

USER'S MANUAL



ISLANDHUNTER VER1.0

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1. Software Requirements

User needs to have Java Runtime on the machine. Java Runtime can be obtained from:

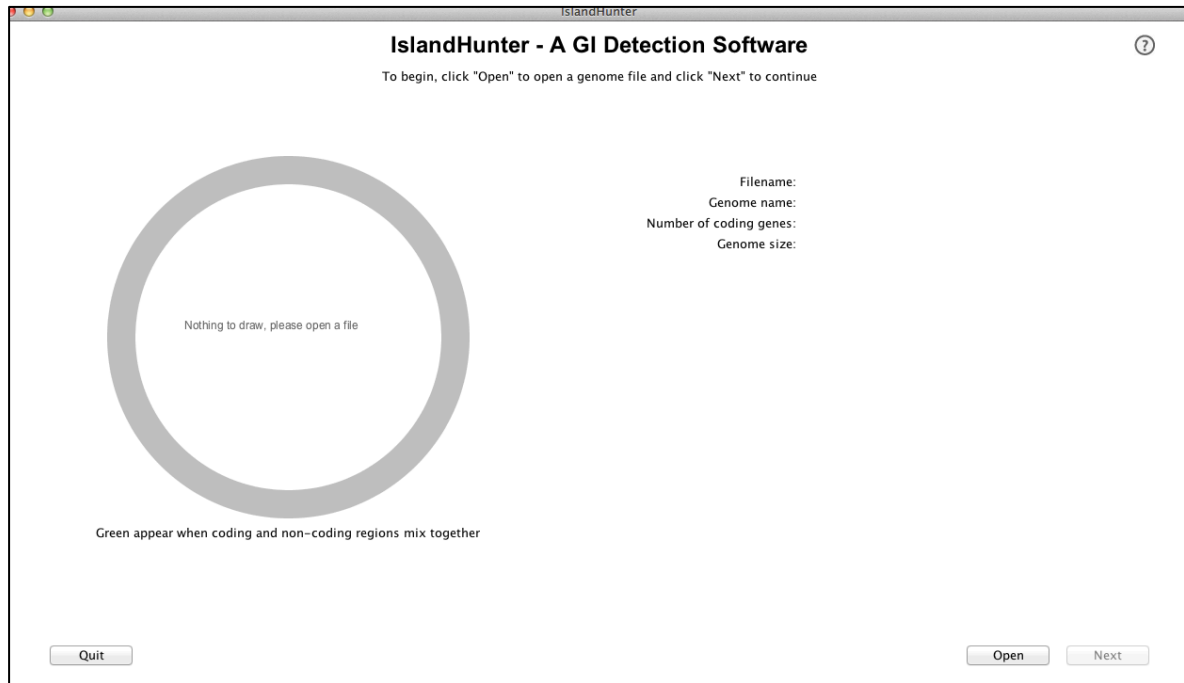
<https://www.java.com/en/download/>

2. Introduction

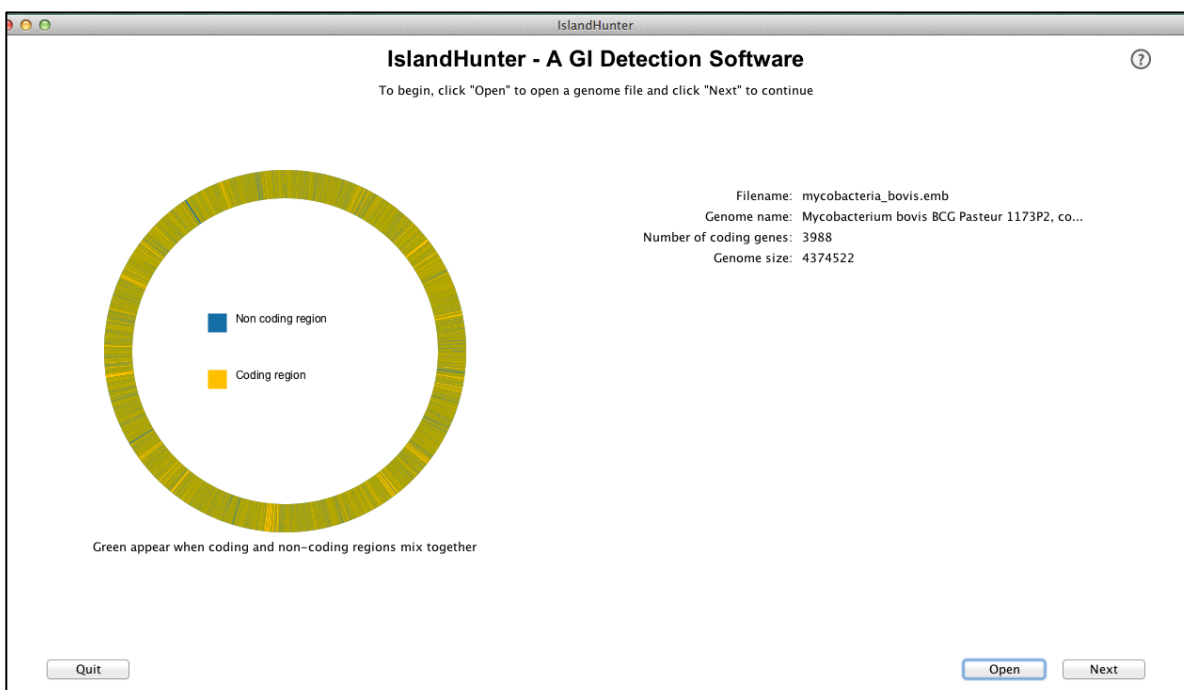
Genomic islands (GIs) are clusters of genes in prokaryotic genomes of probable horizontal origin. For decades, it has been a challenge for biologists to identify GIs within a bacterial genome as they usually evolve very rapidly. This makes it difficult to analyse the DNA sequences and to be up-to-date with bacterial evolution. Thus, bioinformatics is the solution to this problem. "Genomic Islands Detection Tool" (GIDT) detects GI regions by using a number of nucleotide-based statistical methods such as GC-content, codon usage bias, dinucleotide frequency bias, tetranucleotide frequency bias, k-mer signature analysis and identification of mobility genes. It takes genome files in the embl-format as input and returns the probable GI regions in a tree-view display along with a circular-view display. On a conclusive note, GIDT is a simple tool which uses six GI identification algorithms and visually displays the probable GIs in a given genome and it runs on Mac, Microsoft windows as well as on Linux.

3. Getting Started

- Click on “Open” to upload a genome file (.fasta, .gbk, .embl).

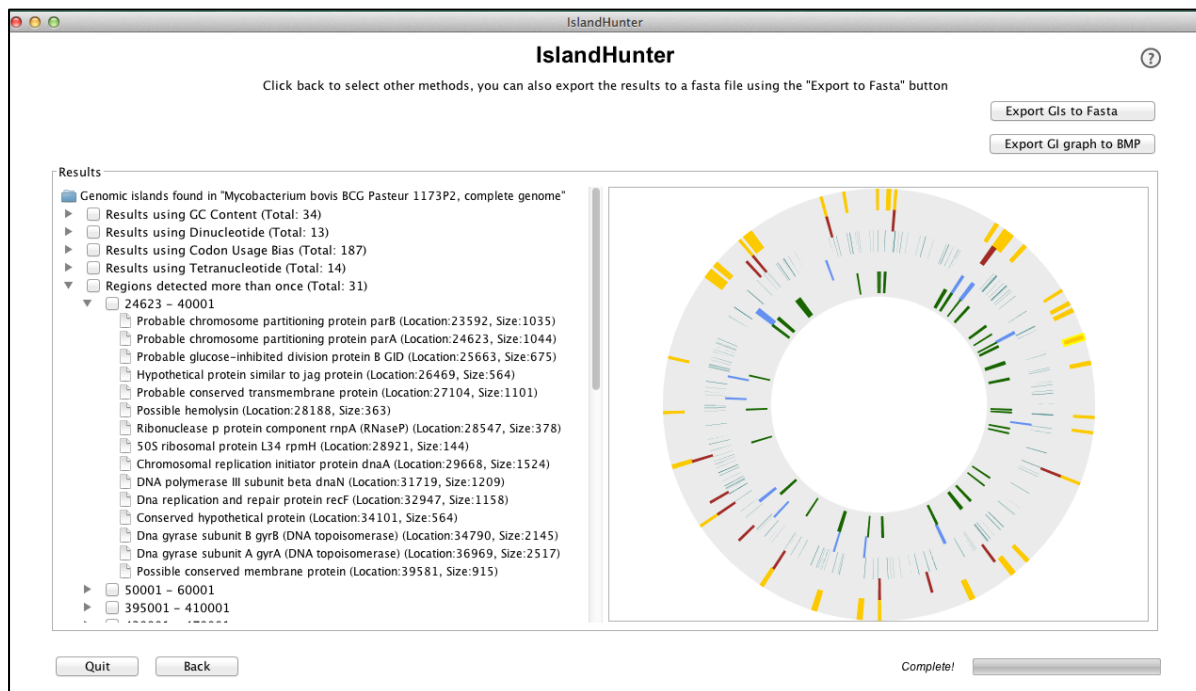


- Click on “Next” to continue.



- Choose the methods by selecting the checkboxes. Standard deviation controls the “sensitivity” of the methods used. A higher value decreases the sensitivity (i.e. less regions are detected) whereas a lower value increases the sensitivity (i.e. more regions are detected). You can also specify the window size and step size to be used by methods requiring these values.

- Click on “Next” to get the outputs.



The results are displayed in both a tree format and a graphical format. The outputs can be exported to a fasta file which can be used to blast to find the originality of the detected genomic islands (GIs). Select the required results by using either the tree or by simply clicking on the graph at the required region

To blast the identified GI regions, any appropriate BLAST site can be used.