

A Distributed Annotation System Client

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Abstract

The pace of genomic sequencing has outstripped the ability of sequencing centers to annotate and understand the sequence prior to submitting it to the archival databases. Multiple third-party groups have stepped into the breach and are currently annotating genomic sequence with a combination of computational and experimental methods. But this fractures knowledge about the genome: researchers may have to check multiple Web sites for information about a particular region of interest, download the data in several different formats, and perform a manual integration in order to get the whole picture. The solution to this problem that we advocate allows sequence annotation to be decentralized among multiple third-party annotators and integrated on an as-needed basis by client-side software.

The client software is a web browser like application which allows a researcher to query one or more annotation servers to retrieve features in a region of interest within a genome. Servers respond to a defined set of queries and return data in a structured XML format (server specification is available at: <http://stein.cshl.org/das/>). The client then displays graphical maps of the resulting data. The client is Java based and utilizes the Neomorphic Genome Software Development Kit.