

Using wastewater to monitor COVID-19

Alt-text Figure 4 - Sample collection, RNA extraction, RT-PCR testing and whole genome sequencing of SARS-CoV-2 from wastewater

Illustrative workflow of the wastewater analysis process. 1) Sample collection: picture of water reservoirs. 2) Total RNA extraction: illustration of microtubes, viral particles and RNA molecules. 3) RT-qPCR: a sigmoid graph representing an RT-qPCR result. 4) Sequencing: a basecalling graph. 5) Bioinformatics: laptop with a quality control graph on the screen.

Alt-text Figure 5 - Schematic representation of the data analysis and variant identification pipeline showing the most frequently used tools

Flowchart depicting the following information: Raw FASTQ > Quality control = FastQC, Trimmomatic, bbdut (short reads) or FastQC, BoardION, NanoFilt (ONT reads) > Alignment (mapping) against reference = BWA, bowtie, STARaligner (short reads) or Medaka, BWA, minimap2 (ONT reads) > Coverage check (filtering) = SAMtools, BEDtools > Variant calling = SAMtools, GATK (short reads) or Medaka, SAMtools, GATK (ONT reads) > Consensus fasta > SARS-CoV-2 lineage alignment = Pangolin, custom designed pipelines.