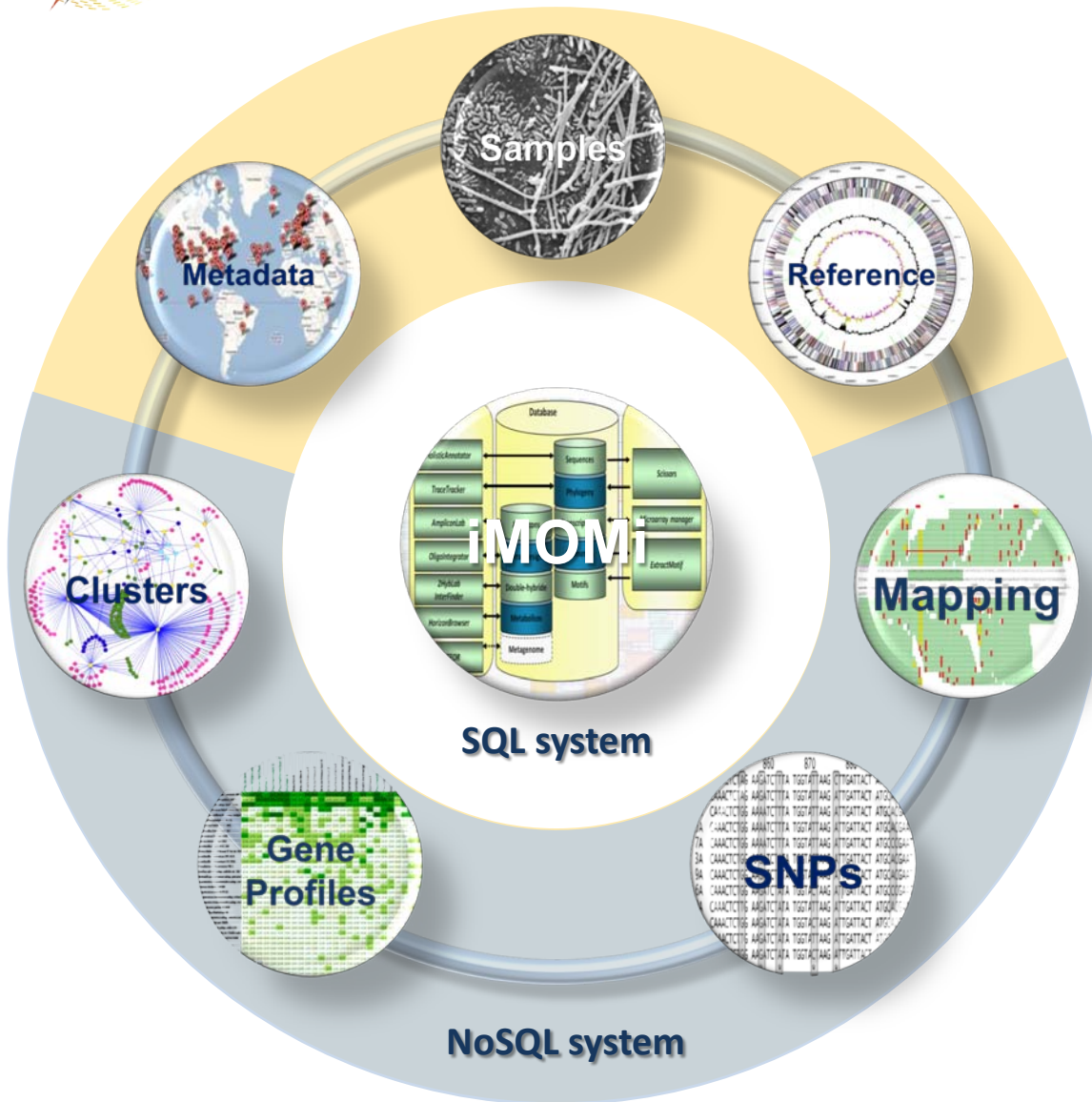
Indexing counting

Analysis



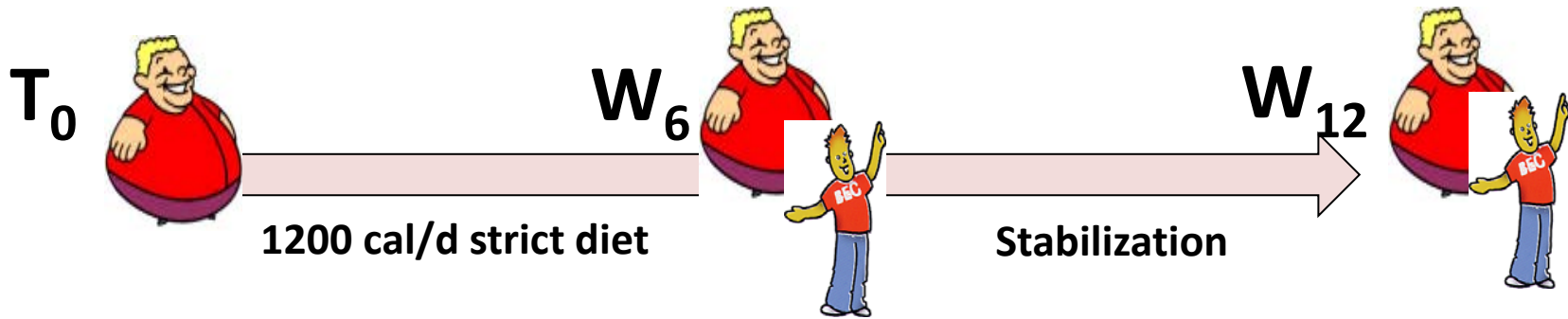


Data management



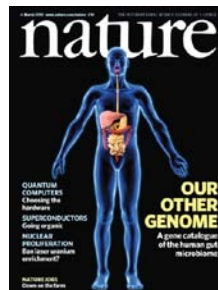
- Projects :
 - Micro-Obes
 - BB-allergy
 - Food-Microbiomes
 - Metaflora
 - Genome mixes
- ~300 samples
- ~500 Gbases
- >100000 files
- >10 To

Micro-Obes project



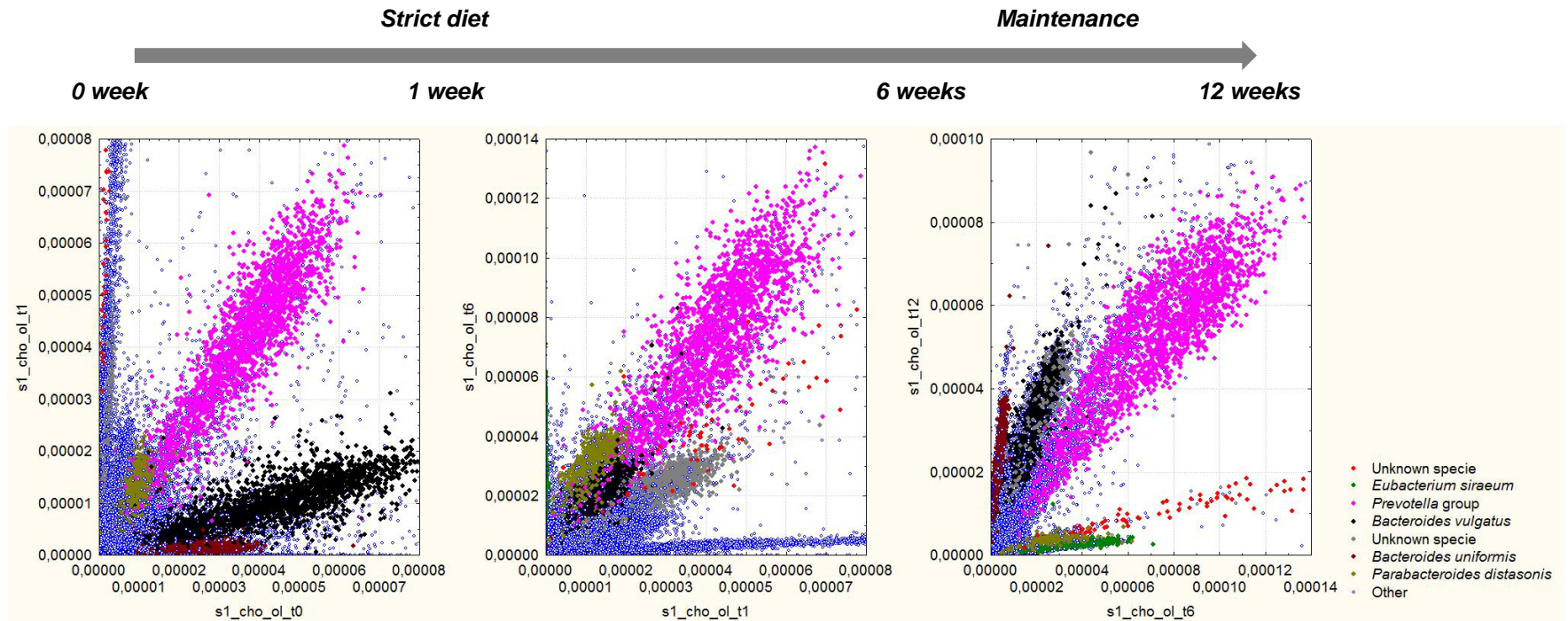
Follow the microbiota dynamic and identify signatures of obesity and nutritional transition in the intestinal microbiote

- DNA sequencing (SOLiD) of **215** faecal samples of **49** obese individuals sequenced at **3** different time-points (**t0**, **w6**, **w12** and extra-time)
 - **300 Gbases sequenced**
- Read projection against the MetaHIT gene catalog (Qin et al., 2010) (3.3 millions genes)
 - **150 Gbases projected**
- Gene clustering and bacteria composition determination



Micro-Obes project

Dynamic of microbiota during the diet

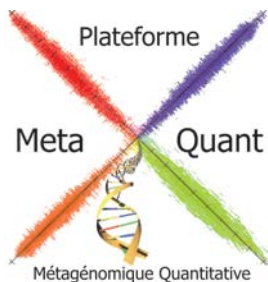


Important variation of gene composition during the first part of the diet
 More stable composition in the second part (stabilization)

Different dynamic profiles observed
 Association with clinical data (ongoing work)

MetaQuant

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Nicolas Pons
Nathalie Galleron
Benoît Quinquis



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Micro-Obes
Food-Microbiomes

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