Sequence analysis

**DASher: a stand-alone protein sequence client for DAS, the Distributed Annotation System**

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**ABSTRACT**

Summary: The rise in biological sequence data has led to a proliferation of separate, specialized databases. While there is great value in having many independent annotations, it is critical that there be a way to integrate them in one combined view. The Distributed Annotation System (DAS) was developed for that very purpose. There are currently no DAS clients that are open source, specialized for aggregating and comparing protein sequence annotation, and that can run as a self-contained application outside of a web browser. The speed, flexibility and extensibility that come with a stand-alone application motivated us to create DASher, an open-source Java DAS client. Given a UniProt sequence identifier, DASher automatically queries the DAS Registry for all active and validated servers which can limit their flexibility.

Several DAS clients are available: SPICE (Prlic et al., 2005), CARGO (Cases et al., 2007), DASMI (http://dasmi.bioinf.mpi-inf.mpg.de/), Jalview (Clamp et al., 2004), PeppeR (http://bioscomp.cnb.uam.es/das/PeppeR/), IGB (http://genoviz.sourceforge.net/), Pfam (Finn et al., 2008), MaDas (http://madas.bioinfo.cnio.es), Dasty2 (http://www.ebi.ac.uk/dasty) and Ensembl protview (Binney et al., 2006). However, only Dasty2, Ensembl and Pfam are focused on protein sequence annotation, yet run in a web browser rather than as a separate application, which can limit their flexibility.

Here we introduce DASher, a lightweight, stand-alone Java DAS client optimized for viewing protein sequence features. As a stand-alone application, DASher offers advantages in responsiveness and interactivity. For example, users can zoom in on a region, and zoom-dependent sequence rendering displays residues automatically at a sufficiently high zoom level. Also, users have full control to customize the appearance of the data being displayed.

**1 INTRODUCTION**

Biological data are accumulated and provided by a large number of laboratories across the world. As a result, today we have hundreds of different web sites with different interfaces and little integration among them. Researchers wanting to compare annotations from disparate sources, even those that relate to the same sequence, must aggregate those annotations themselves, and this is typically a manual, tedious and time-consuming process.

The Distributed Annotation System (DAS) was developed to overcome these problems by creating a standard protocol by which source databases could serve and client programs could access biological sequences and annotations (Dowell et al., 2001). By doing so, DAS establishes two huge advantages over the previous system: (i) DAS creates a standard way to access data, so all sources which comply with that standard can be viewed with the same software, and additional sources can be added effortlessly; (ii) DAS separates the databases responsible for serving data from the software which shows those data to the end user, so the software can be specialized for particular needs, and users can choose whichever way of looking at that data they feel is best.

Since its inception the DAS universe has grown broadly. There are different flavors of DAS suited to sequence, structure and protein interaction annotation. The DAS server registry allows users to view DAS-compliant data sources both manually through the web site and automatically through software (Prlic et al., 2007). Several DAS clients are available: SPICE (Prlic et al., 2005), CARGO (Cases et al., 2007), DASMI (http://dasmi.bioinf.mpi-inf.mpg.de/), Jalview (Clamp et al., 2004), PeppeR (http://bioscomp.cnb.uam.es/das/PeppeR/), IGB (http://genoviz.sourceforge.net/), Pfam (Finn et al., 2008), MaDas (http://madas.bioinfo.cnio.es), Dasty2 (http://www.ebi.ac.uk/dasty) and Ensembl protview (Binney et al., 2006). However, only Dasty2, Ensembl and Pfam are focused on protein sequence annotation, yet run in a web browser rather than as a separate application, which can limit their flexibility.

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**2 OVERVIEW**

**2.1 Implementation**

DASher is written in the object-oriented, platform-independent programming language Java (http://java.sun.com). It is based on the Sfixem platform (Chalk et al., 2004) and uses the Dasobert library to handle DAS stream input and output (http://www.spice-3d.org/dasobert/). DASher has been tested and runs on Apple OS X, Windows XP and GNU/Linux operating systems.

One-click installation is available via Java Web Start from the DASher website. DASher is licensed under the GNU General Public Licence.

**2.2 User interface**

To see annotations for a protein, the user enters a UniProt name or accession number in the search box. DASher automatically queries the DAS Registry for all active and validated servers which
Fig. 1. The DASher main window. When a UniProt identifier is entered in the top left box, DASher fetches annotations from relevant DAS servers which are each displayed on a separate row, color-coded by feature type. In this example, we analyze the transmembrane topology of a largely unclassified human protein. Yellow denotes cytoplasmic regions; white, non-cytoplasmic regions; and brown, transmembrane regions. Tracks from top to bottom are the query sequence, UniProt, three transmembrane topology predictors, Kyte-Doolittle hydrophobicity (blue) and predicted solvent accessibility (green).

We have developed DASher to provide a lightweight, stand-alone DAS client application specialized for comparing protein sequence annotations quickly and easily. DASher is compliant with the latest DAS specification 1.53E (Jenkinson et al., 2008) and is freely available as open source.

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Conflict of Interest: none declared.

REFERENCES
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