



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

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

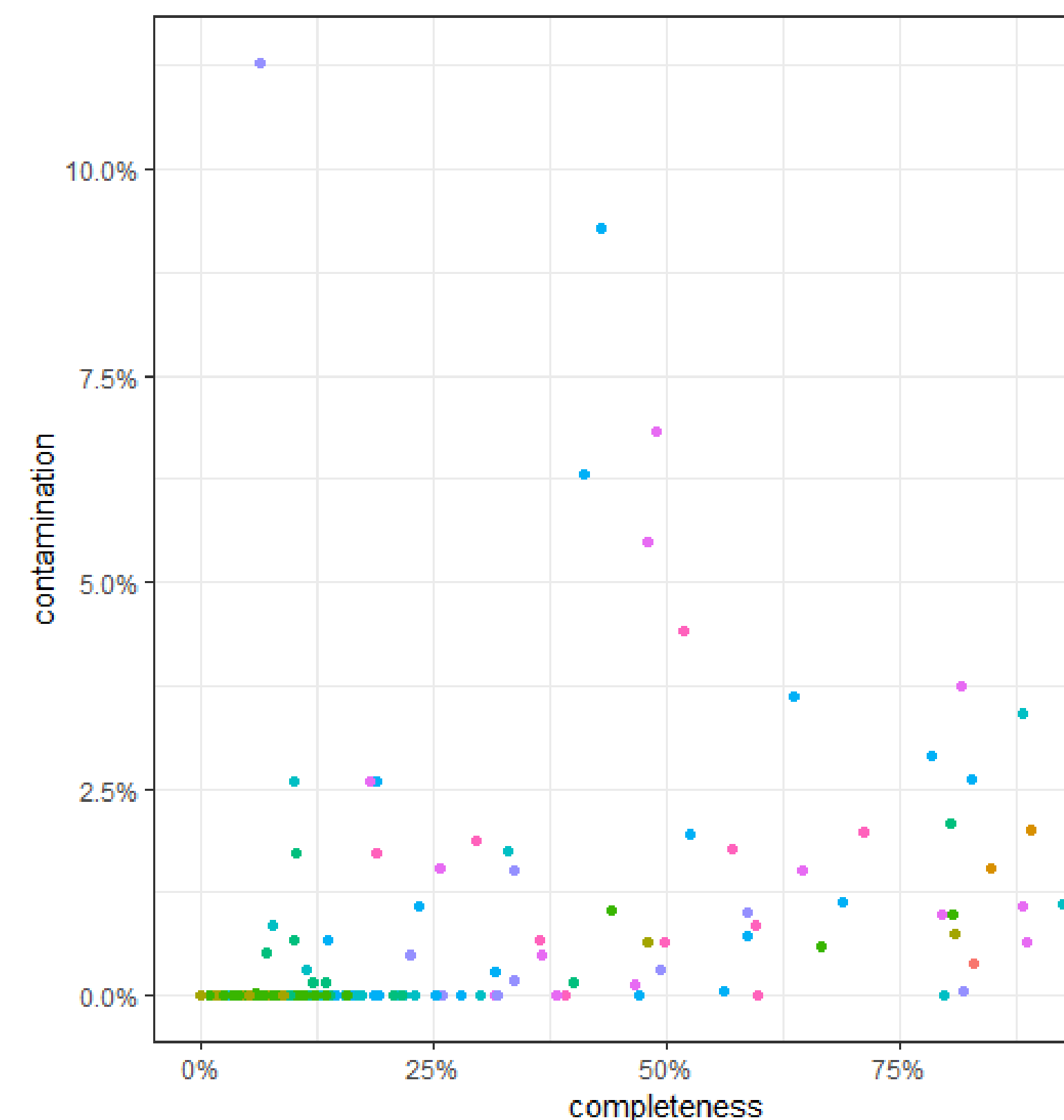
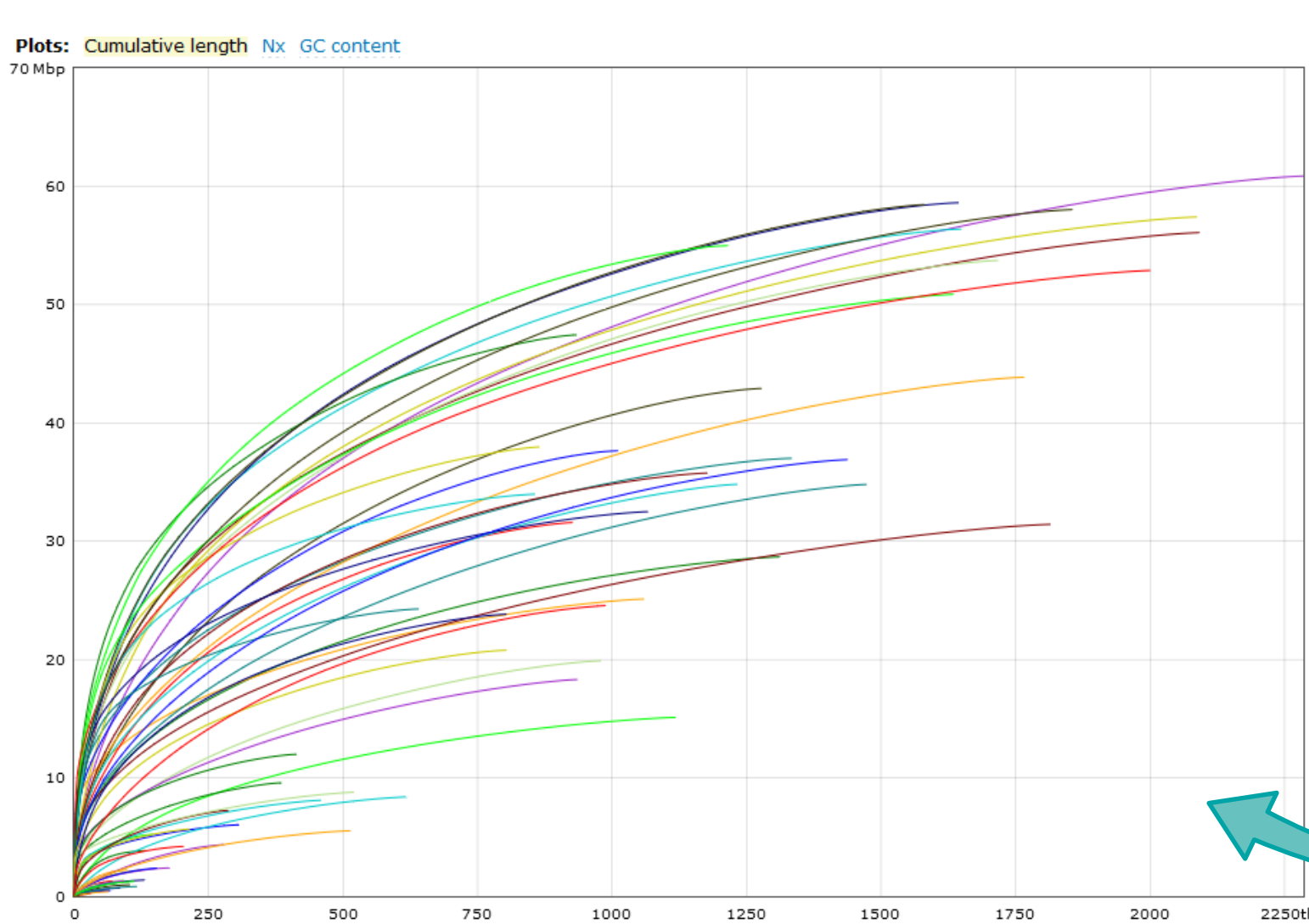
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## ➤ Data

- 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



Nb contigs : [1,4] [9,16] [25,36] [49,64] [81,100] [16,25] [36,49] [64,81] [100,Inf]

## ➤ 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 ...

