# Molecular Models for G-quadruplexes 

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## Motivation

Independent surveys of human gene promoter regions have demonstrated an overrepresentation of G_3X_\{n1\}G_3X_\{n2\}G_3X_\{n3\}G_3 motifs which are known to be capable of forming intrastrand quadruple helix structures.
In spite of the widely recognized importance of G-quadruplex structures in gene regulation and growing interest around this unusual DNA structure, there are at present only four such structures available in the Nucleic Acid Databank.
In the present work we generated by molecular modeling feasible G-quadruplex structures which may be useful for interpretation of experimental data.

## Methods

We have used all quadruplex DNA structures deposited in the Nucleic Acid Databank in order to select a list of fragments entailing a strand of three adjacent G's paired with antother strand of three adjacent G's separated by a loop of one to four residues. These fragments were further clustered and representative fragments were finally selected. Further fragments were generated by assemblying the two strands of each fragment with loops from different fragments whenever the RMSD between the anchor G's were superimposable.
The fragments were used to assembly G quadruplex based on a superimposability criterion.

## Results

Molecular models have been generated for a large number of G_3X_\{n1\}G_3X_\{n2\}G_3X_\{n3\}G_3 sequences. For a given sequence not all topologies are possible with the available repertoire of fragments due to steric hindrance. Since all molecular models are generated by fragments coming from observed quadruplex structures, molecular models are in principle reliable and may be used for interpretation of experimental data. Some examples of applications are given.

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