Office of Science
Financial Assistance
Funding Opportunity Announcement
DE-FOA-0000143

Computational Biology and Bioinformatic Methods to Enable a Systems Biology Knowledgebase

SUMMARY:

The Office of Biological and Environmental Research (BER) of the Office of Science (SC), U.S. Department of Energy (DOE) advances world-class biological and environmental research and provides scientific facilities to support DOE missions in scientific discovery and innovation, energy security, and environmental responsibility. BER hereby announces its interest in receiving applications for potential funding of computational biology and bioinformatic methods and analytics to enable the planned Systems Biology Knowledgebase. The goal of systems biology is to understand living systems, a simple microbe or a complex ecosystem, so well that we can develop predictive, computational models of the systems that "behave" the same way as the living system. Such predictive models would enable scientists to accurately predict an organism's or a more complex system's behavior.

DOE and the Biological Systems Science Division (BSSD) have made significant investments in large scale genome sequencing and systems biology research on the capabilities of plants and microbes to provide breakthrough technologies for biofuel production, carbon biosequestration and waste cleanup. This work has produced petabytes of scattered data and information, much of which is in decentralized archives and databases that are inaccessible to the larger research community. Scientific progress in bioenergy, biogeochemistry and the carbon cycle missions will require much greater access to this information by the entire research community. To address this challenge, a Systems Biology Knowledgebase (Knowledgebase) will be developed in the near future. This will serve as a foundation on which scientists can integrate modeling, simulation, experimentation, and bioinformatics. It will not only give scientists free and broad access to diverse data types but will also provide sophisticated tools for data analysis, visualization, and integration.

This funding will lead to the development of new computational biology and bioinformatic methods and analytics to enable the Systems Biology Knowledgebase. There are four objectives that may be addressed by applicants responding to this FOA: (1) develop methods to integrate together multiple data types, (2) develop new methods to infer and curate (meta)genomic functional annotations (3) develop methods to couple multiple cellular pathways and processes and (4) develop new methods to model whole cellular processes.

Preapplication

Potential applicants are **required** to submit a brief preapplication, referencing Funding Opportunity Announcement DE-FOA-0000143 for receipt by **DOE by 4:30 p.m., Eastern Time, November 5, 2009.**

Preapplications are limited to **three pages total**, including cover page. Preapplications should be sent as a single PDF file attachment via e-mail to: **SBKBioinformatics@science.doe.gov** with **"Preapplication DE-FOA-0000143"** as the subject. No FAX or mail submission of preapplications will be accepted.

Potential applicants must submit a brief preapplication that consists of **three pages** of narrative describing the research objectives, the technical approach(s), and the proposed team members and their expertise. The intent in requesting a preapplication is to save the time and effort of applicants in preparing and submitting a formal project application that may be inappropriate for the program. Preapplications will be reviewed relative to the scope and research needs as outlined in the summary paragraph and in the SUPPLEMENTARY INFORMATION. The preapplication should identify, on the cover sheet, the title of the project, the institution or organization, principal investigator(s) name(s), telephone number, fax number, and e-mail address. No budget information or biographical data need be included, nor is an institutional endorsement necessary.

Preapplications will be reviewed for conformance with the guidelines presented in this solicitation and suitability in the technical areas specified in this solicitation. A response to the preapplications encouraging or discouraging formal applications will be communicated to the applicants by **November 23, 2009**. Applicants who have not received a response regarding the status of their preapplication by this date are responsible for contacting the program to confirm this status. Only those preapplicants that receive notification from DOE encouraging a formal application may submit full applications. **No other formal applications will be considered.**

APPLICATION DUE DATE: January 29, 2010

Formal applications submitted in response to this FOA must be received by January 29, 2010, 8:00 p.m. Eastern time, to permit timely consideration of awards. **APPLICATIONS RECEIVED AFTER THE DEADLINE WILL NOT BE REVIEWED OR CONSIDERED FOR AWARD.**

IMPORTANT SUBMISSION INFORMATION:

The full text of the Funding Opportunity Announcement (FOA) is located on FedConnect. Instructions for completing the Grant Application Package are contained in the full text of the FOA which can be obtained at: https://www.fedconnect.net/FedConnect/?doc=DE-FOA-0000143&agency=DOE. To search for the FOA in FedConnect click on "Search Public Opportunities". Under "Search Criteria", select "Advanced Options", enter a portion of the title "Computational Biology and Bioinformatic Methods to Enable a Systems Biology Knowledgebase", then click on "Search". Once the screen comes up, locate the appropriate Announcement.

In order to be considered for award, Applicants must follow the instructions contained in the Funding Opportunity Announcement.

WHERE TO SUBMIT: Applications must be submitted through Grants.gov to be considered for award.

You cannot submit an application through Grants.gov unless you are registered. Please read the registration requirements carefully and start the process immediately. Remember you have to update your CCR registration annually. If you have any questions about your registration, you should contact the Grants.gov Helpdesk at 1-800-518-4726 to verify that you are still registered in Grants.gov.

Registration Requirements: There are several one-time actions you must complete in order to submit an application through Grants.gov (e.g., obtain a Dun and Bradstreet Data Universal Numbering System (DUNS) number, register with the Central Contract Registry (CCR), register with the credential provider, and register with Grants.gov). See http://www.grants.gov/GetStarted. Use the Grants.gov Organization Registration Checklist at http://www.grants.gov/assets/OrganizationRegCheck.pdf to guide you through the process. Designating an E-Business Point of Contact (EBiz POC) and obtaining a special password called an MPIN are important steps in the CCR registration process. Applicants, who are not registered with CCR and Grants.gov, should allow at least 21 days to complete these requirements. It is suggested that the process be started as soon as possible.

IMPORTANT NOTICE TO POTENTIAL APPLICANTS: When you have completed the process, you should call the Grants.gov Helpdesk at 1-800-518-4726 to verify that you have completed the final step (i.e. Grants.gov registration).

Questions: Questions relating to the registration process, system requirements, how an application form works, or the submittal process must be directed to Grants.gov at 1-800-518-4726 or support@grants.gov. Part VII of the FOA explains how to submit other questions to the Department of Energy (DOE).

All applications should be in a single PDF file.

GENERAL INQUIRIES ABOUT THIS FOA SHOULD BE DIRECTED TO:

Technical/Scientific Program Contact:

> **Program Manager:** Susan Gregurick, Ph.D.
> **Phone:** 301-903-7672
> **E-Mail:** Susan.Gregurick@science.doe.gov

SUPPLEMENTARY INFORMATION:

The Office of Biological and Environmental Research (BER) Genomic Science program funds a portfolio of systems biology research that produces up to petabytes of data annually; examples include: genomic sequences on microbes, plants, and complex environmental samples; mass

spectroscopic proteomic data; microarray expression data; isotopic flux data for pathway analysis; protein binding data for functional annotation; data from imaging of proteins localized in subcellular compartments; and metadata associated with diverse experimental conditions and sampling techniques.

A fully functional Systems Biology Knowledgebase is envisioned to be a cyber-infrastructure for systems biology information and data that not only includes data storage, retrieval and management, but also enables new knowledge acquisition and management, through free and open access to data, analysis tools, and information for the scientific research community. The need for a Knowledgebase has been articulated in a number of scientific workshop reports and is a necessary component of the BSSD Information and Data Sharing Policy (http://genomicsgtl.energy.gov/datasharing/). The 2005 Genomics:GTL Roadmap (http://genomicsgtl.energy.gov/roadmap/) laid the foundation for a comprehensive Knowledgebase as the heart of the Genomics:GTL systems biology program. In May, 2008, an international workshop was held to promote and develop a data and information management system, or Systems Biology Knowledgebase. The report from this workshop can be found electronically at: http://genomicsgtl.energy.gov/compbio/

Projects that exhibit strong collaboration between experimental data generators, bioinformatics and computational biologists and computer scientists are encouraged. Collaborative applications involving multiple institutions, which may include universities, national laboratories, and/or other private institutions are not required but are encouraged. Collaborative applications must identify one lead PI and institution and justify each partner.

Applications are solicited for basic research in computational systems biology that both address DOE's missions in energy and the environment and that will support development of the Systems Biology Knowledgebase in the following areas:

'Omic Data Integration: New computational methods to integrate multiple data types including (meta)genomic, proteomic, metabolomic, transcriptomic, expression and phenotypic data are desired. This could also include the development of data standards, data quality and assessment, ontologies and controlled vocabularies. Methods that significantly improve data visualization and data analysis are also encouraged. This could include new methods for complex web (internet) interfaces and third party tool development. Methods for analysis across different data types is a priority.

Genomic Annotation: New methods for computational gene annotation that include integration of data and information into the assignment of gene functions are encouraged. This should not be an extension of existing methods in genomic annotation, but could include cDNA, clustering and neighborhood gene analysis, expression and phenotypic data, protein folds and structures and phylogenetic profiling data in annotations. Methods for estimating and embedding uncertainty and confidence levels in annotation assignments are a priority.

Integrated Pathway Reconstructions: Significant improvements in methodologies to couple metabolic and regulatory pathways and including integration of data and information are encouraged. This can include new methods in correlational analysis and iterative analysis that

would dynamically link data to model development. New methods in dynamical pathway reconstruction for on-the-fly pathway analysis are also encouraged. Significant improvements that support the integration of expression data with transcription and protein association and localization with pathway simulations are also encouraged.

Whole Cellular Simulations: New methods to model complex cellular processes are encouraged. This could include the integration of multiple data types with additional information such as two and three-dimensional imaging and spectroscopic data with cellular models or simulations.

Information and Data Sharing Policy: The Genomics:GTL information-sharing policy requires that all publication related research software developed with GTL funding that result in a peer-reviewed software publication is to be made accessible through either an open source license or deposited to an open source software community. All Principal Investigators (PIs) within the GTL program will be required to construct and implement an Information and Data-Sharing Plan that ensures this accessibility as a component of their funded projects. As an element of an Information and Data Sharing plan, OBER will require that all publishable information resulting from GTL funded research must conform to community recognized standard formats when they exist, be clearly attributable, and be deposited within a community recognized public database(s) appropriate for the research conducted. All experimental data obtained as a result of GTL funded research must be kept in an archive maintained by the Principal Investigator (PI) for the duration of the funded project. Any publications resulting from the use of shared experimental data must accurately acknowledge the original source or provider of the attributable data. Information about the data-sharing policy and related materials can be found at http://genomicsgtl.energy.gov/datasharing/.

Merit Review

Applications will be subjected to scientific merit review (peer review) and will be evaluated against the following evaluation criteria which are listed in descending order of importance codified at 10 CFR 605.10(d):

1. Scientific and/or Technical Merit of the Project;
2. Appropriateness of the Proposed Method or Approach;
3. Competency of Applicant's Personnel and Adequacy of Proposed Resources; and
4. Reasonableness and Appropriateness of the Proposed Budget.

The evaluation process will include program policy factors such as the relevance of the proposed research to the terms of the announcement and the agency's programmatic needs. Note that external peer reviewers are selected with regard to both their scientific expertise and the absence of conflict-of-interest issues. Both Federal and non-Federal reviewers may be used, and submission of an application constitutes agreement that this is acceptable to the investigator(s) and the submitting institution.

PROGRAM FUNDING:

It is anticipated that up to $5,000,000 will be available for approximately 15 awards to be made in Fiscal Year 2010. The number of awards will be contingent on satisfactory peer review, the availability of appropriated funds, and the size of the awards. Applications may request project support for up to three years, with out-year support contingent on the availability of funds, progress of the research and programmatic needs. Annual budgets for project applications are expected to range from $100,000 to $500,000 in total cost.

DOE is under no obligation to pay for any costs associated with the preparation or submission of an application. DOE reserves the right to fund, in whole or in part, any, all, or none of the applications submitted in response to this FOA.

The Catalog of Federal Domestic Assistance (CFDA) number for this program is 81.049, and the solicitation control number is ERFAP 10 CFR Part 605.

Posted on the Office of Science Grants and Contracts Web Site
August 31, 2009.