



National Science Foundation
4201 Wilson Boulevard
Arlington, Virginia 22230

NSF 10-006

Dear Colleague Letter: Mathematical and Statistical Research for understanding the “Omics” (genomics, proteomics, transcriptomics, etc.) of biological threats.

Dear Colleague,

The Division of Mathematical Sciences (DMS) at the National Science Foundation (NSF) has a long history of supporting scientific research to develop technology to secure the national defense. We have formed a partnership with the Defense Threat Reduction Agency (DTRA) to develop the next generation of mathematical and statistical algorithms for the detection of chemical and biological threats. In FY 2009, DMS issued a Dear Colleague Letter, [NSF09010](#), still in effect, that defined an Area of Emphasis within the Computational Mathematics program. This Dear Colleague letter describes an additional new Area of Emphasis for FY 2010.

The introduction of the next generation of massively parallel sequencing technologies led to an exponential increase in the amount of available DNA sequence information for biological threats. As sequence data is now produced faster than it can be meaningfully analyzed, new approaches to the analysis of this information is one of the most important recent challenges for the mathematical sciences. New and improved mathematical and statistical methods and high performance algorithms are needed to clear this bottleneck. Beyond methods to sample and organize the sheer amount of data in a meaningful way, challenges include development of quantitative methods and models to estimate errors for the various sequencing platforms; algorithms and mathematical estimates of the reliability of genomes assembled from short gapped reads; approaches to distinguish sequence-determination errors from biological polymorphism and mutation; and means to distinguish among multiple genomes within a single dataset, particularly when those different genomes are represented at vastly different abundance.

Challenges especially relevant to the area of bio-detection include the development of tools and models for fast identification of the differences between the genomes of individuals of a species, and for distinguishing between naturally-occurring biological heterogeneity and newly-emerged or artificially produced pathogenic sequences in complex samples. Mathematical models and methods to estimate the significance of genomic variability as related to the corresponding phenotypic variability belong to this area of research as well.

Approaches originating from all areas of the mathematical sciences are welcome including but not limited to probability theory and statistics, computational mathematics, applied mathematics, algebraic geometry and topology.

The purpose of this letter is to make the mathematical sciences community aware of this opportunity and to encourage the community to formulate ideas and collaborations, and to assemble diverse groups of mathematical sciences researchers who are actively working in these areas.

DMS and DTRA recognize the needs and opportunities for the mathematical sciences community to develop technology for controlling and reducing the threat from biological and chemical attack. We seek ambitious, transformative, and creative research proposals from individual PIs and collaborative groups

in the mathematical sciences community. While experimental collaborations may serve an appropriate supporting role for a project, proposals submitted should primarily emphasize mathematical, statistical and algorithmic development rather than experimental design. Proposals should include "ATD:" (Algorithms for Threat Detection) at the start of the title and should be submitted to the Mathematical Biology program http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=5690&org=DMS&from=home of DMS within the submission window from December 18, 2009 to January 13, 2010.

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Sincerely,

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