



*a platform for quantitative metagenomic  
profiling of complex ecosystems*

Nicolas Pons, Jean-Michel Batto, Sean Kennedy, Mathieu Almeida,  
Fouad Boumezbeur, Bouziane Moumen, Pierre Léonard,  
Emmanuelle Le Chatelier, S. Dusko Ehrlich and Pierre Renault

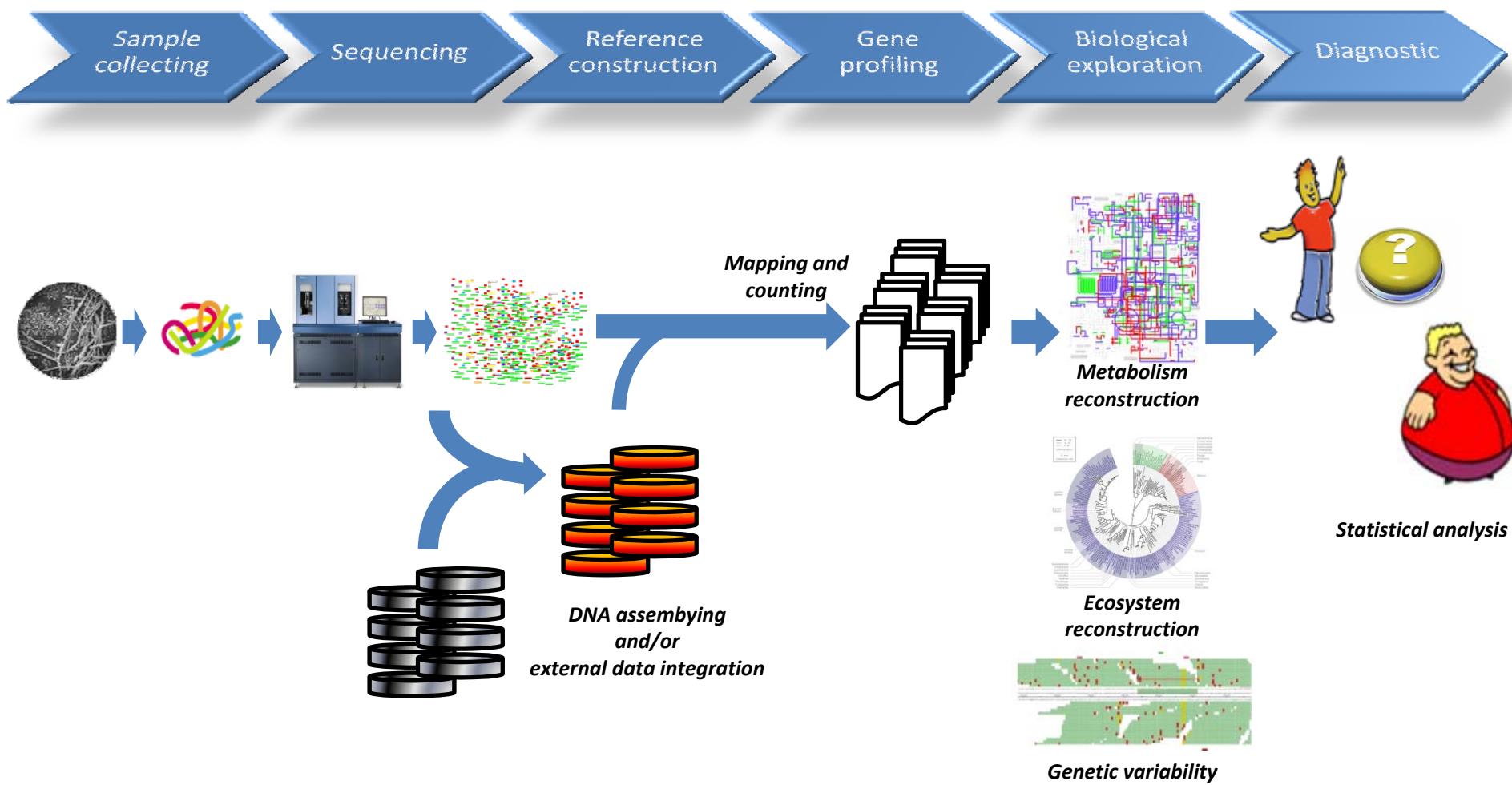


*Micalis - MetaQuant Platform  
Jouy-en-Josas*



**Poster 19**

# What is quantitative metagenomic ?



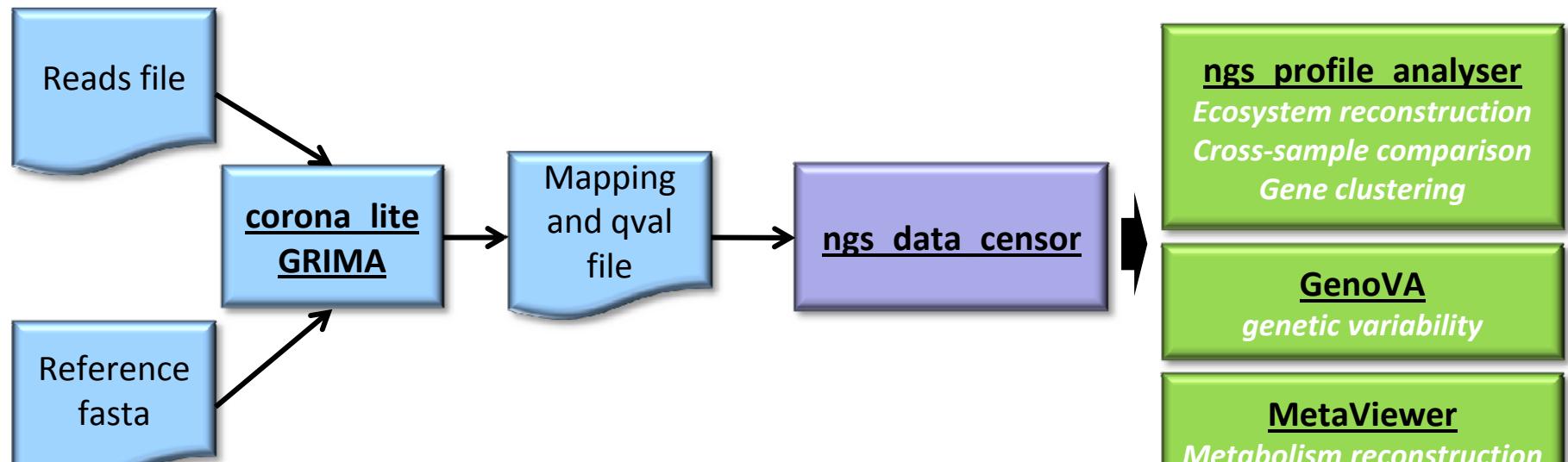


# METagenomic ExploratOR

*Mapping*

*Indexing    counting*

*Analysis*



METEOR data sets

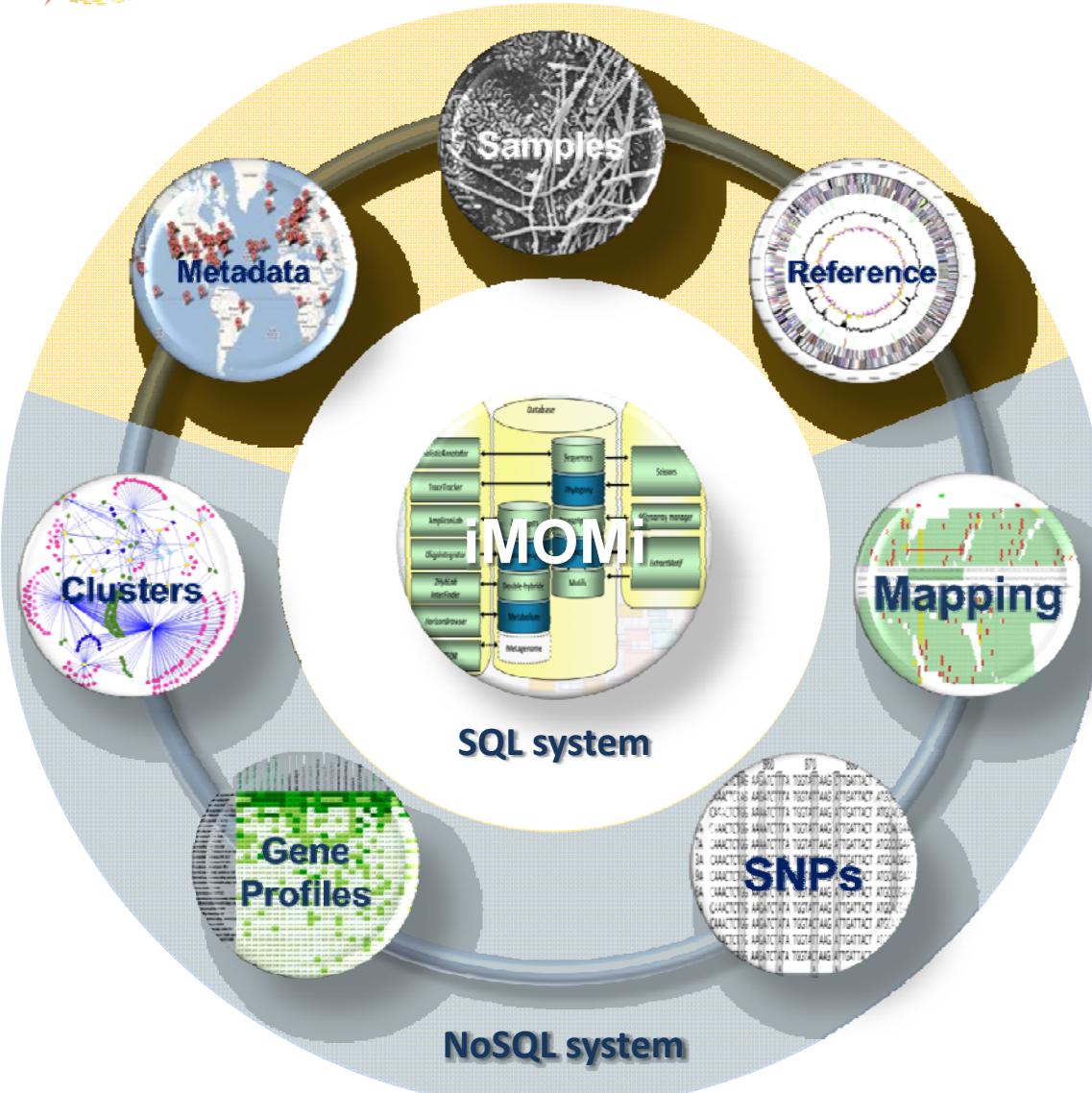
reference manager

sample manager

project manager

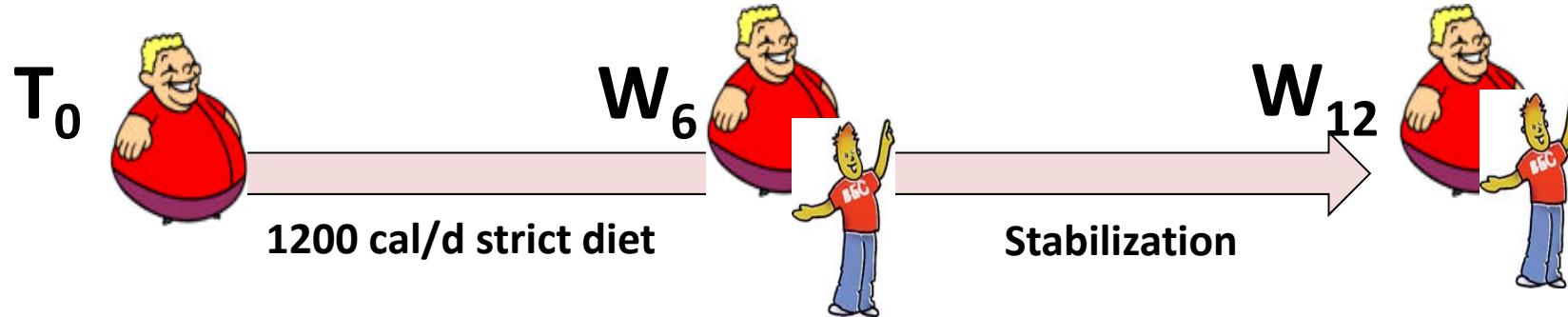


# Data management



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

# Micro-Obes project



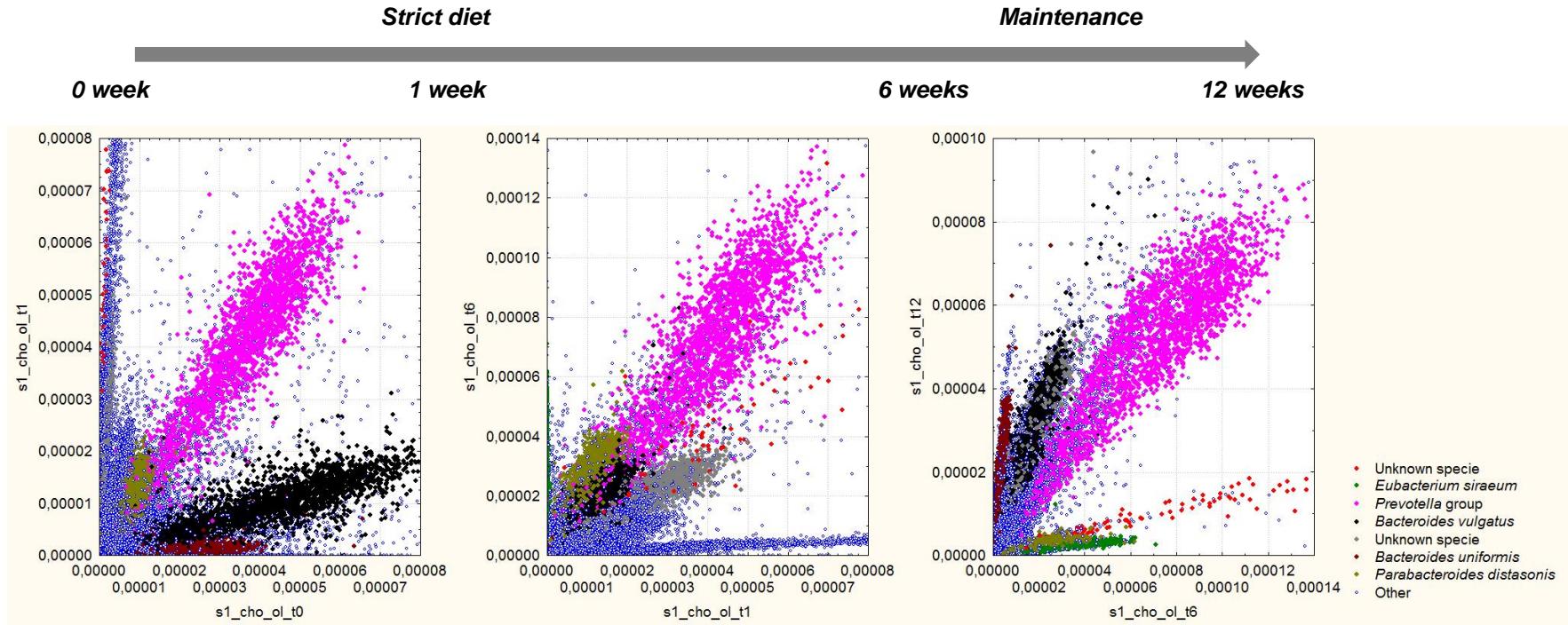
**Follow the microbiota dynamic and identify signatures of obesity and nutritional transition in the intestinal microbiote**

- 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

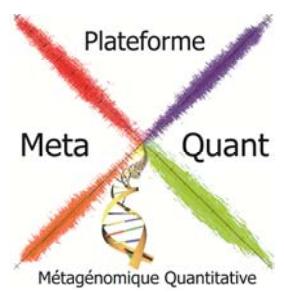
## Dynamic of microbiota during the diet



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**  
Dusko Ehrlich  
Sean Kennedy  
Nicolas Pons  
Nathalie Galleron  
Benoît Quinquis



**Team « Informatique »**  
Jean-Michel Batto  
Pierre Léonard  
Bouziane Moumen



**Team « Bactéries Alimentaires et Commensales »**

**Bioinformatic**  
Emmanuelle Le Chatellier  
Mathieu Almeida  
Fouad Boumekbzeur

**Biology**  
Christine Delorme  
Eric Guédon  
Séverine Layec  
Céline Gautier  
Nicolas Sanchez

Pierre Renault



[http://www.netvibes.com/metahit#Live\\_News](http://www.netvibes.com/metahit#Live_News)



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<http://paper.li/metahit/microbiomics>