# Development of tracking tools for selected bacteria using 16S rDNA sequences: An approach based on repeating tuples and probabilities of dinucleotides

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**Abstract**

Our interest lies in identifying the distinguishing sub-sequences of the selected bacterial group, based on 16S rDNA sequence data, which could be used further for generating genus specific tracking protocols. We have used two criterions the identification of repeating consistent k-tuple of varying in sizes and secondly, discriminating dinucleotide feature.

We have developed a program ***Repeat Tuple Search*** that selected the consistent repeating tuple in set of sequences. The sub-sequences with in the genus specific repeating tuple were superimposed to study the conservation of nucleotides at different positions using Shannon's entropy. The exercise yielded a genus specific 16S rDNA signature. Alternatively, discriminating dinucleotide features were identified which will be used to generated genus specific patterns.

We have designed a set of primer based on aforesaid approach, which has been tested as tracking tool for genus ***Pseudomonas.***