svist4get: a simple visualization tool for genomic tracks from RNA-Seq, Ribo-Seq and other high-throughput sequencing data

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High-throughput sequencing acts as a major data provider for life sciences. Many experimental protocols involving high-throughput sequencing produce signal tracks of genomic coverage estimated from read mapping to a known genome assembly. There are many tools for visualizing genomic tracks, from interactive genomic browsers to R packages for programmatic generation of images. We present svist4get [1], console-based tool for visualization of genomic signal tracks in user-defined genomic windows, either arbitrary selected by genomic coordinates or anchored to particular transcripts or genes. We illustrate svist4get usage in [2], where figures were produced with svist4get Python API.

Svist4get is implemented in Python 3 and runs on Linux. It is able to generate both vector and high-resolution bitmap images, and is highly customizable through command-line parameters and configuration files.

Project homepage: https://bitbucket.org/artegorov/svist4get