Sfixem—graphical sequence feature display in Java

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ABSTRACT
Summary: Sfixem is an sequence feature series (SFS) visualization tool implemented in Java. It is designed to visualize data from sequence analysis programs, allowing the user to view multiple sets of computationally generated analysis to assist the analysis process. SFS is used as the data exchange format.

Availability: Sfixem is available for direct usage or download for local usage at http://sfixem.cgb.ki.se. A protein sequence analysis workbench using Sfixem is available at http://sfinx.cgb.ki.se.

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INTRODUCTION
Sequence analysis can be greatly improved by using graphical tools. Such tools allow expert human interpretation of algorithmic analysis, often from multiple sources. Having all the relevant data and analysis output available in a graphical form simplifies the analysis process, increasing the reliability of human interpretation.

Several systems exist that can be used for sequence segment display. Most of these are integrated systems that are fairly large, often involving substantial frameworks for complex data types. These systems include ChromoScope (Zhang et al., 1994), bioWigets (Searls, 1995), APIC (Bisson and Garreau, 1995), the BDGP java sequence viewer (Rubin, 1996), GAIA (Bailey et al., 1998), ACEDB (Eeckman and Durbin, 1999) and Artemis (Rutherford et al., 2000). We consider the investment of time required to generate and parse complex data types (e.g. ASN.1) excessive, and for the data we display (segments and curves), a simple tabular format is sufficient. We therefore use the sequence feature series (SFS) format (Sonnhammer and Wootton, 2001), which we briefly describe below. To make Sfixem more useful, we plan to make it compatible with data standards, such as DAS and XML in the future.

Two existing viewers that handle curves and segment data using SFS are Blixem (Sonnhammer and Durbin, 1994) and Dotter (Sonnhammer and Durbin, 1995). Both tools were primarily designed to display specialized sequence analysis data, with added SFS viewing functionality. A disadvantage with these and many other tools is the need to install the software locally. Local software installation, while trivial, is often a factor in tools being under-utilized by the biological community. Reasons for this can be lack of administrator rights on the machine, operating system incompatibility or simply reluctance to install external software.

SFIXEM
The visualization tool Sfixem was designed to visualize curve and segment data relating to a single sequence, considering SFS format data as input from any sequence analysis tool. In contrast to Blixem and Dotter, where SFS display capabilities were added to existing specialized analysis tools, Sfixem was written from scratch with generalized SFS display as the single purpose. It is hence a cleaner implementation and more ergonomic to use. The implementation as a Java applet removes the need to install the program locally, the applet requires the Java 2 Runtime Environment version 1.4.

The viewer has zoom functionality with variable amount of detail shown (i.e. coloured boxes or individual residues) dependent on zoom level. The user can get an overall view and zoom in on areas of interest to examine details at the single residue level. For segments, the residues will be shown in the coloured boxes when zoomed into sufficient detail. Additional functionality includes a series picker—allowing the user to select only a subset of the full amount of analysis data to view, and the modification of curve and the segment height.

DATA FORMAT
The SFS data format contains two primary data types that are used by most prediction programs: segments and curves. The segment type is similar to the popular GFF format (http://www.sanger.ac.uk/Software/formats/GFF/); GFF format can in fact be embedded in the SFS data. However, SFS also allows other types of data, for instance for drawing curves which is

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often more illustrative rather than segments. There is also a
native support for passing the sequence itself in the SFS file,
which is useful for many visualization tasks. The simplicity
of the SFS format minimizes the overhead for both the analysis
software and the visualization tool to achieve graphical and
user-friendly display of results. A full specification of the SFS
format is given in Sonnhammer and Wootton (2001) and on
the Sfixem website (see Availability). We here include a brief
description on some definitions in SFS to illustrate the basic
features. The SFS data are in Courier font. Data fields enclosed
by ‘<’ must be single words, while data fields enclosed by
’[]’ may consist of multiple words.

**Header**

```
# SFS format 1.0
```

**Sequence data**

```
# SFS type SEQ <sequence> <seqname> [annotation]
```

**Segment data**

```
# SFS type SEG
<score><seqname><seriesname>
=start><end> <look> [annotation]
```

**XY data (curves)**

```
# SFS type=XY <seqname> <seriesname>
<look> [annotation]
<x-value> <y-value>
<x-value> <y-value>
```

**HSP data**

```
# SFS type=HSP
<score><qname><qframe><qstart><qend>
<sname><sframe><sstart><send>
<sequence>
```

An example of Sfixem usage is shown in Figure 1,
in which a collection of transmembrane (TM) topo-
logy, signal peptide, and structure predictions for
GAA4_BOVIN (Swissprot:P20237) are viewed, along
with homology matches (produced by the Sfinx server,
http://sfinx.cgb.ki.se). Visualizing collections of predictions
from different algorithms allows the user to make a more
informed decision based on all available data. For instance, it
is quite clear that the PhD and Memsat predictions are missing
internal TM segments in this case, and that the N-terminal TM
segment predicted by most methods is really a signal peptide.
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REFERENCES


