The Jena Prokaryotic Genome Viewer – a new tool for exploring the universe of prokaryotic genomes

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Introduction

GenColors [1,2] is a new web-based software/database system aimed at an improved and accelerated annotation of prokaryotic genomes considering information on related genomes and making extensive use of genome comparison. It offers a seamless integration of data from ongoing sequencing projects and annotated genomic sequences obtained from GenBank. With GenColors dedicated genome browsers containing a group of related genomes can be easily set up and maintained. The tool has been efficiently used for Borella garrini [3,4] and is currently applied to various ongoing genome projects on Legionella, Pseudomonas and E. coli genomes. The GenColors-based Spirochetes Genome Browser is freely accessible at sgb.fli-leibniz.de. Another GenColors-based tool is the Jena Prokaryotic Genome Viewer (JPGV). Contrary to the dedicated browsers it offers information on almost all finished bacterial genomes. As of July 27, 2006 it includes 1140 genomic elements of 293 species. Due to this large number we were not yet able to generate precomputed data for all genome pairs that are required for specific genome comparison methods offered by the dedicated browsers such as the generation of gene core sets and their translation are displayed in the Basemap view.

In the central part of the sheet general gene information is provided. If the corresponding protein sequence is included in UniProt its description and all the external database links are also shown. The GenColors [5] annotation and comparative genomics of prokaryotic genomes at various stages of completeness, Bioinformatics 2005, 15, 3689-71.

The Jena Prokaryotic Genome Viewer

A brief description of the options offered by JPGV is available from the homepage.

Jena Prokaryotic Genome Viewer

Quicksearch | Genomes | Methods | Contacts | Options | Contact

The Jena Prokaryotic Genome Viewer (JPGV) is a freely accessible web tool aimed at visualization and analysis of prokaryotic genomes.

JPGV currently includes 1140 genomic elements of 293 species.

You can view JPGV on:

- GenColors dedicated genome browsers containing a group of related genomes can be easily set up and maintained. The tool has been efficiently used for Borella garrini [3,4] and is currently applied to various ongoing genome projects on Legionella, Pseudomonas and E. coli genomes. The GenColors-based Spirochetes Genome Browser is freely accessible at sgb.fli-leibniz.de. Another GenColors-based tool is the Jena Prokaryotic Genome Viewer (JPGV). Contrary to the dedicated browsers it offers information on almost all finished bacterial genomes. As of July 27, 2006 it includes 1140 genomic elements of 293 species. Due to this large number we were not yet able to generate precomputed data for all genome pairs that are required for specific genome comparison methods offered by the dedicated browsers such as the generation of gene core sets and their translation are displayed in the Basemap view.

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Gene information sheet

The most detailed information on a gene can be found on the Gene information sheets (Figure 5). These sheets start on top with a Gene environment graph. The DNA bases of both strands and their sequence are displayed in the Basemap view.

Horizontal gene transfer

Horizontal gene transfer (HGT) is an important evolutionary mechanism in bacterial genomes. In JPGV horizontally transferred genes are predicted with the program SIGI-HMM [5]. In addition to the SIGI-HMM results related information such as GC-content, presence of mobility islands and tRNAs is offered. The data can be displayed both in tabular form and as clickable global genome representations (Figure 6).

Genome plots

JPGV generates circular and linear genome plots (PNG, PDF, Postscript) using annotation data and calculating quantities such as GC-content, GC-skew and purine and keto excess. Different features of one or more genomes can be displayed in one representation facilitating comparative analysis.

Outlook

The current work is primarily aimed at the improvement and extension of genome comparison options in JPGV that are already operating in dedicated browsers. We are also working on an improved analysis of intergenic regions, the incorporation of alternative prediction methods for horizontal gene transfer and the analysis of microRNAs.

References