



Implementation of a Nanopore metagenomic workflow for time-series of complex microbial communities: MAG catalog and functional annotation.

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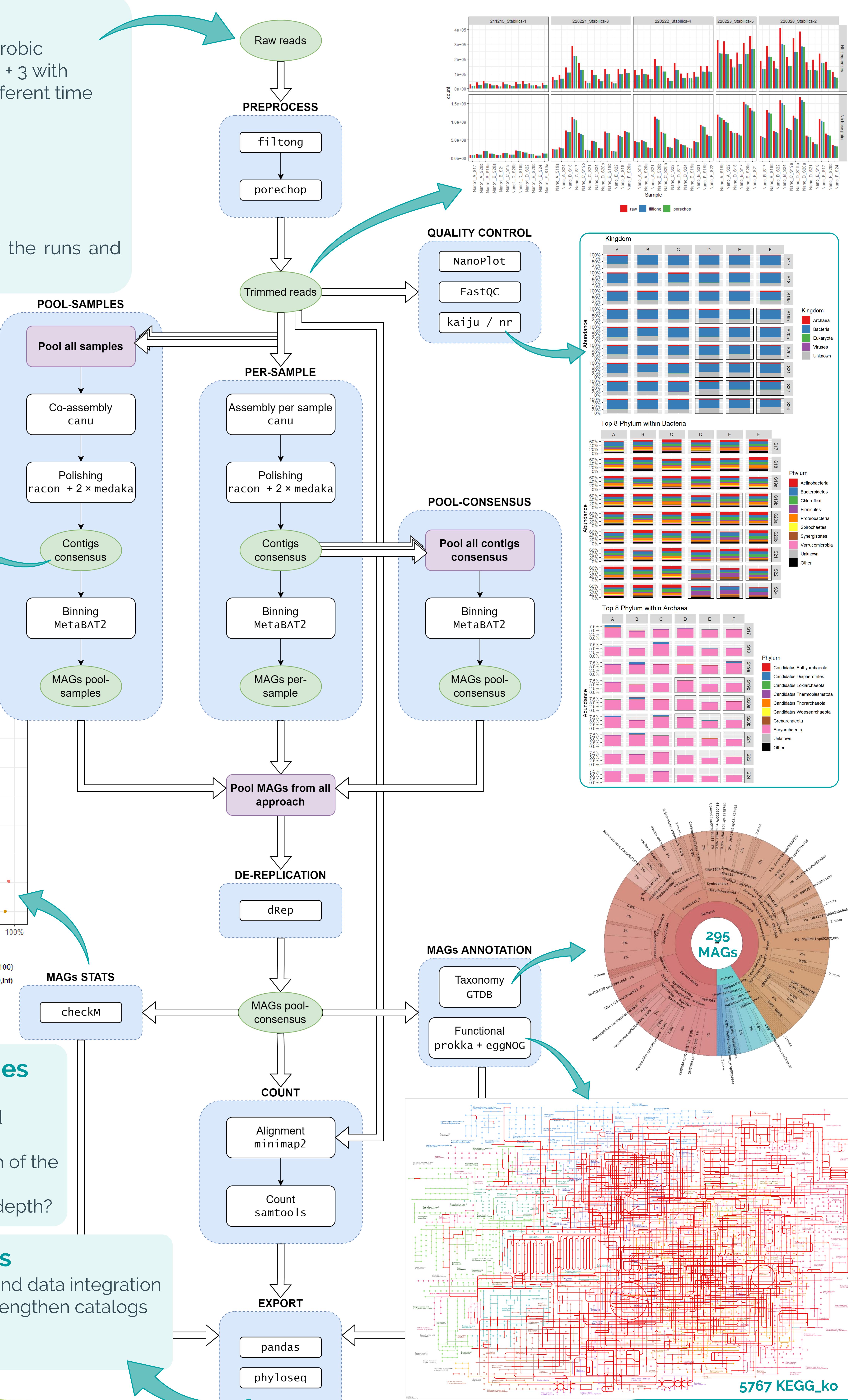
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► Data

- Samples come from 6 anaerobic digesters (3 controls: A, B, C + 3 with perturbation: D, E, F) at 9 different time points ($n = 54$)
- Lab-made sequencing :
 - MinION Mk1C
 - Flow-cells R9.4.1
 - Rapid Barcoding Kit
 - Multiplexing
- Throughput increases over the runs and our experience



► Statistical Challenges

- How to normalize count?
- Are reads correctly distributed between MAGs?
- Should we consider the length of the reads for normalization?
- Which effects of sequencing depth?

► Perspectives

- Statistical analysis and data integration
- Add new data to strengthen catalogs
- Workflow sharing
- Publications ...



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Snakemake workflow available
<https://forgemia.inrae.fr/cedric.midoux/nanosnake>