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Functional Genomic and Computational Assessment of Threats (Fun GCAT)

The biological sciences have experienced extraordinary growth over the past decade. Technological advances in DNA synthesis, sequencing, large gene construction, and data analysis are expanding biological research and the bioeconomy, and are likely to enable revolutionary advances in medicine, agriculture, and materials. At the same time, these advances have intensified security concerns around the accidental or deliberate misuse of biotechnologies. One special concern regards DNA synthesis technologies that can be used to create novel organisms. Today, most global DNA synthesis activity is not screened for health or environmental risks, and existing screening tools are limited to matching sequences to known organisms. They offer little protection against novel threats. Additionally, current DNA screening practices are inefficient and costly due to hits for genes that are likely to be harmless, but require extensive manual follow up¹. The Fun GCAT program seeks to decrease risks from DNA synthesis by reducing the ambiguity that currently exists in bioinformatic screening and by assessing the threat potential of unknown genes. If successful, Fun GCAT will result in systems that can screen DNA sequences to prevent accidental or deliberate health hazards to humans and agricultural assets.

The Fun GCAT program intends to develop better approaches and tools for characterization and analysis of biological threats based on gene function. Currently, threats are organized based on genetic relatedness, resulting in static, threat-based lists that fail to emphasize biological functions. In order to better characterize known threats, and improve our capacity to understand the relative risk posed by new and emerging threats, the Fun GCAT program will seek to characterize biological threats from a functional perspective and will seek to develop new and better computational and bioinformatics tools to analyze biological data, predict structure/function relationships, and ascribe a relative risk potential to unknown genes.

Fun GCAT is anticipated to be a two-phase program with two separate thrust areas:

- Thrust 1: Apply functional genomics and other approaches to biological threats in order to categorize genes based on threat potential. The focus in Thrust 1 during Phase 1 will be the significant advancement of the characterization and prediction of gene function. The performers will choose genes from bacterial or viral models, or host genes involved in the response to infection. During Phase 1 this thrust will focus on using model genes to demonstrate and validate experimental approaches, methods development, data analysis, and validation. The model pathogens chosen do not need to be select agents. The data and approaches need to inform the development of technical approaches and models that can be applied to predict the function of novel genes.
- Thrust 2: Develop bioinformatic and computational tools and approaches that accelerate data analysis, inform threat potential, predict structure and functions of unknown genes, or develop computational models of threat risk based on gene functions in order to improve our ability to screen DNA sequences.

Phase 2 will maintain both thrusts and will focus on curating the function of genes from select agents or other genes of concern, with an emphasis on data integration and analysis. Bioinformatic tool development and the development of computational models of threat risk will continue in this phase in order to advance capabilities of

predicting functions of unknown genes. The end result should be a set of tools that will improve existing DNA synthesis screening practices. Collaborative efforts and teaming among potential performers are highly encouraged. It is anticipated that teams will be multidisciplinary, including expertise in virology, microbiology, immunology, proteomics, transcriptomics, immunology, functional genomics, bioinformatics, computational modelling of structure, and statistical analysis. IARPA anticipates that academic institutions and companies from around the world will participate in this program. Researchers will be encouraged to publish their findings in academic journals following government review.

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Solicitation Status: CLOSED

IARPA-BAA-16-08 (https://beta.sam.gov/opp/1c36cb90ac60df61ed0448da5118d026/view?keywords=iarpa%2016-08&sort=-relevance&index=&is_active=false&page=1&date_filter_index=0&inactive_filter_values=false)

BAA Release Date: September 22, 2016

BAA Question Period: September 22, 2016 - October 12, 2016

Proposal Due Date: November 8, 2016

Additional Information

Program Description (</index.php/research-programs/fun-gcat>)

IARPA-BAA-16-08 Q&A (round one)

(https://beta.sam.gov/api/prod/opps/v3/opportunities/resources/files/c5c55270254cc774290ba895127aeda3/download?api_key=O4kzViWGVYNumPqhAzUhYGiZZZwW3RKUEYJOI6ii&status=archived&token=)

IARPA-BAA-16-08 Q&A (round two)

(https://beta.sam.gov/api/prod/opps/v3/opportunities/resources/files/c2aad06ebbd8baea99fe2bfb4330a9/download?api_key=O4kzViWGVYNumPqhAzUhYGiZZZwW3RKUEYJOI6ii&status=archived&token=)

IARPA-BAA-16-08 Q&A (round three)

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Proposers' Day Briefings

Fun GCAT Proposers' Day Briefing (/images/files/programs/fungcat/FUNGCAT_proposers_day.pdf)

Applied BioInformatics Laboratory (poster) (</images/files/programs/fungcat/ABiL%20FunGCAT%20Poster.pdf>)

Battelle Memorial Institute (poster) (</images/files/programs/fungcat/Battelle%20FunGCAT%20Poster.pdf>)

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