

## **Bridging Existing Bioinformatics Resources Into the Semantic Web**

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We have identified the need for, and built, client-side software (“Seahawk”) in Bioinformatics that facilitates the *ad hoc* composition of Semantic Web Services (SWS) by biologists. Through user studies, we have also identified the unavailability of existing services from trusted sources as a barrier to adoption of SWS by biologists. We explore how to make the range of tools biologists already use conform to an established SWS protocol in the Life Sciences (BioMoby). We attack the problem of wrapping existing software with a semantic layer from three perspectives: 1) legacy data format conversion (both to and from), 2) semantic annotation of software interfaces and 3) end-user programming/wrapping for widespread adoption.

For service provision, we present a suite of four SWS wrapping tools that build on one another to cover a wide spectrum of semantic wrapping scenarios, namely 1) Java-language servlet annotation, 2) command-line bioinformatics tool annotation, 3) WSDL Web Services annotation, and 4) HTML/CGI form annotation (in progress at time of writing). Guiding principles behind the design of these tools are to distribute the wrapping work appropriately between those who are most motivated to use them, and those who can specify the annotations best. Code re-use is also strongly emphasized.

For service usage and basic workflow construction, we present the applet Seahawk, which provides a hypertext interface to BioMoby services, and workflow-by-example capabilities (reusable in the Taverna workflow engine) that provide a gentle learning curve for large-scale analysis by biologists without the assistance of a bioinformatician.

The software (“Daggoo”) and its source code can be found on the Java developer’s homepage of the BioMoby Web site ([www.biomoby.org](http://www.biomoby.org)). Like all BioMoby repository code, tools mentioned are available under the terms of the Perl Artistic License.