Providing Context to In Vitro High-throughput Screening Data via Annotation and Visualization Tools

A. L. Karmaus[1], J. Rooney[1], P. Ceger[1], J. Abedini[1], J. Phillips[2], S. Bell[1], D. Allen[1], and N. Kleinstreuer[3]

[1]ILS, Research Triangle Park, NC, United States; [2]Sciome LLC, Research Triangle Park, NC, United States; and [3]NIH/NIEHS/DNTP/NICEATM, Research Triangle Park, NC, United States

A wide variety of in vitro high-throughput screening (HTS) assay data is available to the public. These data have the potential to facilitate the development of computational approaches for chemical hazard assessment, but linking HTS data to regulatory endpoints remains a challenge and requires detailed information about the assays as well as an understanding of their biological context. Here we present the results of our efforts to facilitate HTS data integration with in vivo bioassays and other data sources through a mechanistic mapping approach. This approach provides an assay grouping schema with a toxicological endpoint-based framework that is applicable beyond HTS datasets. We used expert curation and molecular/cellular process annotations to map assays to regulatory endpoints of interest through structured vocabularies that allow data to be searched, grouped, and visualized by regulatory endpoint. Furthermore, these annotations are publicly available in the Integrated Chemical Environment (ICE, https://ice.ntp.niehs.nih.gov/). Increased accessibility to annotated HTS data provides context that facilitates the identification of data gaps, insight into mechanistic plausibility, and investigation into regulatory-relevant endpoints such as endocrine disruption, carcinogenicity, developmental toxicity, and systemic effects. This effort highlights that while single assay results are generally insufficient for regulatory application, leveraging annotations across diverse data sources within ICE helps integrate results in a weight of evidence framework. Associated data visualizations assist users in reviewing a chemical's potential activity for selected regulatory endpoints. This presentation will walk through specific case studies that demonstrate how to access and interpret the annotations within the ICE tool. This project was funded with federal funds from the NIEHS, NIH under Contract No. HHSN273201500010C.

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