NUCLEIC ACIDS RESEARCH ANNUAL WEB SERVER ISSUE IN 2011

The 2011 Web Server Issue of *Nucleic Acids Research* is the ninth in a series of annual special issues dedicated to web-based software resources for analysis and visualization of molecular biology data. It is freely available online under NAR's open access policy. The present issue reports on 92 web servers.

Topics

This year’s special emphasis is on next-generation sequencing data analysis, molecular network and pathway analysis, and biological text mining. A total of 16 papers deal with these topics. The major categories of papers cover analysis involving DNA and RNA (17 papers); protein structure, docking and functional site prediction (19 papers); gene enrichment, gene function annotation and protein function annotation (13 papers); and alignment and homology search (9 papers).

The 2011 Web Server issue continues two special sections, one for stand-alone programs that analyze high-throughput data, such as next-generation sequencing data and one for large collections of popular web services for automated analyses that can be utilized programmatically rather than through manual interaction with a web browser. Seven papers fall in these categories.

Also included is the Bioinformatics Links Directory 2011 update by Michelle Brazas, Francis Ouellette and their colleagues at the Ontario Institute for Cancer Research. The directory, at http://bioinformatics.ca/links_directory, is a searchable compilation of web servers published in this and previous Web Server issues together with other useful tools, databases and resources for life sciences research.

Special note on the tsunami in Japan

The tragic March 11 tsunami which devastated the northeast coast of Japan and the resulting nuclear catastrophe at the Fukushima Dai-ichi nuclear power plant have had a major impact on the Japanese nation, and our scientific colleagues there. We wish them well and hope that they and their loved ones remain safe and unharmed. The resulting blackouts of electrical power and network disruptions caused significant difficulties for authors and reviewers located in Japan and required that several authors arrange alternative web sites for their servers. I admire their fortitude and resiliency in the face of this overwhelming tragedy.

Instructions for submissions

To streamline the review process, authors are required to send a one-page summary of their web server to the editor, Dr Gary Benson (narwbsrv@bu.edu), for pre-approval prior to manuscript submission. For the 2011 issue, 297 summaries were submitted and 135, or 45%, were approved for manuscript submission. Of those approved, 92, or 68%, were ultimately accepted for publication.

Review of a summary includes evaluation of the proposal and extensive testing of web server functionality. The key criteria for pre-approval are high scientific quality, wide interest, the ability to do computations on user-submitted data and a well designed, well implemented and fully functional web site. Note that there is a minimum 2-year interval before publication in the Web Server issue for web servers, or essentially similar web servers, that have been the subject of a previous publication, including publication in journals other than *NAR*.

With respect to the web site, the following are guidelines for approval.

(i) It should have an easy-to-find submission page with a simple mechanism for loading test data and setting test parameters. The preferred method is one-click loading. Additional mechanisms that assist the user in submitting data should be implemented where appropriate, for example, automatic download of a pdb structure file once the user has entered the appropriate identifier.

(ii) Output should be dynamic and rich in detail. Wherever possible, supporting evidence used in calculations and/or links to external databases containing additional information should be provided. Numerical, textual and visual output should be mixed and any visualization tools that add information or increase the user’s understanding should be utilized (for example, the java plug-in tools jmol for structure visualization and jalview for sequence alignment visualization). Note that output that consists merely of a few numerical values, a static spreadsheet or a series of files to be opened in other programs will not be approved.

(iii) Web servers that do not finish their calculations immediately must implement a mechanism for returning results to the user. Notification by email may be provided as an option, but an alternative that returns a web link at the time of data submission, which the user can then bookmark and access at a later time, is required. This link
should ideally report the status of the job (queued, running, finished). Note that uploaded data and the results of analysis for each user must be private and not viewable by other users.

(iv) The web site should be supported by an extensive help section or tutorial that guides the user through the submission process, contains details about input file formats and parameters and, importantly, explains the meaning of the output. Whenever possible, the help pages should link to dynamic output examples similar to those provided by the web site.

(v) Any proposal for a web server that is ‘predictive’ must include details on validation of predictions from new data not used in training. N-fold cross-validation methods will not be considered sufficient. Details should include size and composition of the validation data set (number of positive and negative cases) and several measures of predictive performance, including sensitivity, specificity and precision. Proposals are regularly rejected for lack of adequate prediction validation information.

(vi) Web sites not clearly designed to accept and analyze user-submitted data will be rejected. This applies to those established primarily for lookup or exploration in a data set or serve the function of ‘data aggregators’. Authors of web sites that provide novel data should consider the NAR Database Issue as a possible venue (see the instructions at http://www.oxfordjournals.org/our_journals/nar/for_authors/msprep_database.html).

(vii) Proposals that describe a novel analysis method are generally not appropriate for the Web Server issue because limited space makes adequate method description and validation problematic. Authors of such methods might instead consider sending their manuscript to NAR as a regular computational biology paper (see the instructions for authors at http://www.oxfordjournals.org/our_journals/nar/for_authors/criteria_scope.html#Computational%20Biology).

Special emphasis for 2011

For the 2011 issue, the topics of special emphasis will be the analysis of next-generation sequencing data, including read mapping and genetic variation detectors; network and pathway analysis; and biological text mining.

Deadlines for 2012

Authors wishing to submit manuscripts for the 2012 Web Server issue must submit their one-page proposal along with the URL address of the fully functional web site to narwbsrv@bu.edu by 31 December 2011. Detailed instructions and requirements are presented at http://www.oxfordjournals.org/nar/for_authors/submission_webserver.html. This information should be consulted before sending in the summary. The deadline for submission of articles is 31 January 2012.

Requirement for references links

Manuscripts submitted for the 2012 issue must format their References section to include active links to electronic versions of the cited papers, including links to PubMed, PubMed Central and a DOI link. Instructions for incorporating these links into the manuscript are presented at http://www.oxfordjournals.org/nar/for_authors/submission_webserver.html.

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Gary Benson
Executive Editor
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