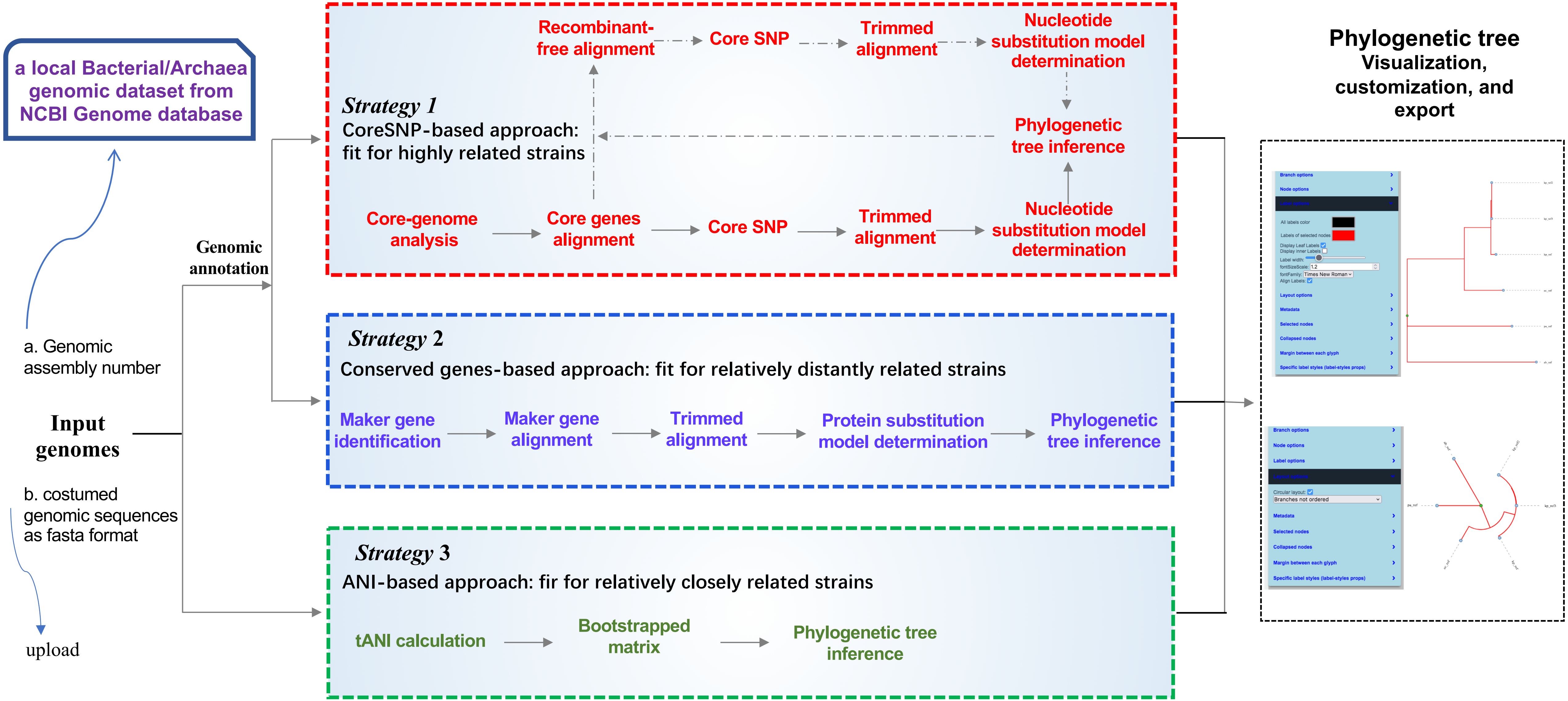

Figure1. The workflow for pubAutoTree. Users have the option to either provide the assembly numbers of the genomes they wish to analyze or upload genome sequence files. Upon providing the assembly numbers, pubAutoTree will promptly retrieve the corresponding genome sequences from its local genomic database, which is updated daily with the NCBI genome database. From among the three available methods, users can select one to construct a maximum likelihood tree. Once the phylogenetic tree is completed, users can instantly visualize, customize, and export the phylogenetic tree map in either SVG or JPEG format.