Novel bioinformatics tools for microbial monitoring and clinical diagnostics.

Mohamed Mysara^{1,2*}, Britto B. Xavier², Pieter Monsieurs¹, Surbhi Malhotra-Kumar², Natalie Leys¹

SCK · CEN

1 Unit of Microbiology, Belgian Nuclear Research Centre (SCK-CEN), Mol, Belgium. 2 Laboratory of Medical Microbiology, University of Antwerp, Wilrijk, Belgium.

OCTOPUS pipeline

Mysara M. et al. (2017) Gigascience

IPED

- IPED algorithm developed for correcting sequencing errors in Illumina MiSeq pairedend reads
- It is able to predict positions in the sequencing reads potentially containing errors.
- IPED detects double the amount of errors compared with the second best algorithm.



BacPipe pipeline

- open-access tools were screened to select the appropriate tools for each stage of analyses. Within BacPipe, including tools for: quality control check, assembly, as well as specialized tools for bacterial and plasmid typing, and for resistance and virulence gene predictions.
- As some of these specialized tools required annotation, these were divided within BacPipe into those that required assembly (post-assembly tools) or annotation (post-annotation analysis)
- BacPipe is designed to run multiple tools simultaneously which considerably reduces the time-to-result.

To increase the user-friendliness of the pipeline, we also integrated a

graphical user interface (GUI) Chromosomal DNA DNA shearing High throughput sequencing BacPipe Reads (Trim Galore) trimming Assembly (SPAdes) and scaffolding Genotyping Virulence identification (MLST, emm typing) Post (VirulenceFinder) assembly Acquired resistance identification Plasmid identification Outbreak analysis (ResFinder) (PlasmidFinder) (ParSNP) (Prokka) Annotation tRNA



<u>Monitoring</u>



SCK•CEN || Boeretang 200 || BE-2400 Mol || www.sckcen.be || info@sckcen.be || Posternr: