Nextflow processes

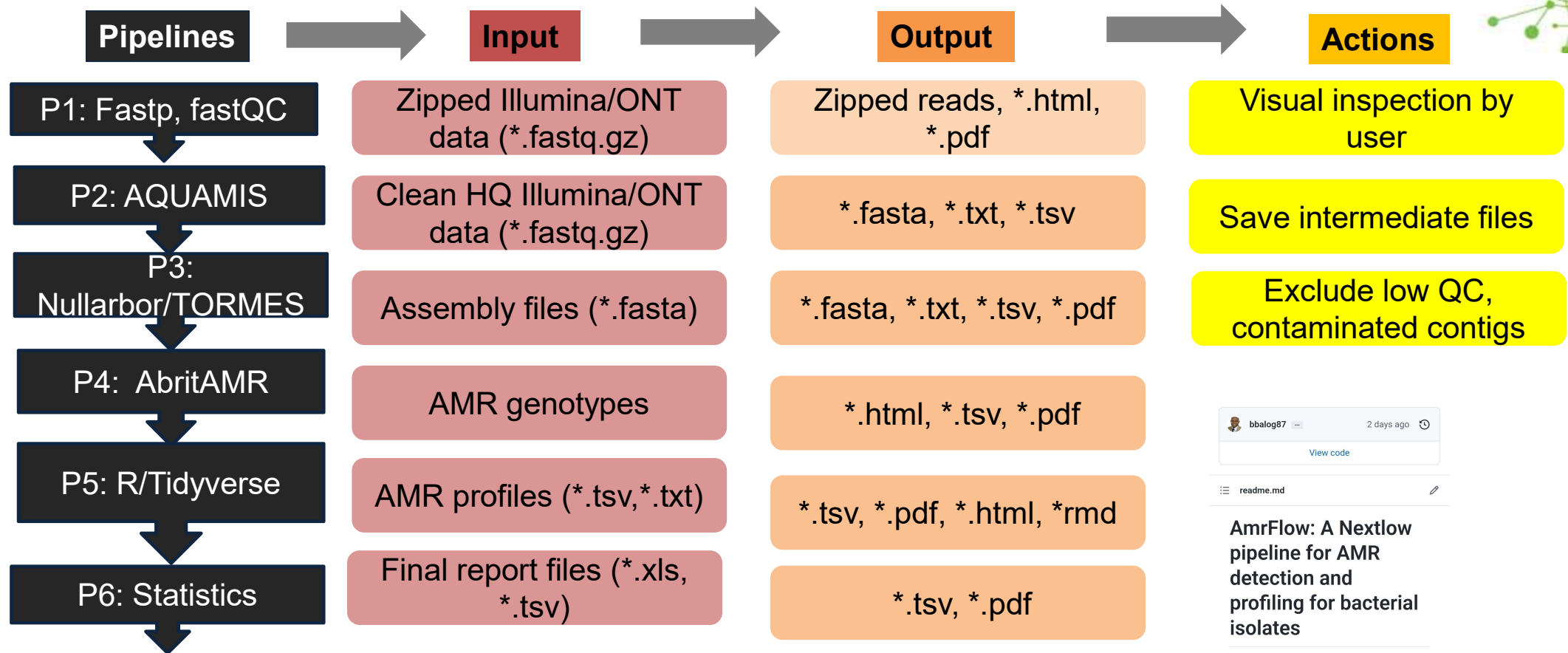| Pipelines		Input		Output		Actions
P1: Fastp, fastQC	→	Zipped Illumina/ONT data (*.fastq.gz)	→	Zipped reads, *.html, *.pdf	→	Visual inspection by user
P2: AQUAMIS		Clean HQ Illumina/ONT data (*.fastq.gz)		*.fasta, *.txt, *.tsv		Save intermediate files
P3: Nullarbor/TORMES		Assembly files (*.fasta)		*.fasta, *.txt, *.tsv, *.pdf		Exclude low QC, contaminated contigs
P4: AbritAMR		AMR genotypes		*.html, *.tsv, *.pdf		
P5: R/Tidyverse		AMR profiles (*.tsv,*.txt)		*.tsv, *.pdf, *.html, *rmd		
P6: Statistics		Final report files (*.xls, *.tsv)		*.tsv, *.pdf		

bbalog87 ··· 2 days ago

View code

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AmrFlow: A Nextlow pipeline for AMR detection and profiling for bacterial isolates

A Nextflow pipeline for NGS antimicrobial resistance profiling; from raw NGS FASTQ to rendered AMR profiles.