**Personalized Song Creation Using Genomic DNA Sequencing**

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**ABSTRACT**

This project is a design and implementation of parsing genetic sequences to be represented as musical compositions.

**Introduction**

(Currently detailed in proposal)

**Motivation**

(Currently detailed in proposal)

**Approach**

The implementation uses the R language, as well as the packages tuneR and Biostrings. The implementation uses FASTA file formatted nucleotide data, which is opened in to a parsable format using Biostrings. The sequence is parsed 4 nucleotides at a time, using the first two to decide the pitch, the third to decide the length, and the fourth to determine the determine whether or not to play a chord.

**Algorithms**

Initialization:

sequence = readDNAStringSet(“sequence.fasta”)

sample.rate = 16000 #customizable

Main iteration:

For i=1, …, N - 3

notes <- parsePitch(subseq(s, start = i, end = i + 3)

parsePitch:

pitch = value(dict(subseq[1:2])) #get values from A3 to C5, with two rests values of 0 from dictionary

duration = value(dict(subseq[3])) #get length of pitch from whole to sixteenth note

chord = value(dict(subseq[4])) #get chord type, no chord, minor 3rd, major 3rd, major 7th

output:

For i = 1, …, length(notes)

#concatenate all notes together