

Opportunity Title: Bioinformatics Scientist Opportunity Reference Code: EPA-ORD-NCCT-2018-01

Organization	U.S. Environmental Protection Agency (EPA)
Reference Code	EPA-ORD-NCCT-2018-01
How to Apply	A complete application consists of:
	An application
	 Transcripts – Click here for detailed information about acceptable transcripts
	 A current resume/CV, including academic history, employment history, relevant experiences, and publication list
	Two educational or professional references
	All documents must be in English or include an official English translation.
	If you have questions, send an email to EPArpp@orau.org. Please include the reference code for this opportunity in your email.
Description	The EPA National Center for Computational Toxicology (NCCT) is responsible for developing new computational tools and providing quantitative analysis for improving environmental risk assessments and regulatory decisions pertaining to chemical safety and sustainability.
	The NCCT is using gene expression profiling in multiple cell types to rapidly screen thousands of environmental chemicals fo their potential biological effects. Targeted RNA-Sequencing

types to rapidly screen thousands of environmental chemicals for their potential biological effects. Targeted RNA-Sequencing (high-throughput transcriptomics/HTTr) has been used to generate concentration-response data on all genes (~21,000) for thousands of environmental chemicals. A multidisciplinary research team including scientists at EPA and other partners, is developing a computational infrastructure to manage, process and analyze this large-scale HTTr dataset. Our primary objectives are to predict the putative molecular targets of each chemical based on gene expression changes and to estimate the corresponding concentrations where perturbations in biology occur. The predicted mechanisms of chemicals will be validated using independent/orthogonal assays. The resulting data will be used to support chemical prioritization and safety assessment processes as well as for computational modeling efforts.

Through this research project, the research participant will gain education and training in the development of computational methods for evaluating chemical safety using gene expression and other large-scale data. Prior experience in these areas would clearly be of value. Research findings will be







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> communicated through peer-reviewed publications, national meetings of professional societies, and work-in-progress seminars. The training the participant will receive, coupled with a productive publishing record, will make it possible for the research participant to move into any of these areas or continue down a transdisciplinary path at their discretion. The research participant will be involved in highly visible predictive toxicology efforts as part of the computational toxicology research projects and will be engaged with researchers world-wide. The research participant will have an opportunity to be published in peerreviewed journals and present research results at local and national meetings.

> This program, administered by ORAU through its contract with the U.S. Department of Energy (DOE) to manage the Oak Ridge Institute for Science and Education (ORISE), was established through an interagency agreement between DOE and EPA. The initial appointment is for one year, but may be renewed upon recommendation of EPA and is contingent on the availability of funds. The participant will receive a monthly stipend commensurate with educational level and experience. Proof of health insurance is required for participation in this program. The appointment is full-time in the Research Triangle Park, North Carolina area. Participants do not become employees of EPA, DOE or the program administrator, and there are no employment-related benefits.

The mentor for this project is Imran Shah (shah.imran@epa.gov).

Qualifications Applicants must have received a masters or doctoral degree within five years of the desired starting date. The applicant must be generally knowledgeable in at least one of the following fields: bioinformatics, computational biology, biostatistics, mathematical modeling. The ideal applicant would be proficient in bioinformatics including, but not limited to, gene expression data processing and analysis, and have a demonstrated interest in one or more of the fields listed above.

Preferred skills include:

- Solving human health/environmental/biomedical problems using large-scale molecular datasets in R/Python and describing the research in peer-reviewed manuscripts
- Writing custom programs in R/Python to organize multi-step analysis workflows (e.g. Jupyter notebooks) including database storage/retrieval, visualization, report generation, etc.
- Processing Affymetrix/RNA-Sequencing data to analyze expressed genes from in vitro/in vivo samples
- Using data from public gene expression repositories: GEO (NCBI), ArrayExpress (EBI), CMap/LINCS (Broad Institute)



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- Analyzing differential gene expression with R/Bioconductor (Im/DESeq etc.) for intensity and count data
- Experience with using optimization/curve-fitting libraries in R/Python for dose-response analysis
- Interpreting differential expression data using pathway analysis, GSEA or other approaches
- Using machine learning approaches to reduce dimensionality of gene expression data or to classify outcomes
- Eligibility Requirements
- **Degree:** Master's Degree or Doctoral Degree received within the last 60 month(s).
- Academic Level(s): Postdoctoral or Post-Master's.
- Discipline(s):
 - Chemistry and Materials Sciences (12 (1))
 - ∘ Computer, Information, and Data Sciences (5 ●)
 - Engineering (4 𝕗)
 - Environmental and Marine Sciences (1 ()
 - Life Health and Medical Sciences (11 (1))
 - Mathematics and Statistics (5 ⁽⁵⁾)
 - Physics (16 ♥)