

Report 90: Implementing integrated systems based approach for environmental health sciences

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Brief History:

Environmental effects on disease are complex and understanding these effects requires an integrated, comprehensive approach.

Emerging technologies allow for transformative analysis of genome structure and sequence, gene expression, methylation, the metabolome, proteome, phenotypes, etc. but there is currently no coordination between these experiments. Strategies that facilitated integration of such data in the context of environmental exposures would permit greater synergy between EHS researchers, and improve our basic understanding of environmentally associated diseases.

We propose a paradigm shift in the way that this data is collected and integrated to allow a broad systems biology approach for studying the effects of the environment on human biology.

Discussion Highlights:

Identify useful exposure models, bring together stakeholders with pre-existing interests and/or data, and identify gaps in data. Work within DIR, DERT, etc. to fill in those gaps.

Involves building a framework to build a standardized data set (agreed upon conditions, quality control, format, genetic background), and a collaborative effort to populate this with different kinds of 'omic data. Could kick start this initiative using current interests/ strengths within NIEHS, and build upon this with targeted extramural funding and intramural hires.

Develop new tools for integration of databases as well as optimized methods for statistical analysis and mining data in order to maximize utility and ease of access to data generated. If the data is of high quality and easy to mine, others will opt to use the standard conditions and our database will continue to grow.

Initial framework can be built upon in a flexible manner as new technologies are developed and new models are added.

Recommendations:

The NIEHS should take a leadership role in connecting the people studying environmental exposures and the various systems biology data sets, and facilitate synthesis of the wealth of data being generated. In addition, we should help direct new research toward further developing these comprehensive strategies and their accessibility.

Develop an overarching framework for how comprehensive analyses of effects of exposures of both model organisms and humans can be conducted, including sequencing of genomes, methylomes, epigenomes, metabolomes, microbiomes, etc.

This framework would entail collaboration across the NIEHS, involving DIR, DERT and the NTP, as well as leveraging the infrastructure and knowledge present at the other ICs.

Discussion Participants: Adelman, Bernstein, Fasman, Holsapple, Mural, Pollock, Taylor, Umbach, Archer, Fargo, London, Fessler, Gilliland, Gould, Hall, Hanawalt, Kiley, Ladd, McAllister, Nicholas, Paules, Tice, Vogt, Worth, Zeisel