IslandViewer: More Flexible, Integrated Prediction and Visualization of Genomic Islands, Virulence Factors, and Antimicrobial Resistance Genes in Bacterial Genomes

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Genomic Islands (GIs)

- GI definition: segment of a bacterial or archaeal genome of probable horizontal origin (commonly defined as being larger than 8 kb).
- Shown to disproportionately contain genes encoding notable adaptations including antimicrobial resistance and virulence. Associated with a large, novel gene pool.

GL Prediction with IslandViewer*

- Web-accessible tool for GI prediction and analysis.
- Integration of the three most accurate GI prediction methods: SIGI-HMM, IslandPath-DIMOB (sequence composition based approaches), and IslandPick (comparative genomics approach).
- Pre-computed analyses for all NCBI complete microbial genomes.
- Option for users to upload a genome for customized analysis.

IslandViewer improvements provide a much more flexible interface to aid analysis of GI regions of medical and adaptive interest in bacterial genomes, coupled with capabilities of wider interest for microbial genome analysis.

Draft Genome Analysis

- As more bacterial genomes are being sequenced, a higher proportion of them are not being finished (becoming one high quality contiguous sequence).
- To accommodate this, IslandViewer now accepts draft genomes as input.

IslandViewer Features Overview

- Customizable genome plot can display different combinations of prediction methods and/or annotations.
- GI features are listed in more detail in this table (colour-coded by the prediction method), including the size of an island and the genes found in the island. Genes, proteins, and genomic sequences are available for download.

Pathogen-associated genes, which are present in genomes of multiple pathogen species but absent from non-pathogenic species, were generated using a set of 2783 finished genomes annotated as pathogenic or non-pathogenic.

Incorporation into IRIDA

- IRIDA (Integrated Rapid Infectious Disease Analysis, www.irida.ca): platform being developed to support real-time infectious disease outbreak investigation in Canada.
- Command line IslandViewer for custom analysis will be incorporated into IRIDA’s Galaxy platform.
- IRIDA will also incorporate:
  - Whole-genome sequence
  - Genotype
  - Virulence factors
  - Resistance gene and pathogen-associated gene annotations
  - Remaining tracks identify GI predictions and are clickable to highlight genes in hover box to the right.

Horizontal view of genome from which users can zoom in. The first two tracks are forward and reverse genes (clickable with overlapping virulence factor, resistance gene and pathogen-associated gene annotations). Remaining tracks identify GI predictions and are clickable to highlight genes in hover box to the right.

References


*New IslandViewer paper released in April!