

# A Composition Designer for Bioinformatics Web Services

Zhiming Wang, John A. Miller, Jessica C. Kissinger,  
Rui Wang, Douglas Brewer, Cristina Aurrecoechea  
*University of Georgia, Athens, GA, 30602*

*{zhiming@cs., jam@cs., jkissing@, very@, twisted@, aurreco@}uga.edu*

With the advances in technology and computational approaches, the quantity of biological data is increasing explosively. How biologists share data and analytical tools efficiently is becoming a fundamental issue. One of the promising technologies to handle this challenge is Web service technology. Web services provide advanced data-sharing features such as language independence, platform independence and ease of programmatic access. Given the increasing prevalence of Web services that access biological data from multiple different locations and databases, we have seen an increasing interest in biological Web services composition in order to generate an analysis pipeline to perform a bioinformatics task. Although there are some research efforts towards composing biological Web services, such as BioMoby and Taverna, the challenge these tools face is that they are still too difficult to be widely used by the average biologist. Therefore, lowering the learning curve for Web service composition is becoming a critical need. With this objective in mind, we introduce WS-BioZard, a comprehensive framework that addresses this need by using graphical wizards and a semantic framework to provide a suite of tools that support practical semi-automatic composition of Web services in the biological domain.

The architecture of WS-BioZard includes a Semantic Process block (service annotation, and service registration), a Model block (semantic engine, BPEL model, editor externalization) and a User Interface block (service discovery and service composition). Multiple technologies are used in our framework to lower the complexity of service composition. First, Web services are annotated with Radiant using Semantic Annotation for WSDL (SAWSDL), and then registered in a semantic UDDI registry to assist service discovery and data mediation. Web service semantic annotation and registration is a fundamental task that is required prior to the user performing Web service discovery and composition. Our framework provides a design and implementation to facilitate service providers to accomplish this task. Second, a semantic Web service discovery tool is implemented to help biologists discover and browse the available services. Third, a multi-faceted wizard is used in a friendly and intuitive Web services composition editor to assist the user. This wizard acts like an assistant and can hide most of BPEL's complexity from the user. Furthermore, with the help of the METEOR-S Discovery API and a new algorithm (Data Mapping Algorithm) that we have developed, the wizard can help users achieve data mediation (a process used to convert data format from service provider to service consumer), which is an important challenge in the biological Web service composition. These tools permit users to rapidly compose Web services and store the composition persistently in BPEL format, a business language accepted and supported by industry. The BPEL composition can then be executed in a standard BPEL engine and the composition itself is a standard Web service that can be reused by other applications or Web services.