As whole genome sequence data of microorganisms are becoming easily accessible and cheap to produce, a transformation of the traditional methods used for typing, phenotyping and phylogenetic analysis of microorganisms is on the way. Following the anticipation that most clinical microbiological and food safety laboratories will soon have a sequencer in use on a daily basis, there is a growing need for easy-to-use bioinformatics methods that can quickly convert the sequence data into useful information on, e.g., the type of bacteria, whether it is resistant towards any types of antibiotics, and whether it is part of an outbreak. The Center for Genomic Epidemiology, which is located at the Technical University of Denmark, has since its beginning in 2010 developed such bioinformatics methods and made them freely available as web-services. These web-services and their use is the focus of this chapter.