

THE PARIS-GENEVE CLINICAL METAGENOMIC GROUP



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Infection • Antimicrobials • Modelling • Evolution



KUDOS TO MAUD SALMONA (PARIS, FRANCE)



(if you like the slides, she's the one to credit)

CURRENT SITUATION IN OUR HOSPITALS

Significant decrease of
sequencing cost



Implementation of NGS
sequencers in care
facilities



CMg in the hospital as complementary care tool

Heterogeneity
between the
teams



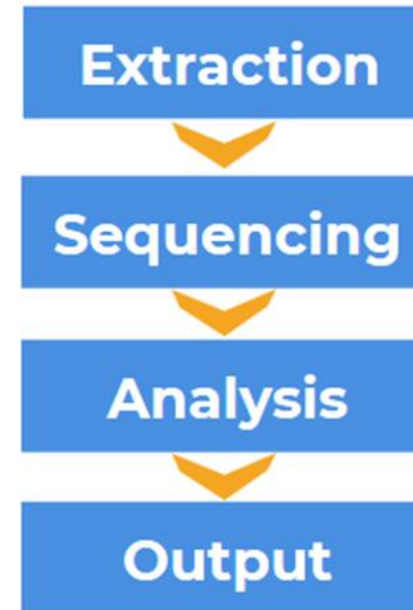
Need to harmonize practices

OBJECTIVES OF THE GROUP



Establish consensus guidelines for CMg implementation at APHP

- ✓ *Shotgun Clinical Metagenomic*
- ✗ *Targeted Metagenomic (16S,...)
Microbiome analysis*



COMPOSITION OF THE GROUP

18 lab experts



Biologists, Engineers and Bioinformaticists



7 Hospitals



PRE-ANALYTICAL



- **All samples** are relevant
- **DNA** and **RNA** must be extracted (RNA virus)
- **No minimum** of acid nucleic quantity
- **Internal control** (DNA and RNA) necessary
- **Negative and Positive controls** necessary
- **Dedicated workflow**



- Samples pre-treatment **by bead-beating?**
- **Host nucleic acid depletion?**

SEQUENCING



- **Illumina Sequencers**


Nanopore too experimental

- **Minimum depth** : 2x5 M reads / sample


Or more (Virus++)

- **Reads size** : 150nt sufficient

INFORMATICS AND BIOINFORMATICS



- **Curated Database** is necessary
No curated database to date
RefSeq curation ongoing (Bichat)
- Use of **MOABI** (AP-HP) for patients' data



- **Analysis Strategy**
(Cleaning, Mapping, Metrics and cut-off)
→ Different pipeline available in each site

OUTPUT

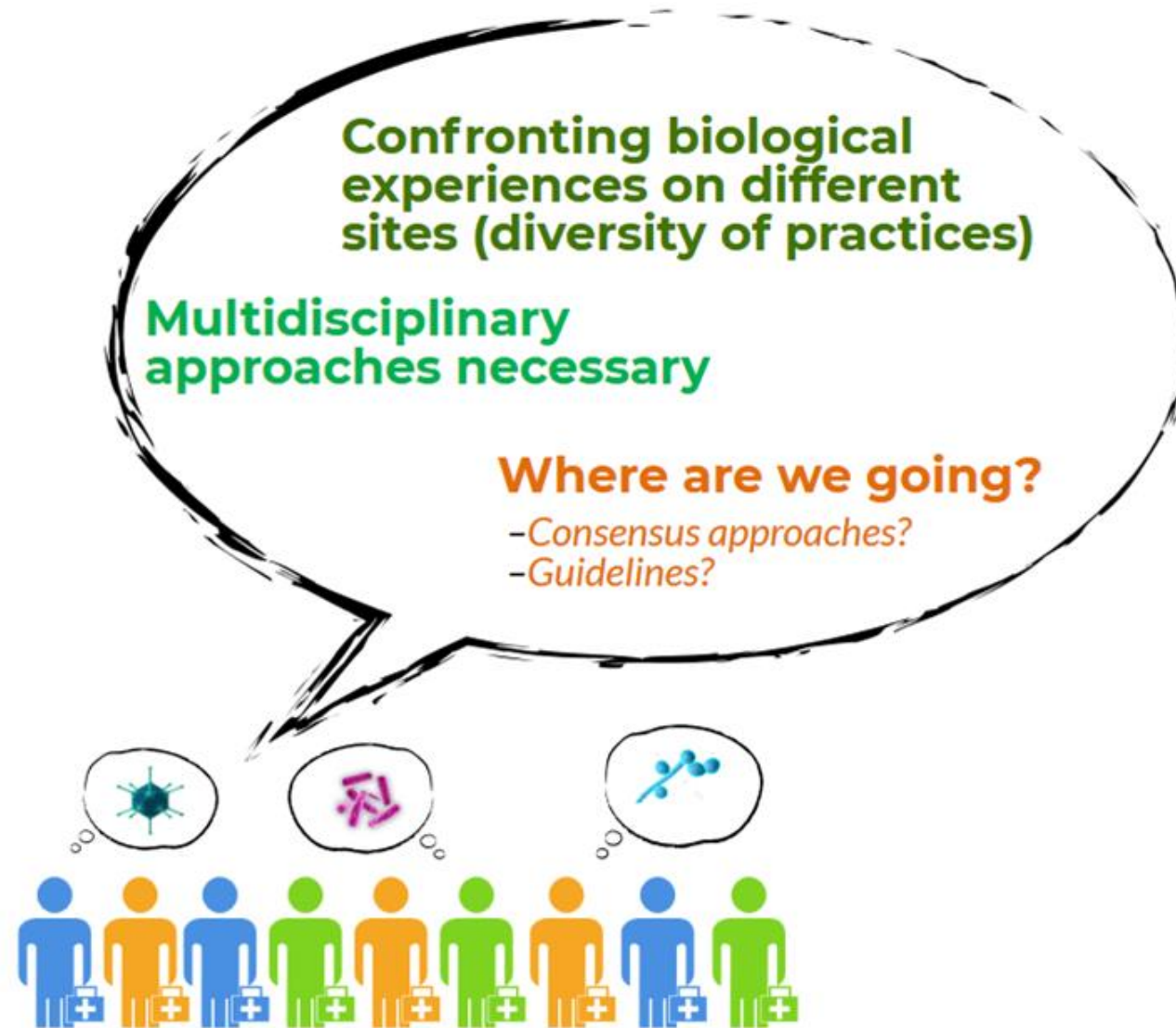


- First technical report interpreted by a **microbiologist trained in metagenomic sequencing**
Includes **various bioinformatics parameters**
- Second report **clinician friendly**



- **What should be reported to the clinician?**
So far quite dependant on the interpretation of the biologist

CONCLUSION



ACKNOWLEDGEMENTS

