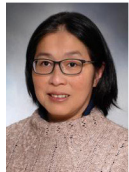


ITS Panel Workshop on Single-Cell RNA Sequencing Friday January 20: All are welcome



The ITS Core will offer a **Single-Cell RNA Sequencing Workshop** on Friday **January 20** from 11:00 AM–1:00 PM, Room 121 Kettering. Box lunches by *Aynies* will be available on a first come, first served basis (sign-in required). Expert speakers and topics will include

[Mario Medvedovic, PhD](#); Professor and Director of the Division of Biostatistics and Bioinformatics, UC Department of Environmental and Public Health Sciences: **Analyzing and learning from scRNA-seq data.**



[Chia-I Ko, PhD](#); Adjunct Assistant Professor, Division of Environmental Genetics and Molecular Toxicology (EGMT): **Identification of AHR function in preimplantation embryonic differentiation by scRNA-seq.**



[Rathnakumar Kumaragurubaran, PhD](#), Assistant Professor, Pediatrics and Developmental Biology, and Director, scRNA-seq Core, CCHMC: **Single Cell Genomics Core: Overview and Services.**



[Xiang Zhang, PhD](#), Research Associate Professor and Director of the Genomics & Epigenomic Sequencing Core (GES): **Overview of GES Core and single cell sequencing.**

Lessons Learned on the Road to Environmental Cleanup

Available now! A collaborative, interactive **educational resource** produced by the UC Center for Environmental Genetics (NIEHS P30 ES006096), UPenn's Center of Excellence in Environmental Toxicology (P30 ES013508), and the MIT Superfund Research Program (P42 ES02770). To access the **Lessons Learned** modules online, use the QR code here or **[click on the CEG web page here.](#)**



At left, UC team members Kayla McGill, Joyce Bentle, Kent Meloy, and Susan Pinney. At right, the team debuts the new modules to DEPHS students, faculty and guests.



Recent Publications

Ma J, Niklewski PJ, **Wang HS**. Acute exposure to low-dose bisphenol A delays cardiac repolarization in female canine heart - Implication for proarrhythmic toxicity in large animals. *Food Chem Toxicol.* 2022 Dec 28;172:113589. **PMID: [36584932](#).**

Zhen Y, Ren Y, **Medvedovic M**, Adams DE, Wang D, **Shao WH**. Axl regulated survival/proliferation network and its therapeutic intervention in mouse models of glomerulonephritis. *Arthritis Res Ther.* 2022 Dec 28;24(1):284. **PMID: [36578056](#). PMCID: [PMC9795606](#).**



Funded by NIEHS award P30 ES006096

<http://med.uc.edu/eh/centers/ceg>

Follow us online

YouTube

The CEG Bioinformatics and Integrative Health Sciences Facilities Cores will host **[Devin C. Koestler, Ph.D.](#)**, Director of the Quantitative 'Omics Core, Kansas Institute of Precision Medicine, for a **February 9** online workshop on strategies for analyzing DNA methylation data in epidemiological studies using high-throughput profiling techniques. **12 Noon - 1:00 PM Thursday Feb 9.**



Devin Koestler

DNA methylation (DNAm) based cell mixture deconvolution (CMD) has become a quintessential part of epigenome-wide association studies (EWAS) when DNAm is profiled in heterogeneous tissue-types. CMD refers to the application of computational and statistical techniques aimed at estimating the proportion of cell types in a mixed or heterogeneous biospecimen (e.g., whole-blood). Among other themes, Dr. Koestler will discuss the potential for confounding due to cellular heterogeneity along with the motivation for DNA methylation-based deconvolution methodologies and their importance to EWAS.

Watch your email for the Feb 9th webinar link and details