W2H: a WWW Interface to Applications in Bioinformatics

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The availability of World-Wide-Web browsers for many computer systems made it possible to develop platform-independent graphical user interfaces for command-line-driven UNIX applications. We followed this trend with our development of a WWW-interface for the widely used GCG sequence analysis package and its derived systems like HUSAR. Using HTML-forms together with JavaScript on the client side and the Perl programming language on the server side, it is possible to achieve fast access and a high level of portability. Security requirements concerning the data flow via networks (e.g. Internet) are fulfilled by using Secure Socket Layer (SSL) encrypted HTTP data streams.

Instead of creating individual interfaces for each application, we decided to employ meta-data. This enables the administrator to add new applications by simply writing a new meta-data file containing the application-specific configurations. Additionally, this strategy results in a common graphical user interface for all applications.

The current W2H implementation comprises

- different user levels: a “Simple Mode” for beginners and an “Advanced Mode” with full functionality for experienced users,
- a graphical data manager for UNIX directories and files,
- a converter for graphical application output into standard Web formats,
- support for the separation of different user projects,
- support for site-dependent post-processors on application results (cross-linker to SRS included).

At the moment W2H is mostly adapted to the GCG system but non-GCG command-line applications can be incorporated by using the meta-data mechanism of W2H. W2H can be adopted to any other command-line driven system with only minor modifications.

We are currently extending the meta-data mechanism of W2H, not only to describe interfaces to individual applications but also to complete tasks. In this context a task is understood to be a chain or even a network of applications together with its data flow. To achieve this, a mechanism is needed which describes the control- and data-flow within one task. Meta-data for such tasks will not only contain parameters of single applications, but also dependency and incompatibility rules for the interrelationship between different applications belonging to the same task.

W2H is freely available on the World Wide Web:

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http://genome.dkfz-heidelberg.de/w2h/ (Germany)
http://industry.ebi.ac.uk/w2h/        (UK)
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Reference: M.Senger, T.Flores, K.-H. Glatting, P. Ernst, A. Hotz-Wagenblatt, S. Suhai (1998) *W2H: WWW interface to the GCG sequence analysis package*, Bioinformatics, 14, 452-457