

- **Title**

Fundamentals of Toxicogenomics: Introduction to Computational Toxicology Methods and Tools

- **Names and affiliations for instructors**

Elaine Cohen Hubal, Stephen Edwards, David Reif, Imran Shah
US EPA, Office of Research and Development

- **Contact information for lead instructor**

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- **Brief biography for each instructor**

Elaine Cohen Hubal, Ph.D.

Senior Scientist (Chemical Engineer), National Center for Computational Toxicology

Dr. Cohen Hubal has over 10 years experience in the field of exposure science. The focus of Dr. Hubal's current research is on applying a systems approach to characterize complex relationships between environmental factors and health outcomes with an emphasis on early-life exposure.

David Reif, Ph.D.

Computational Biologist, National Center for Computational Toxicology

Dr. Reif's research focuses on integrating environmental exposure information with physiological biomarker data to address public health issues. He comes to EPA from Vanderbilt University, where he earned his M.S. (Applied Statistics) and Ph.D. (Human Genetics) degrees developing strategies for comprehensive analysis of genetic, transcriptomic, proteomic, and annotation data.

Imran Shah, Ph.D.

Computational Systems Biologist, National Center for Computational Toxicology

Dr. Shah's current research focuses on design of computational, systems-based models that support improved assessment of the public and ecological health implications of environmental stressors. He comes to EPA from Icoria, a clinical data company, where he was head of computational systems biology and led the development of their metabolomic biomarker discovery pipeline.

Stephen Edwards, Ph.D.

Systems Biologist, National Human and Environmental Effects Research Laboratory

Dr. Edwards comes to EPA from Rosetta Inpharmatics (Merck & Co.) where he identified several pharmacologically relevant biological pathways using genetics and gene expression

data. His current interest is in applying this approach to the elucidation of mode of action for environmental stressors.

- **Description**

Recent technological advances have led to the development of the field of toxicogenomics in which the effects that chemicals have on living organisms and/or the environment can be examined using genomic, transcriptomic, and proteomic methods. These emerging tools in molecular biology provide the potential to develop cellular and molecular indicators of exposure that can be used to assess the vulnerability of humans to environmental stressors. Better understanding of genetic factors, genomic expression, and proteomic levels will also provide insight into factors impacting differences in susceptibility to chemical exposure that is seen in the human population. In this course we will:

- Introduce terminology
- Introduce molecular biology methods with a focus on those tools used to collect data for characterizing genetic variation and gene expression
- Introduce environmental informatic tools with a focus on publicly available computer tools to interpret and visualize toxicogenomic data
- Present a case study to demonstrate available computer tools for interpreting a publicly available toxicogenomic data set
- Discuss the potential and challenges of using toxicogenomics and other computational toxicology tools to improve risk assessment

Course participants will be introduced to and develop an awareness of the types of technologies, data, and tools that are being applied in the field of toxicogenomics.

- **Target audience**

1. Exposure scientists
2. Industrial, regulatory, and public health professionals
3. Environmental scientists and engineers
4. Industrial hygienists

- **Course level**

Introductory

- **Prerequisites or expected proficiency**

None

- **Number of students**

20+

- **Course length**

One half day

- **Course Outline**

Introduction (Elaine Cohen Hubal, NCCT)

- Motivation (Rapid advances in molecular biology and computation)
- Definitions (Ecogenetics, Toxicogenomics, Environmental Bioinformatics)

- Promise and Challenge for Risk Assessment

Molecular Biology Techniques (Steve Edwards, NHEERL)

Experimental measurement methods organized along the central dogma of molecular biology (DNA, RNA, Protein)

- Genetics/Genomics (Sequencing, SNP chips)
- Transcriptomics/Toxicogenomics (expression microarrays)
- Proteomics (protein arrays, HTP MS)

Environmental Bioinformatics (Imran Shah, NCCT)

Publicly available tools for managing, evaluating, and visualizing toxicogenomic data

- Knowledge based categorical analysis tools (pathways, ontologies)
- Analytical tools (clusters, trees, etc.)

Case Example (David Reif, NCCT)

A case example will be presented to demonstrate available computer tools for interpreting a publicly available toxicogenomic data set