



Figure S17. ProkEvo’s computational workflow with both mlst and stringMLST included for ST-based classification.

Top-down flow of tasks for the ProkEvo computational pipeline. The squares represent the steps, while the bioinformatics tool used for each step is shown in brackets. The sub-workflow on the left includes all the steps of the current ProkEvo platform, for which the steps needed for obtaining ST classifications with mlst are colored in orange. The sub-workflow on the right includes all the steps of the alternative path in the ProkEvo platform, where stringMLST was integrated for ST-based classification.