National Advisory Council for Human Genome Research
February 22/23, 2021
Concept Clearance for PAR

Title: Investigator Initiated Research in Computational Genomics and Data Science (R01/R21 Clinical Trial Not Allowed)

Purpose: The purpose of this funding opportunity announcement (FOA) is to invite applications for research efforts in computational genomics, data science, statistics, and bioinformatics relevant to one or both of basic or clinical genomic science, and broadly applicable to human health and disease. This FOA supports fundamental genomics research that focuses on early-stage development of innovative analytical and computational approaches and tools, as well as refinement or hardening of software and tools of demonstrated high value to the biomedical genomics community. Work supported under this FOA should be enabling for genomics, and generalizable across diseases and biological systems. All applications should address how the approaches and tools would scale to address increasingly larger data sets.

New or renewal/modified initiative: Renewal
Only minor changes are being proposed from the active Computational Genomics and Data Science (CGDS) PARs. The research topic examples will be updated to reflect the latest science and the special review criteria will be updated to more closely align with the NHGRI mission and CGDS goals. The proposed PAR will also utilize three standard receipt dates instead of two special receipt dates to streamline the application process for investigators. A related SBIR/STTR funding opportunity (PAR-19-061) is not being proposed to be renewed since program staff have determined the parent SBIR/STTR announcements are sufficient.

Current PAR: https://grants.nih.gov/grants/guide/pa-files/PAR-18-844.html (R01)
https://grants.nih.gov/grants/guide/pa-files/PAR-18-843.html (R21)

Mechanism of Support: Research Project Grant / R01, R21

Appendix 1: Awards under previous rounds of the CGDS FOAs (FY19-21)

PAR-18-843, PAR-18-844

Act. Code	Grant	PI	Title	Early Stage Inv	New Inv	Total Cost/Yr
R01	HG010731	LI, GEN	Tensor Array Methods for RNA-Seq Analysis	YES	YES	$215,172
R01	HG010749	GERSTEIN, MARK BENDER	Enhancing open data sharing for functional genomics experiments: Measures to quantify genomic information leakage and file formats for privacy preservation	NO	NO	$523,409
R01	HG010753	LI, WEI	Modeling Functional Elements using CRISPR Screening	YES	YES	$446,250
R01	HG010757	QUINLAN, AARON R	Scalable detection and interpretation of structural variation in human genomes	NO	NO	$692,048
R01	HG010759	BANSAL, VIKAS	Computational methods for variant calling and haplotyping using long-read sequencing technologies	NO	NO	$381,728
R01	HG010773	HE, XIN; NOVEMBRE, JOHN	Refining mutation rates and measures of purifying selection with an application to understanding the impact of non-coding variation on neuropsychiatric diseases	NO	NO	$416,226
R01	HG010774	KERN, ANDREW D	Deep learning for population genetics	NO	NO	$529,154
R01	HG010798	WANG, XIAOFENG; TANG, HAIXU T	Secure and Privacy-preserving Genome-wide and Phenome-wide Association Studies via Intel Software Guard Extensions (SGX)	NO	NO	$375,868
R01	HG010805	GE, XIJIN	An interactive tool for in-depth and reproducible analysis of RNA-seq data	NO	NO	$179,821
R01	HG011138	GAMAZON, ERIC R	Advancing Multi-Omics and Electronic Health Records Computational Methodologies	NO	NO	$330,670
R01	HG011139	IRIZARRY, RAFAEL ANGEL	Next Generation Computational Tools for Functional Genomics	NO	NO	$665,458
R01	HG011392	LANGMEAD, BENJAMIN THOMAS	Personal and panel references for improved alignment	NO	NO	$381,528
R21	HG010748	GUSEV, ALEXANDER	Efficient methods for identifying cryptic relatedness in millions of individuals	N/A	N/A	$165,232
R21	HG010789	ZACHAREWSKI, TIMOTHY R	Advancing chemical and drug safety testing using single-cell RNA-sequencing	N/A	N/A	$234,750