

| Label  | Value   |
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| <b>Core Facility Name</b>  | Computational Biology Consulting Core   |
| <b>Last Name</b>   | Florea  |
| <b>First Name</b>  | Liliana   |
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| <b>Phone</b>   | (443) 287-5624  |
| <b>Amount of Funding Requested</b>   | \$25000   |
| <b>Briefly describe the core services you offer:</b>                                 | <p>Next generation sequencing of DNA and RNA has marked a revolution in biomedical sciences, however the ability to analyze the complex and large amounts of data is not the purview of basic and clinical researchers. The Computational Biology Consulting Core (CBCC), organized as part of the Center for Computational Biology (CCB), offers advanced bioinformatics solutions to the Johns Hopkins biomedical community, as data analyses and consultations. We have experience with any type of sequencing data, from Sanger to second generation Illumina and to long Pacific Biosciences reads, and from single-cell to pooled experiments, and with a variety of genomics applications. We employ best practices solutions, verified and optimized in house, for common workflows such as RNA-seq, ChIP-seq and metagenomic data analyses. Additionally, we draw upon our expertise with developing algorithms for next generation data analysis to evaluate and incorporate the latest software and develop new methods to meet the needs for custom analyses.</p>   |
| <b>What specific services do you plan to offer as part of this RFA?</b>              | <p>Deep sequencing of RNA (RNA-seq) is the first line of investigation in tracing the molecular bases of disease and other cellular manifestations. Our group has extensive expertise developing algorithms and software dedicated to analysis of RNA-seq data. Over the past 3 years since CBCC's inception, we have also analyzed thousands of RNA-seq data sets generated with different sequencing strategies and from a wide variety of experiments. We are also actively evaluating and improving existing bioinformatics solutions for the analysis of metagenomic data from host:microbiome communities. While there is significant interest in this area at JHU, there is currently no on-site offering and no cost efficient local solution, a gap that we aim to fill. The Core Coins grant, if awarded, will allow us to publicize our capabilities in these two areas and others, as well as our commitment to offering the highest quality services, in a timely manner and at affordable prices, to JHU biomedical researchers.</p> <p>We have recently simplified our pricing for projects; a schematic of the price estimates for the two types of services, namely RNA-seq and metagenomic data analyses, depending on the number of samples will be made available to applicants. In particular, the suggested maximum amount per award of \$5,000 would cover the analysis of up to 10 RNA-seq samples and up to 60 16S rRNA metagenomic samples.</p> |
| <b>How do these services address the goals of the pilot program?</b>                 | <p>Historically, most of the CBCC projects came from junior investigators or were exploratory projects aimed to provide proof of concept for grant applications. During the cycle of a potential project, we would meet with the investigator, discuss data requirements and strategies to meet the science and analysis goals, then undertake the analyses and present the investigator the details of the methods and results. Our offering through the RFA will be targeted primarily to small-to-medium (up to \$5,000) projects from young or new investigators, and to pilot studies for grants, thus continuing to provide targeted solutions to address critical gaps.</p> <p>At the same time, the RFA would help publicize our specific capabilities and create visibility for our iLab presence.</p>   |
| <b>How would you select recipients to receive core services? Please describe the</b> | <p>The first step will be to publicize the RFA through our iLab portal (<a href="https://johnshopkins.corefacilities.org/service_center/show_external/3770">https://johnshopkins.corefacilities.org/service_center/show_external/3770</a>), the CBCC web site hosted at CCB (<a href="http://ceb.jhu.edu/cbcc">http://ceb.jhu.edu/cbcc</a>), and via School of Medicine-wide messaging. The tentative deadline for a first round of applications will be July 31, with awards announced by August 15. We will evaluate eligible projects using criteria such as scientific soundness</p>  |

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| <p><b>process and criteria you might use.</b></p>  | <p>and match to the RFA, and availability of data within the FY2018 timeframe. Priority will be given to projects initiated by junior investigators and grant pilots, as well as to projects involving analysis of new data. Agreement to acknowledge the Core in subsequent publications resulting from the data analysis, and to allow us to list the publications on our site, will also be considered. If necessary, the RFA will remain open and applications will be evaluated at the end of each month subject to funding availability. Recipients will be required to submit a one page update of the project and outcomes (e.g., publications, grants submitted and/or received) within a year of the award, by August 15, 2018.</p>   |
| <p><b>How do you plan to allocate the amounts available to individual investigators?</b></p> | <p>We request up to \$25,000 in Core coins to help provide timely and on target services that address areas of need. We will award each selected project up to \$5,000 to cover and/or defray the costs. For example, this amount is sufficient to cover the cost of analysis for experiments with up to 10 RNA-seq samples or up to 60 metagenomic samples, which encompass the vast majority of exploratory projects we have encountered. Diagrams of price estimates will be made available with the RFA and on our web site, since any exceeding costs will be the responsibility of the investigator. We expect most of the exploratory projects to be in the range of \$3,000-5,000, thus ensuring that every investigator has ready access to affordable bioinformatics services to bridge areas of critical need in their research and funding.</p> |