**National Advisory Council for Human Genome Research**
**February 12/13, 2024**
**Concept Clearance for PAR**

**Title: Investigator Initiated Research in Computational Genomics and Data Science (R01/R21/R15/R41/R42/R43/R44 Clinical Trial Not Allowed)**

**Purpose:** The purpose of these renewing Notices of Funding Opportunity (NOFOs) is to support investigator-initiated research efforts fostering innovation in computational genomics, data science, statistics, bioinformatics, and data visualization and exploration. These NOFOs support research developing innovative analytical methodologies and approaches and early-stage development of tools and software for genomics. Applications should be enabling for genomics, broadly applicable to human health and disease, and generalizable across diseases and biological systems.

**New or renewal/modified initiative: Renewal**
The following changes are being proposed from the current NOFOs (PAR-21-254, PAR-21-255):

- NOFOs resulting from this concept will feature a narrowed scope focused on projects that emphasize innovation in computational genomics and data science. Projects focused on advancing basic genome sciences and genomic medicine, instead of on developing innovative computational genomics and data science methods and approaches, would be considered out of scope for these NOFOs but could be appropriate for submission to NHGRI under the NIH Parent Announcements or other funding opportunities.

- NOFOs will no longer support efforts to refine or harden existing software and tools. Very few applications proposing refinement were received or funded through previous NOFOs.

- The NIH Research Enhancement Award (R15) mechanism will be used to broaden the NHGRI's reach in fostering innovation in computational genomics and data science. The R15 mechanism aims to support meritorious research, expose students to research, and strengthen the research environments at institutions that provide degrees for a significant number of the Nation's research scientists but that have not been major recipients of NIH support.

- Parallel NOFOs may be developed to support computational genomics and data science research using Small Business Technology Transfer (STTR, R41/42) and Small Business Innovation Research (SBIR, R43/44) mechanisms.

**Mechanism of Support:** R01/R21/R15/R41/R42/R43/R44

# Appendix 1: Awards Funded Through PAR-21-254, PAR-21-255 (FY22-24)

| Activity Code | Grant | PI | Title | Study Section | Total Cost / Year 1 |
|---|---|---|---|---|---|
| R01 | HG009299 | Clark, Nathaniel | Functional Annotation of Genomes via Phenotypic Convergence within Large Multi-species Alignments | GCAT | $529,944 |
| R01 | HG012558 | Sheffield, Nathan | Novel methods for large-scale genomic interval comparison | BDMA | $383,973 |
| R01 | HG012573 | Park, Peter | Development and Application of Computational Methods for Single Cell DNA Sequencing Data | GCAT | $747,149 |
| R01 | HG012784 | Rigoutsos, Isidore | Specialized Tools and Auto-updatable Scalable Interactive Databases to Study isomiRs, tRFs and rRFs in Human and Mouse | BDMA | $553,060 |
| R01 | HG013104 | Morrison, Jean | Mendelian randomization for modern data: Integrating data resources to improve accuracy of causal estimates | GCAT | $358,755 |
| R01 | HG013317 | Greenleaf, William | Fast, powerful, scalable, usable, and distributable methods for multi-modal single cell analyses | BDMA | $716,630 |
| R21 | HG012639 | Azizi, Elham | Computational toolbox for spatial transcriptomic analysis of complex tissues | BDMA | $435,475 |
| R21 | HG012978 | Ray, Debashree | Statistical methods for identifying pleiotropy between complex human traits | BDMA | $245,625 |
| R21 | HG012981 | Zang, Chongzhi | A multi-level bias correction model for bulk and single-cell CUT&Tag data | GCAT | $444,125 |
| R21 | HG012998 | Tintle, Nathan | Novel methods to improve the utility of genomics summary statistics | GCAT | $426,811 |
| R21 | HG013433 | Langmead, Benjamin | Efficient and scalable pangenomes with the move structure | GCAT | $198,495 |
| R56 | HG013117 | Song, Yun | Scalable Computational Methods for Genealogical Inference: from species level to single cells | ZRG1 | $315,000 |