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Chapter 6 - Whole-Genome Analyses: Average Nucleotide Identity

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Abstract

Average nucleotide identity (ANI) was proposed almost 10 years ago as a means to compare genetic relatedness among prokaryotic strains. It was found that values around 95% corresponded to the 70% DNA–DNA hybridization cut-off value that is widely used to delineate archaeal and bacterial species. ANI calculations are one of the many aspects and approaches that can be derived from comparative genomic data and used for taxonomic purposes. Here, an overview about the impact and current usage of ANI values is given together with details of the existing user-friendly package tool, the biology-oriented software package JSpecies, which can be used to generate two types of ANI calculations based on BLAST and MUMmer software packages.

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