Genome analysis

GSDS 2.0: an upgraded gene feature visualization server

Bo Hu1,2,†, Jinpu Jin1,†, An-Yuan Guo3, He Zhang1, Jingchu Luo1 and Ge Gao1,*

1State Key Laboratory of Protein and Plant Gene Research, College of Life Sciences, Center for Bioinformatics, Peking University, Beijing 100871, People’s Republic of China, 2College of Life Science, Beijing Normal University, Beijing 100875, People’s Republic of China and 3Department of Systems Biology, College of Life Science and Technology, Huazhong University of Science and Technology, Wuhan 430074, People’s Republic of China

*To whom correspondence should be addressed.
†The authors wish it to be known that, in their opinion, the first 2 authors should be regarded as Joint First Authors.

Abstract

Summary: Visualizing genes’ structure and annotated features helps biologists to investigate their function and evolution intuitively. The Gene Structure Display Server (GSDS) has been widely used by more than 60 000 users since its first publication in 2007. Here, we reported the upgraded GSDS 2.0 with a newly designed interface, supports for more types of annotation features and formats, as well as an integrated visual editor for editing the generated figure. Moreover, a user-specified phylogenetic tree can be added to facilitate further evolutionary analysis. The full source code is also available for downloading.

Availability and implementation: Web server and source code are freely available at http://gsds.cbi.pku.edu.cn.

Contact: gaog@mail.cbi.pku.edu.cn or gsds@mail.cbi.pku.edu.cn

Supplementary information: Supplementary data are available at Bioinformatics online.

1 Introduction

The visualization of gene features such as composition and position of exons and introns for genes offers visual presentation for biologists to integrate annotation, and also helps them to produce high-quality figures for publication. Thus, several web servers/software including FancyGene (Rambaldi and Ciccarelli, 2009), GECA (Fawal et al., 2012), FeatureStack (Frech et al., 2012), GSDraw (Wang et al., 2013), GPViz (Snajder et al., 2013) and GenePainter (Hammesfahr et al., 2013) have been developed recently. Designing to generate high-quality figures suitable for publication, we developed an online Gene Structure Display Server (GSDS) (Guo et al., 2007), which supported three input formats including sequences, accession number of GenBank (Benson et al., 2013) and exon positions. With more than 1 million hits annually, GSDS has been widely used by world-wide scientists in the functional (Ye et al., 2009; Wang et al., 2010) and evolutionary study (Hu et al., 2010; Yin et al., 2009; Yu et al., 2009) of gene families.

According to the feedbacks from GSDS users, we developed the upgraded GSDS 2.0. Compared with the previous version, GSDS 2.0 supports two more widely used annotation formats, providing more comprehensive support for annotation files. To aid biologists generating suitable figures for publication, GSDS 2.0 offers a powerful interactive interface. Users can customize the size, shape and color of annotation features after their initial render and even fine-tune each element through an integrated visual editor. To facilitate evolutionary analysis, a user-specified phylogenetic tree can be added to the figure. Finally, the generated figure can be exported as either vector graphic (in SVG and PDF format), or raster graphic (in PNG format).
We have updated our GSDS to version 2.0, which supports more types of features and feature describing formats, as well as further modification on the generated figures. By analyzing the usage of GSDS and feedbacks from users, we will continue our efforts to update GSDS to better serve this community.

### 3 Further directions

We have updated our GSDS to version 2.0, which supports more types of features and feature describing formats, as well as further modification on the generated figures. By analyzing the usage of GSDS and feedbacks from users, we will continue our efforts to update GSDS to better serve this community.

### Acknowledgement

We thank all comments from users of GSDS 1.0 and the developers of SVG-edit tool.

### Funding

This work was supported by the China National 973 Program [2011CBA01103]; 863 Programs [2006AA02Z334, 2007AA02Z165]; and the State Key Laboratory of Protein and Plant Gene Research. The research of G.G. was supported in part by the National Outstanding Youth Talent Initiative Program. J.J. was supported partly by the China Postdoctoral Science Foundation Grant [2014M560017].

Conflict of Interest: none declared.

### References

Benson, D.A. et al. (2013) GenBank. *Nucleic Acids Res.*, 41, D36–42.

Fawal, N. et al. (2012) GECA: a fast tool for gene evolution and conservation analysis in eukaryotic protein families. *Bioinformatics*, 28, 1398–1399.

Frech, C. et al. (2012) FeatureStack: perl module for comparative visualization of gene features. *Bioinformatics*, 28, 3137–3138.

Guo, A.Y. et al. (2007) GSDS: a gene structure display server. *Yi Chuan*, 29, 1023–1026.

Hamesfahr, B. et al. (2013) GenePainter: a fast tool for aligning gene structures of eukaryotic protein families, visualizing the alignments and mapping gene structures onto protein structures. *BMC Bioinformatics*, 14, 77.

Hu, R. et al. (2010) Comprehensive analysis of NAC domain transcription factor gene family in *Populus trichocarpa*. *BMC Plant Biol.*, 10, 145.

Rambaldi, D. and Ciccarelli, F.D. (2009) FancyGene: dynamic visualization of gene structures and protein domain architectures on genomic loci. *Bioinformatics*, 25, 2281–2282.

Snajder, R. et al. (2013) GPViz: dynamic visualization of genomic regions and variants affecting protein domains. *Bioinformatics*, 29, 2195–2196.

Wang, S. et al. (2010) Auxin-related gene families in abiotic stress response in *Sorghum bicolor*. *Funct. Integr. Genomics*, 10, 533–546.

Wang, Y. et al. (2013) PIECE: a database for plant gene structure comparison and evolution. *Nucleic Acids Res.*, 41, D1159–1166.

Ye, H. et al. (2009) Identification and expression profiling analysis of TIFY family genes involved in stress and phytohormone responses in rice. *Plant Mol. Biol.*, 71, 291–305.

Yin, Y. et al. (2009) The cellulose synthase superfamily in fully sequenced plants and algae. *BMC Plant Biol*, 9, 99.

Yu, X.H. et al. (2009) BAHD superfamily of acyl-CoA dependent acyltransferases in Populus and Arabidopsis: bioinformatics and gene expression. *Plant Mol. Biol.*, 70, 421–442.