Support for Use of Common Fund Data Sets

Background:

The NIH Common Fund supports programs that are strategic investments designed to solve problems or build resources to catalyze scientific discovery throughout the entire biomedical research enterprise. Many Common Fund programs generate high-value, high content, and widely available data sets. To maximize the impact and engage a broader community of potential end-users for wider adoption of these data sets and/or to develop or enhance the tools available to mine the data, the Common Fund plans to support administrative supplements or small projects that encourage the use of Common Fund data to answer novel and compelling biological questions, generate cross-cutting hypothesis for future research, and/or to enhance computational tools.

Several established Common Fund data sets are well-poised for increased community use:

- 4DNucleome: The 4D Nucleome Data Portal hosts data (e.g., HiC, RNA and DNA-FISH datasets) generated by the 4DN Network and other reference nucleomics data sets, and an expanding tool set for open data processing and visualization
- Genotype-Tissue Expression (GTEx): whole genome sequence and RNA sequence data from multiple human tissues to study tissue-specific gene expression and regulation
- Illuminating the Druggable Genome (PHAROS): integrated source containing data on understudied druggable proteins, including mRNA and protein expression data, phenotype associations, bioactivity data, drug target interactions, and functional information
- Knockout Mouse Phenotyping Program (KOMP2): data on broad, standardized phenotyping of a genome-wide collection of mouse knockouts
- Library of Integrated Network-based Cellular Signatures (LINCS): library of molecular signatures that describes how different types of cells respond to a variety of agents that disrupt normal cellular function
- Metabolomics Workbench: repository for metabolomics data and metadata from studies on cells, tissues, and organisms
- Integrative Human Microbiome Project (iHMP): microbiome, epigenomic, metabolomic, and phenotypic data for 3 cohorts of people with different diseases/conditions (pregnancy, inflammatory bowel diseases, and diabetes)

In future years, additional Common Fund data sets may be added to the list of eligible data sets for these awards.

Proposed support for use of Common Fund data sets:

Beginning in fiscal year 2019, the Common Fund proposes to award 1-year administrative supplements to existing NIH awards, competitive revisions, and/or new small projects to enable exploration and use of Common Fund-supported data sets to address issues that are within the scope of the parent award. This is intended to maximize the NIH investment in Common Fund programs by providing an additional incentive to use Common Fund data and catalyze discovery. Publications resulting from these projects will further enhance the uptake of these data sets by providing case studies of how data can be used. Additionally, feedback provided by the awardees regarding the usability of data sets, web portals, and associated analytic tools may inform future efforts to improve functionality for all researchers. The Office of Strategic Coordination, which oversees the Common Fund, will monitor the impact of these awards.