

GRIL Overview

Genome Inversion and Rearrangement Locator



About GRIL

GRIL is a tool that can be used to identify the location of rearrangements and inversions in the backbone of a set of DNA sequences. GRIL works by identifying exactly matching regions present in all sequences under consideration and organizing them into groups of collinear regions. GRIL removes small regions of collinearity that appear unlikely to be true sequence rearrangements based on user-specified criteria such as the length of the collinear region and the percent sequence identity of the collinear region. The size of sequences that GRIL can be applied to is dependent on the amount of available memory.

GRIL requires approximately 16 bytes of memory per base of the longest input sequence. For example, detecting rearrangements in 7 bacterial genomes, the largest of which is 5.5MB, would require approximately 88MB of memory.

NOTE - GRIL does not perform an actual alignment of genome sequences. If you would like a multiple genome alignment, please consider using Mauve.

Documentation

An [application note](#) describing GRIL has been published in [Bioinformatics](#).

There is a [gril_readme.txt](#) file that provides basic information on using GRIL and an example.

The algorithms behind GRIL are described [here](#).

An example of using GRIL to determine the rearrangements in 5 genomes is [here](#).

Download GRIL

GRIL Version 1.0.0 was released on April 25, 2003.

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