Abstract: Since their introduction in 1970, Bloom filters have been used as space-efficient alternatives to hash functions for testing set membership with a tolerable rate of erroneous acceptance. Bloom filters have been widely applied in the area of dictionaries, relational databases and latter in a wide range of networking problems. Recently, bloom filters caught the attention of researchers in mitigating the challenges posed by overwhelming growth of (meta)-genomic data being generated, processed and stored. In the process of tailoring the data structure to the data, different variants of bloom filters such as sequence bloom trees, bloom filter trie and interleaved bloom filters have been introduced. These variants of bloom filters offered a means to index and search databases which are too big for popular indexing approaches such as k-mer index, suffix trees, and FM-Indices. In this disputation, I will discuss different variants of bloom filters related to processing genomic data and their applications. The presentation will be followed by a short summary of my dissertation titled “Whole Genome Shotgun Sequencing-Based Taxonomic Profiling Methods for Comparative Study of Microbial Communities”