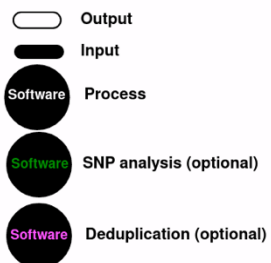


AMR++ bioinformatic pipeline

Pipeline Steps

1. QC trimming
2. Host DNA removal
3. Resistome alignment
4. Taxonomic classification



Pipeline workflows

- standard_AMR (Green line)
- fast_AMR (Brown line)
- standard_AMR_wKraken (Orange line)

Pipeline subworkflows

- eval_qc (Purple line)
- trim_qc (Black line)
- rm_host (Pink line)
- resistome (Dark red line)
- kraken (Dark purple line)
- bam_resistome (Blue line)

