# On the Test of Significant Similarity in an Alignment of DNA/Protein Sequences

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Most human diseases are a result of some kind of genetic mutation occurring at the cellular level. The application of correct statistical methodology is an important aspect towards understanding the complexity of genetics data. In this talk a matching problem of testing hypothesis for similarity between two un-gapped alignment sequences of DNA or protein sequences are considered. A computationally efficient method, based on mutually orthogonal Latin squares, of calculating a more accurate Z-value for a pair-wise alignment of two sequences is proposed.