

**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*.