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CS 199

March 23, 2019

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In this paper, the researchers present web version of AUGUSTUS. This web version is similar to the original AUGUTUS that was developed previously and allows the user to add constraints. Such constraints allow user to enforce alternative splice prediction and identify intron from RT-PCR. AUGUSTUS can be utilized for four different species: Homo Sapiens, Drosophila melanogaster, Arabidopsis thaliana and Brugia malayi. Web version of AUGUSTUS use same constraints that are used in the original AUGUSTUS. There are some restrictions on predicted gene structure, as gene structure must have exon without in-frame stop codon, splice site that obeys gt-ag consensus, gene ending before next gene start and exon and intron whose length do not exceed species dependent minimal level.

The web version takes DNA as input and uses GFF format for constraints. The user has an option to restrict predicted gene structure to be one complete gene or to be any number of complete genes. The user can also lift some of restrictions on predicted gene structure. Output shows predicted protein coding gene sequence and amino acid sequence. It also shows the start and end position of exon, along with its name, type of strand and length.

References

1. Stanke, M., Morgenstern, B. (2005). AUGUSTUS: a web server for gene prediction in eukaryotes that allows user-defined constraints*. Nucleic Acids Research.* Volume 33. 465-467.