As of 2010, more than 1000 bacterial and archaeal genomes are available in public databases, making the number of possible comparisons almost infinite. Several programs such as Artemis Comparison Tool (ACT; Carver et al., 2005), UCSC Genome Browser (Rhead et al., 2010), Mauve (Darling et al., 2004), and Murasaki (Sakakibara et al., 2004), have extensive visualization functions. However, these tools lack the ability to directly add annotations to the publication quality graphics they produce or to fully automate the production of comparative figures. GenomeGraphs (Durinck et al., 2009) is a R package, which allows the visualization of one genomic region with related datasets such as microarray data. It can display several annotations for the same region, but it cannot show several regions in a single plot. The R package genoPlotR is an attempt to fill in those gaps by providing a flexible, automatable tool. It allows the user to graphically represent the comparison between several segments or subsegments of genomes in a linear fashion. It reads data stored in commonly used formats (EMBL, Genbank, BLAST and Mauve outputs) or in user-created tabular files and allows comparisons of one or several subsegments of a genome. A tree can be added to show the phylogenetic relationships between the segments, as can also scales and annotations to each subsegment. The use of R (R Development Core Team, 2009) and its grid package enables the use of its graphical power and flexibility to manipulate data and to integrate gene and genome maps into more complex graphics. The results can be saved either in high-quality raster or vector formats for further editing.

2 INPUT DATA

The R package genoPlotR reads comparison objects using the tabular output of, e.g. BLAST (Altschul et al., 1990) or from user-generated tabular files (Fig. 1A). Hit tables in text format produced by stand-alone or online BLAST programs are suitable for input in genoPlotR. For example, from the NCBI BLAST web page, sequence alignments of genes and genomes can be produced with the option ‘align two or more sequences’. The hit table can then be downloaded. The backbone file produced by Mauve, a multiple-genome alignment tool (Darling et al., 2004), can be transformed into both dna_seg and comparison objects (Fig. 1B).

Both dna_seg and comparison objects can be filtered either by using arguments to the reading functions, or by using R functions, for example, to remove short genes or low-significance comparisons. Objects can be modified to specify color, size or appearance (arrows, lines, etc.) for each element of the DNA segments and of the backbone file produced by Mauve, a multiple-genome alignment tool (Darling et al., 2004), can be transformed into both dna_seg and comparison objects (Fig. 1B).

3 VISUALIZATION

After being read and modified, objects can be passed to the main graphical function plot_gene_map.

The user can define, for each segment, several subsegments that will be represented in the plot. These subsegments can be represented in reverse orientation (e.g. see Fig. 1B, first subsegment on the top DNA segment). The placement of each subsegment on the plot is either automatically determined by minimizing the area of the comparison...
Fig. 1. Examples of gene and genome comparisons with genoPlotR. The code used to generate this figure is available at http://genoplotr.r-forge.r-project.org/screenshots.php. 

(A) Example of minimal code to represent a three-way comparison in genoPlotR. 

(B) Comparison of four *Bartonella* genomes using the backbone output of Mauve. The features are colored according to their order along the second segment (BG), following a rainbow palette. 

(C) BLAST comparison of genes in several subsegments of the same four *Bartonella* genomes. Note the scale of the first subsegment on the top row, which is in reverse orientation. 

(D) Comparison of a 220 kb segment of the Y chromosome in *Homo sapiens* and *Pan troglodytes*. In (C and D), the E-value of the BLAST alignment is represented with shades of blue and red. All datasets used here are present in the package.

**4 CONCLUSIONS**

By using the graphical power and flexibility of R, the package genoPlotR generates reproducible maps of genes and genomes that can be used to generate publication-ready figures, starting from a wide range of formats. Since all the instructions for drawing the figures are contained in R code, it is highly flexible, and thus it is straightforward to automate the process of drawing very similar figures for different datasets. The use of a scripting language makes it particularly suitable for integration into annotation and comparative genomics pipelines.

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