

Framing Our Birth Defects Questions with Systems Biology: Learning from Our Mentors



Elaine M. Faustman, Ph.D. DABT
Professor and Director

*Institute for Risk Analysis and Risk
Communication*



SCHOOL OF PUBLIC HEALTH
UNIVERSITY of WASHINGTON

Disclosure

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Outline

- Summers in Seattle
- Role of environment in the etiology of birth defects (E)
- Role of Genetics and Environment (G x E)
- Role of Context both Risk Assessment and Systems Biology
- Unique aspects of our Societies and our Mentors



Dr. Josef Warkany

Founders in the late 1950s. Left to right:
James Wilson, F. Clarke Fraser, and Josef Warkany.



University Center for Excellence in Developmental Disabilities



This view of the the UW campus shows the newly completed Center.



Center Director Emauel (left) meets with Senator Henry (Scoop) Jackson in the CD150 auditorium in 1973.

Seattle Teratology Club-- Best science but suffers no ties (or formality)



Central Laboratory for Human Embryology



University of Washington



CATALOG OF
**TERATOGENIC
AGENTS** FIFTH
EDITION

Thomas H. Shepard, M.D.

**CATALOG OF
TERATOGENIC AGENTS**

Fifth Edition

Thomas H. Shepard, M.D.

Central Laboratory for Human Embryology
Department of Pediatrics
School of Medicine
University of Washington

THE JOHNS HOPKINS UNIVERSITY PRESS
Baltimore and London

1980 Interview of Dr. J. Warkany Part 4




Role of the Environment in Birth Defects

Role of environmental agents in the overall etiology of birth defects is largely unknown, with estimates of 3-25% of all birth defects due to some type of environmental interaction.

NAS, 2010





“Environment” Broadly Defined in Longitudinal Studies

- **Physical environment:**
 - housing, neighborhoods and communities, climate, radiation...
- **Chemical exposures:**
 - air, water, soil, food, dust, industrial products, pharmaceuticals...
- **Biological environment:**
 - womb, infection, nutrition; inflammatory and metabolic response...
- **Genetics:**
 - influence of genetics on disease; relationships between genes and the environment
- **Psychosocial:**
 - influence of family, socio-economics, community, culture, stress...

Combined Approaches Needed for Children's Exposure Assessment

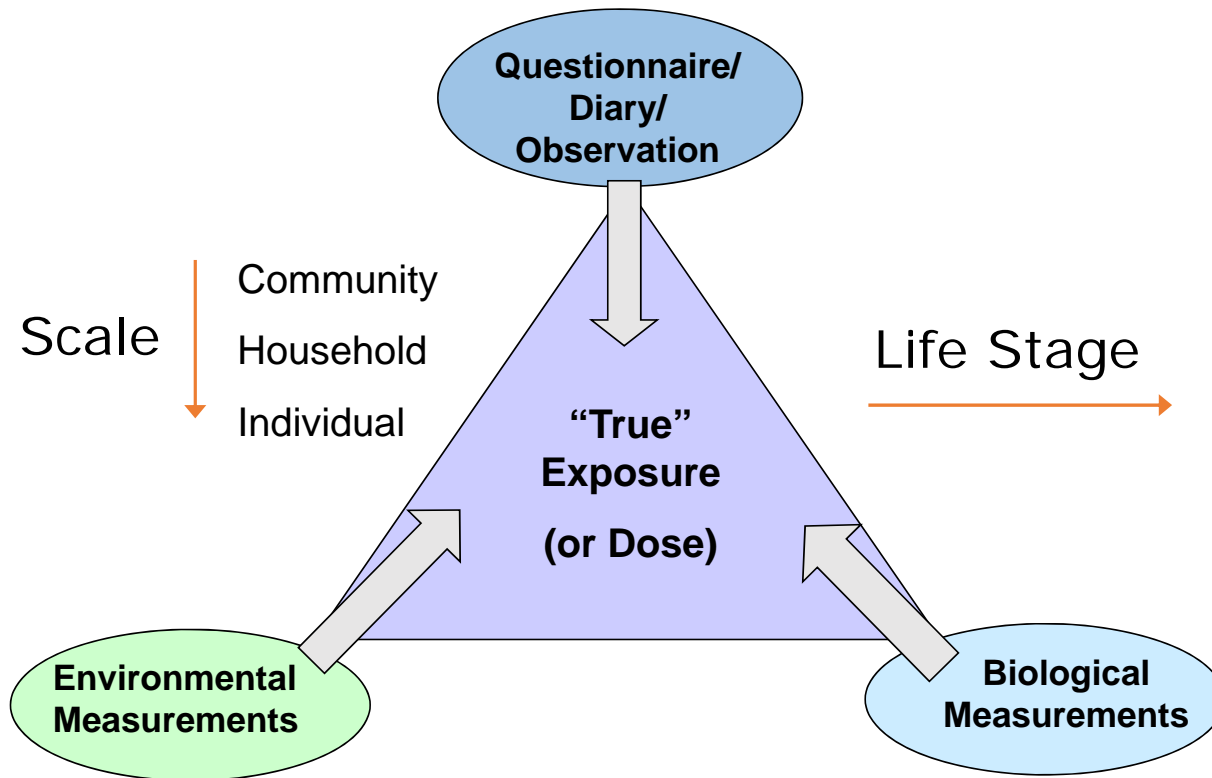
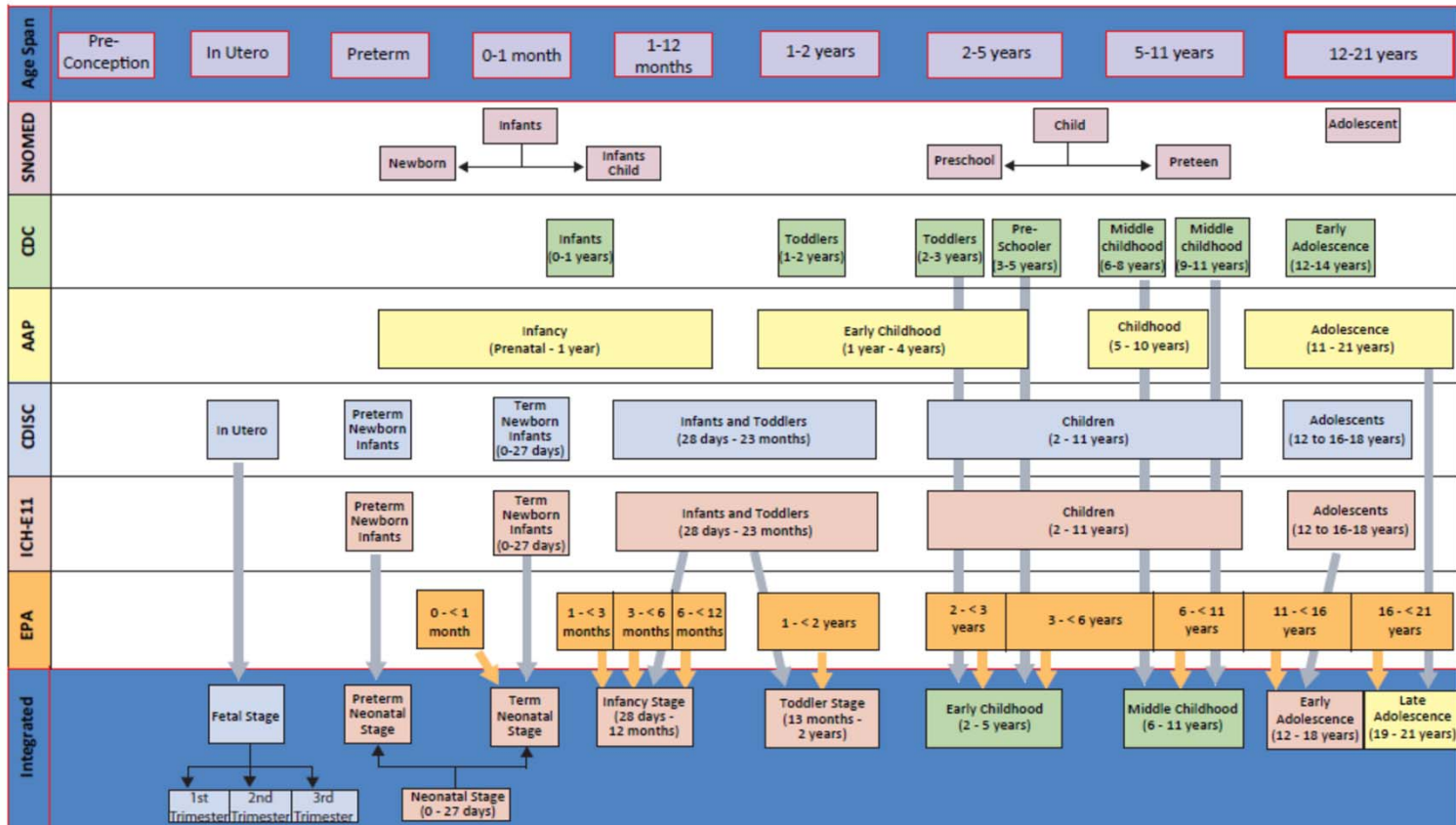


Figure 1

Integrated child-life stages for NICHD Pediatric Terminology as mapped to existing medical terminologies



AAP: American Academy of Pediatrics
 CDC: Centers for Disease Control and Prevention
 CDISC: Clinical Data Interchange Standards Consortium
 EPA: Environmental Protection Agency
 ICH-E11: International Conference on Harmonisation
 SNOMED: Systemized Nomenclature of Medicine

Figure 4

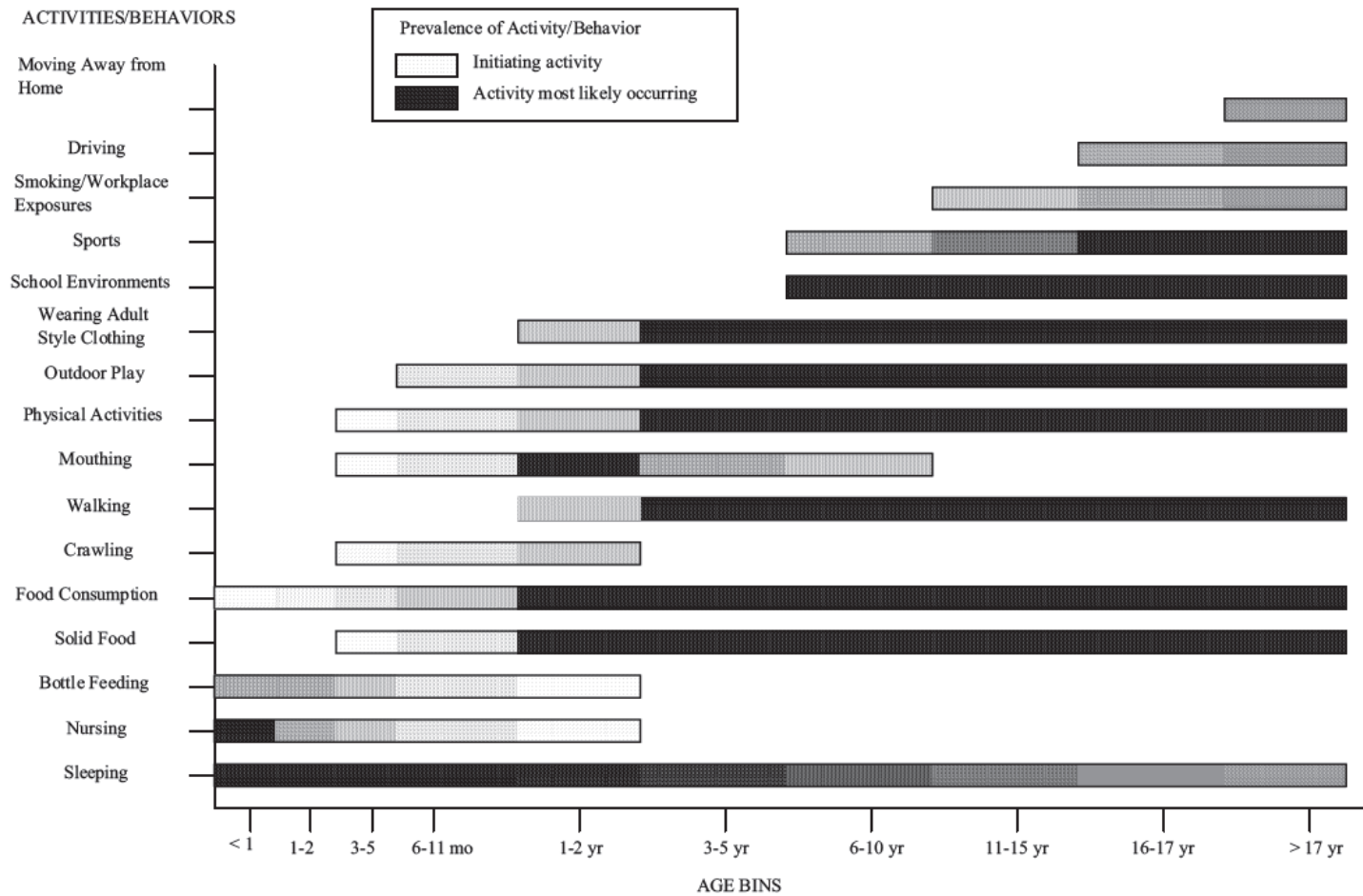


Fig. 14. Children's activities that impact exposure as a function of developmental age (from USEPA, 2003b)

WHO (2006) Principles for Evaluating Health Risks in Children Associated with Exposure to Chemicals, Environmental Health Criteria, 237

 @theNAMedicine



"Health and development each builds on themselves; **each period of development lays the foundation for the next.** This is important when it comes to understanding the drivers of health within a population. Even though the impacts of early exposures may not be evident for years or decades, **they have consequences.**"

Why the United States Needs a National Birth Cohort Study
An NAM Perspective

www.nam.edu/LifelongHealth

 @theNAMedicine



"A national birth cohort study is essential for developing evidence-based policies that are capable of improving the United States' international health standing and ensuring that **every member** of the U.S. population has an **equal opportunity to thrive.**"

Why the United States Needs a National Birth Cohort Study
An NAM Perspective

www.nam.edu/LifelongHealth



Discussion Paper

Why the United States Needs a National Birth Cohort Study

**Anne Riley, Ezekiel Dixon-Román, Barbara Entwisle, Ruth Etzel, Ann Masten,
Kerry Anne McGeary, Hirokazu Yoshikawa**

May 31, 2016

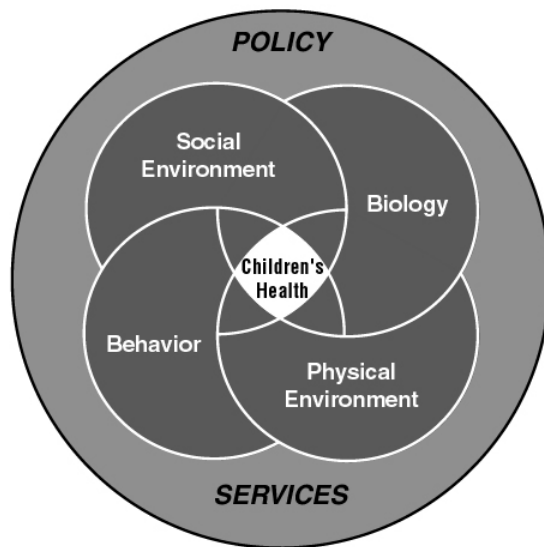
Discussion Paper

Methods for a National Birth Cohort Study

**Greg Duncan, Virginia Lesser, Barbara Entwisle, Graham Kalton, Andy Shih,
Elaine Faustman, Rosalind Wright, Kerry Anne McGeary, Richard Gershon,
Steven Wysmuller, Shelley Merritt, and Charlee Alexander**

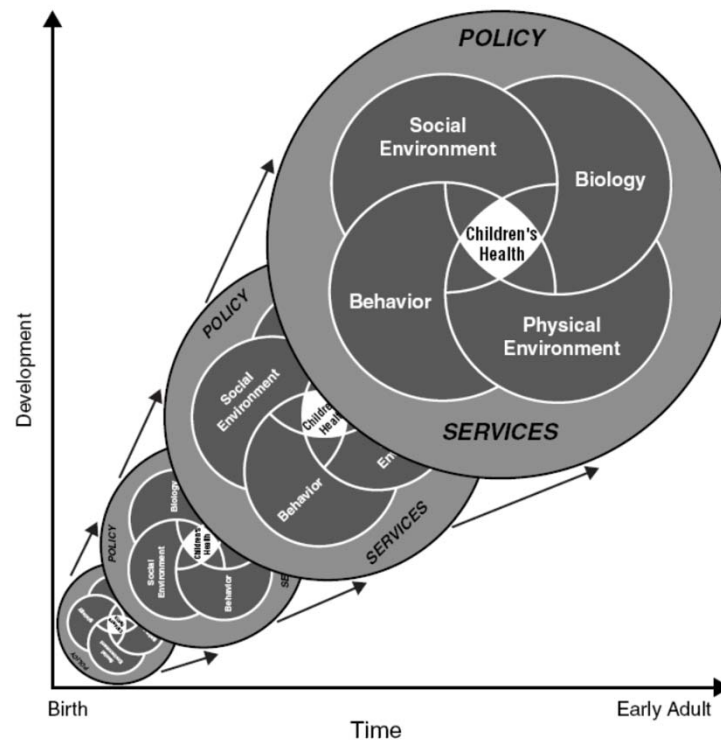
May 31, 2016

Multiple, Interacting Influences Affect Children's health including Chemical and Non Chemical Stressors



IOM, 2004

Life Course Based Model of Children's Health and its Influences:

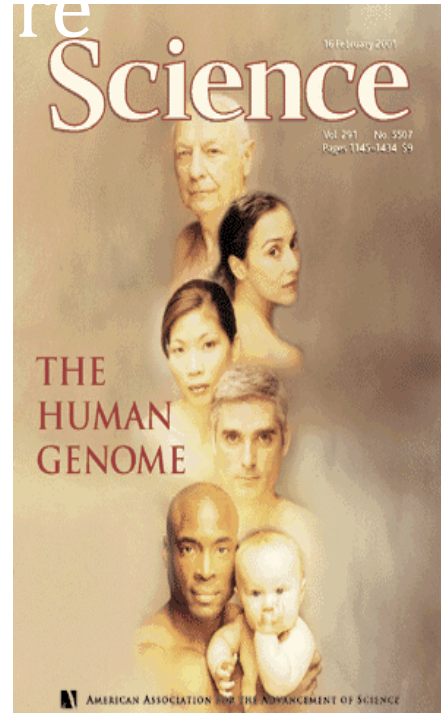
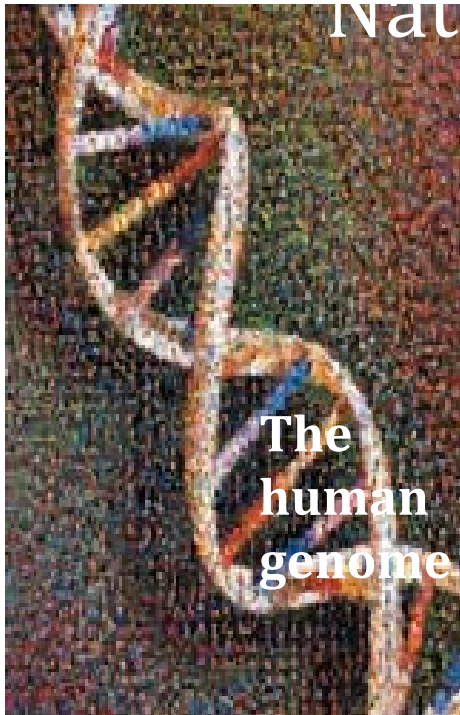


Source: *Children's Health, Nation's Health*, IOM report, 2004



“A Child of Non-disjunction.”
Dr. Josef Warkany

February 2001: Completion of the Draft Human Genome



- Identified 25,000 genes in human DNA
- Identified over 3 billion base pairs
- Provided new avenues for advances in medicine and biotechnology
- Allowed for discovery and annotation of new genes

To date, 46 animal genomes have been sequenced and annotated to some degree.

(<http://genome.ucsc.edu/cgi-bin/hgGateway>)

Genomics Feasibility Study for National Children's Study

Our goal: To build on our team



Elaine Faustman
UW




Jim Swanson
UC Irvine



Bonny Specker
South Dakota State



Jeff Murray
U Iowa



Genomics Feasibility Study for National Children's Study

- **The Trios Project:** A Feasibility Study of Human Whole Genome Sequencing in the National Children's Study
 - Goal to better characterize the full spectrum of variation in the human genome (nucleotide as well as structural variation) and to provide some details about two sources of this variation (the inherited as well as the non-inherited *de novo* components)

Genomics Feasibility Study for National Children's Study

Identify a genomics laboratory for whole genome
sequence



**Debbie
Nickerson**



**Jay
Shendure**



**Mike
Bamshad**



**Evan
Eichler**



**Holly
Tabor**



30 Trios - Genome Variation

Per Genome:

~ 3.8 - 4.4 million single nucleotide substitutions

~ 250,000 small indels

~ 24,000 variants in coding (exome)

12,000 non-synonymous (change aa)

12,000 synonymous (don't change aa)

145 nonsense (truncate)

70 splice

Approximately ~ 6,000 genes carry missense
per individual

Building Capacity: Application

REPORT

Mutations in *ECEL1* Cause Distal Arthrogryposis Type 5D

Margaret J. McMillin,^{1,2} Jennifer E. Below,³ Kathryn M. Shively,¹ Anita E. Beck,^{1,2} Heidi I. Gildersleeve,¹ Jason Pinner,⁴ Gloria R. Gogola,⁵ Jacqueline T. Hecht,⁶ Dorothy K. Grange,⁷ David J. Harris,⁸ Dawn L. Earl,² Sujatha Jagadeesh,⁹ Sarju G. Mehta,¹⁰ Stephen P. Robertson,¹¹ James M. Swanson,¹² Elaine M. Faustman,¹³ Heather C. Mefford,^{1,2} Jay Shendure,³ Deborah A. Nickerson,³ Michael J. Bamshad,^{1,2,3,*} and the University of Washington Center for Mendelian Genomics

The American Journal of Human Genetics 92, 150–156, January 10,
2013

Distal arthrogryposis (DA): group of at least ten disorders characterized by nonprogressive, congenital contractures that typically affect the hands, feet, wrists, and ankles. *ECEL1* is endothelial converting enzyme like 1 (Endopeptidase)

Used linkage analysis and whole-genome sequencing (WGS) of a consanguineous trio to discover that mutations in *ECEL1* cause DA5D and explain ~70% of cases in our cohort

Built Capacity: Application

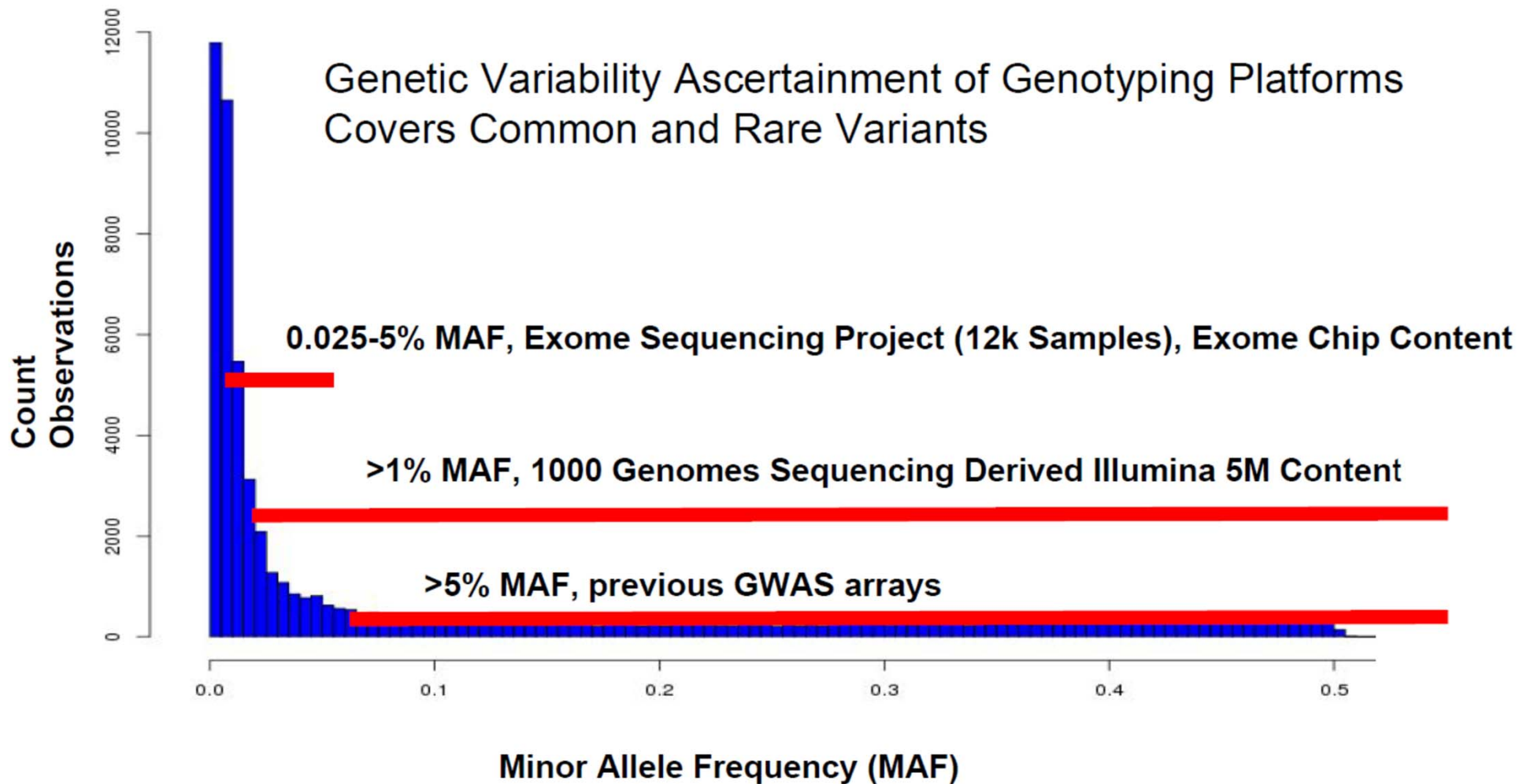
REPORT

Whole-Genome Analysis Reveals that Mutations in Inositol Polyphosphate Phosphatase-like 1 Cause Opsismodysplasia

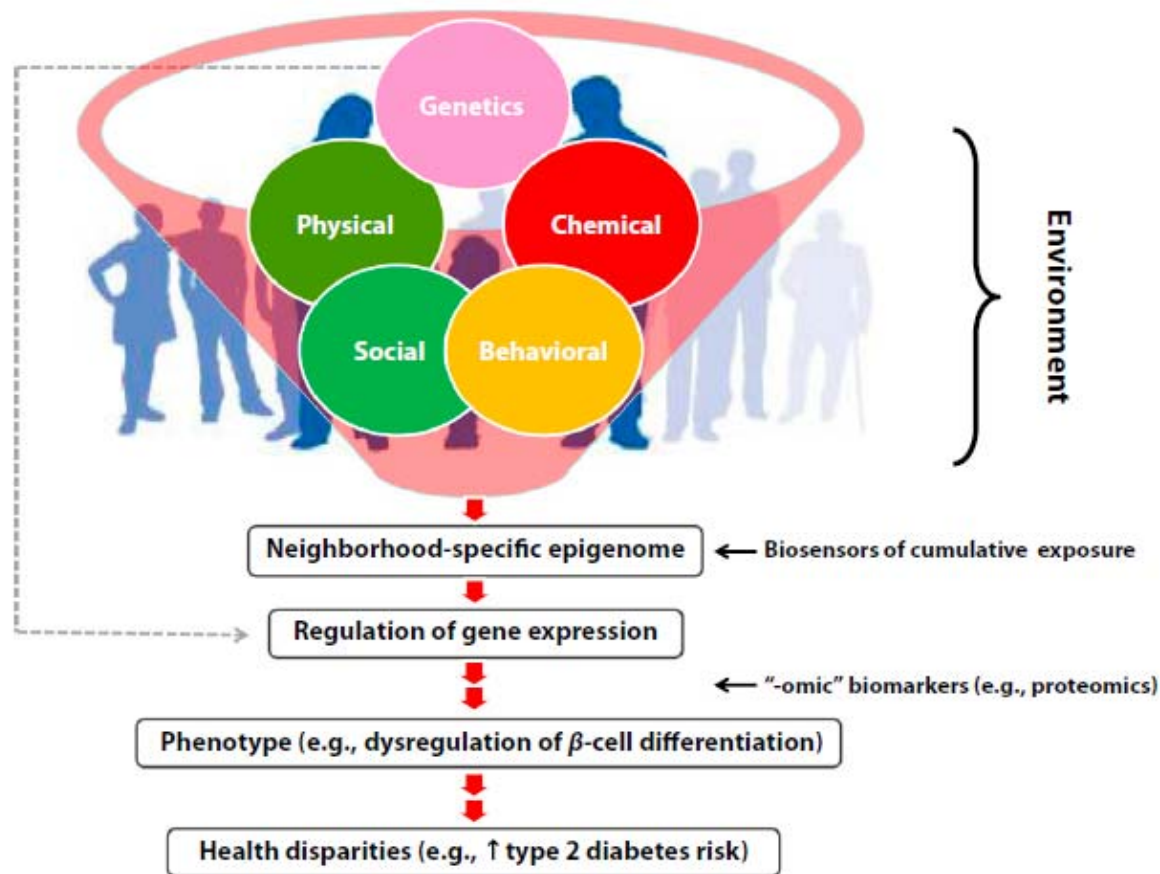
Jennifer E. Below,¹ Dawn L. Earl,^{2,3} Kathryn M. Shively,³ Margaret J. McMillin,³ Joshua D. Smith,¹ Emily H. Turner,¹ Mark J. Stephan,⁴ Lihadh I. Al-Gazali,⁵ Jozef L. Hertecant,⁵ David Chitayat,⁶ Sheila Unger,⁷ Daniel H. Cohn,^{8,9} Deborah Krakow,^{9,10} James M. Swanson,¹¹ Elaine M. Faustman,¹² Jay Shendure,¹ Deborah A. Nickerson,¹ Michael J. Bamshad,^{1,2,3,*} and University of Washington Center for Mendelian Genomics

The American Journal of Human Genetics 92, 137-143, January 10, 2013

- Opsismodysplasia: rare, autosomal-recessive skeletal dysplasia characterized by short stature, characteristic facial features, and in some cases severe renal phosphate wasting.
- Linkage analysis and whole-genome sequencing of a consanguineous trio to discover mutations in inositol polyphosphate phosphatase-like 1 (INPPL1)
- Evaluation of 12 families with opsismodysplasia revealed that INPPL1 mutations explain ~60% of cases overall, including both of the families in our cohort with more than one affected child and 50% of the simplex cases.



Epigenome: Biosensor of Cumulative Exposure to Chemical and Nonchemical Stressors Related to Environmental Justice



Why is social stress relevant to children's environmental health?

- Both physical toxicants and social stress exposure during development can have life-long impacts
- Social stress can be an effect modifier of physical toxicant exposure and disease pathway
- Social stress and environmental toxicants often have overlapping exposure profiles, potentially impacting low income and minority populations most heavily

Epigenomic Factors that Effect our Risk Assessment Approaches

- Epigenomic changes are known to be affected by both chemical and non-chemical stressors
- Epigenomic changes occur after exposure to many chemicals, not related by structure
- Epigenomic or stress changes can be inherited and affect multiple generations.
- Epigenomic changes after chemical and non-chemical stressors can affect the same pathways.
- There are many different types of epigenomic pathways that can be changed by stressor exposure and these occur differentially across time (lifestage) in various biological tissues and can be species, organic and organism specific.
- There are known genetic polymorphisms that affect epigenomic responses

Small Magnitude Effect Sizes in Epigenetic Endpoints are Important in Children's Environmental Health Studies

The Children's Environmental Health and Disease Prevention Research Center's Epigenetics Working Group

Carrie V. Breton, Carmen J. Marsit, Elaine Faustman, Kari Nadeau, Jaclyn M. Goodrich, Dana C. Dolinoy, Julie Herbstman, Nina Holland, Janine M. LaSalle, Rebecca Schmidt, Paul Yosefi, Frederica Perera, Bonnie R. Joubert, Joseph Wiemels, Michele Taylor, Ivana V. Yang, Rui Chen, Kinjal M. Hew, Deborah M. Hussey Freeland, Rachel Miller, and Susan K. Murphy

Under Review, 2016



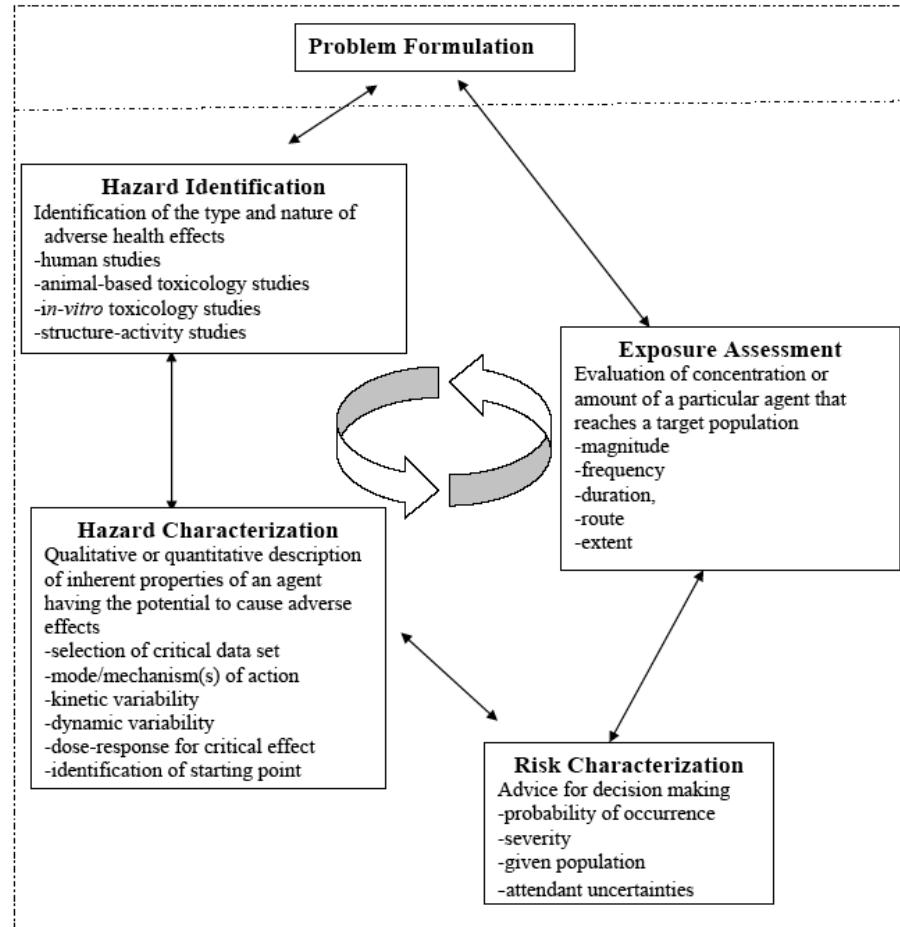
Untitled

Warkany recognized both in his science and in his art a broad definition of environment and in this drawing in particular emphasized under exposure to iodine in underserved populations as a critical missing component for health and development.

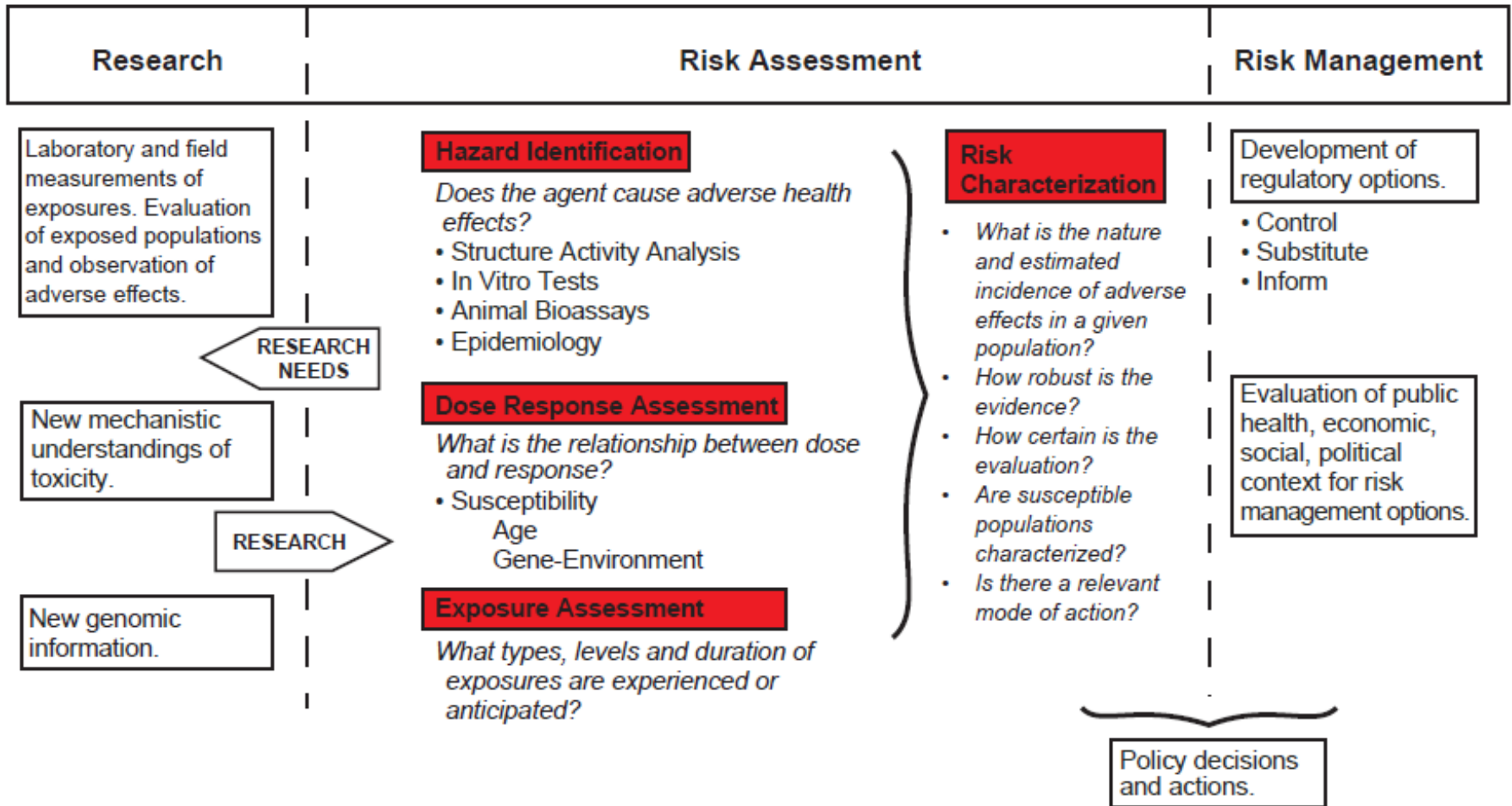


Past Presidents Luncheon, 2009 Annual Meeting, Rio Mar, Puerto Rico. Presidents in attendance (standing, left to right): Richard K. Miller, J.F. Cordero, T.H. Shepard, J.M. Friedman, Lewis B. Holmes, G.P. Daston, M.S. Tassinari, T.B. Knudsen, J.M. Rogers, C.D. Chambers, R.L. Brent, R.W. Tyl, B.F. Hales, J.M. DeSesso, E.M. Faustman, R.J. Kavlock, C.A. Kimmel, K.L. Jones. Standing far right is Louise Winn, Chair of the Education committee, and seated are students and postdoctoral fellows (Photograph by Dr. Robert Parker).

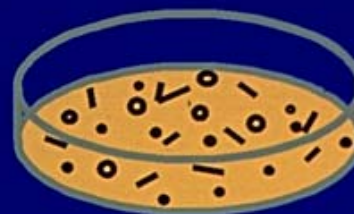
Risk Assessment



WHO, 2006



METHODS TO IDENTIFY TOXICITY



Faustman et al, 2010

Spectrum of Reproductive Toxicity Evaluations

Life Stages

Study Designs:

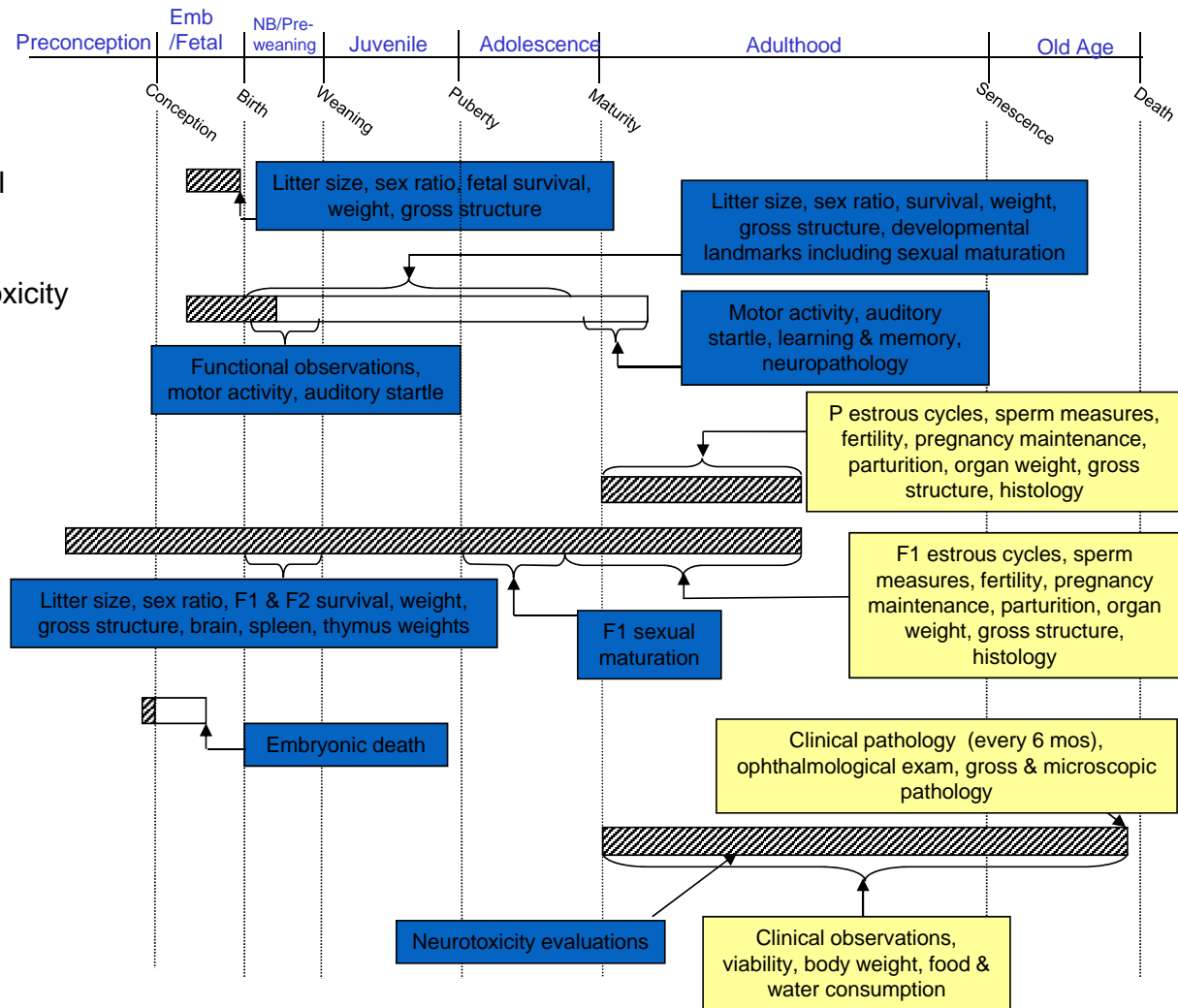
Prenatal Developmental Toxicity Study

Developmental Neurotoxicity Study

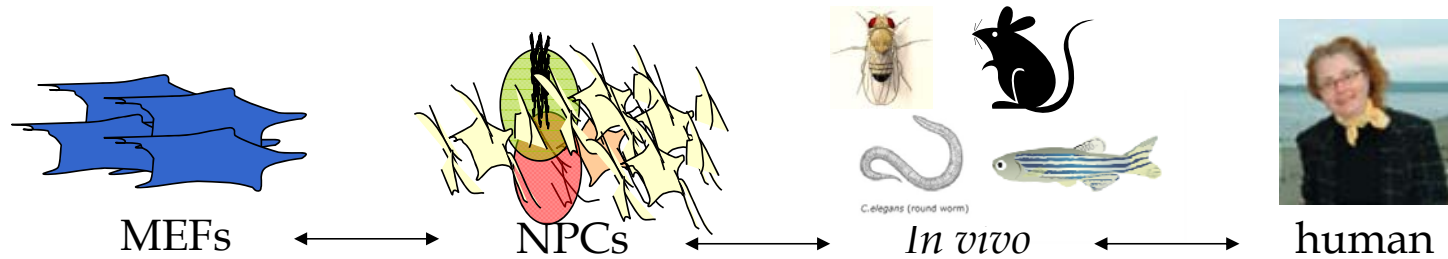
Reproduction and Fertility Study

Dominant Lethal

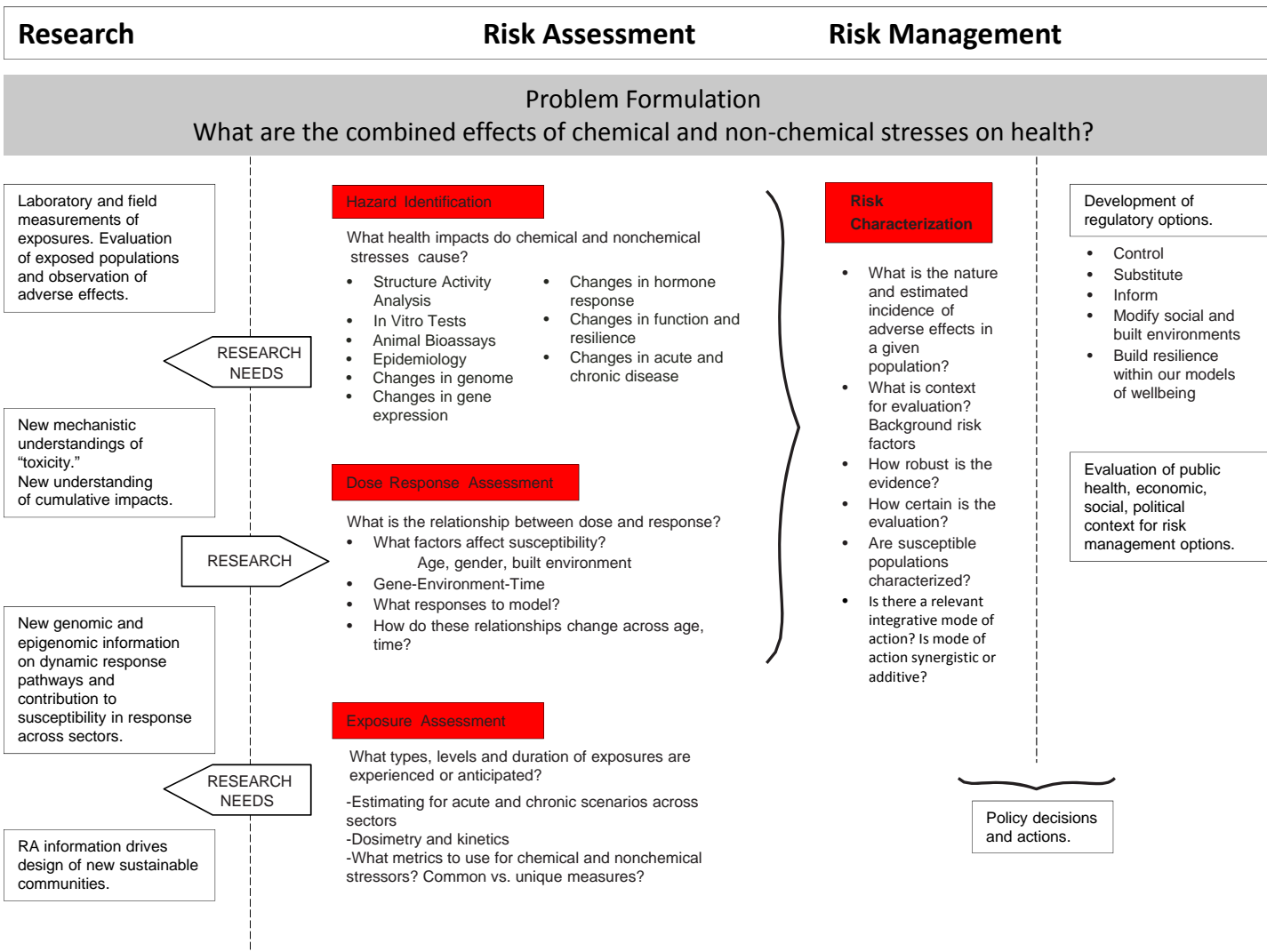
Subchronic/chronic



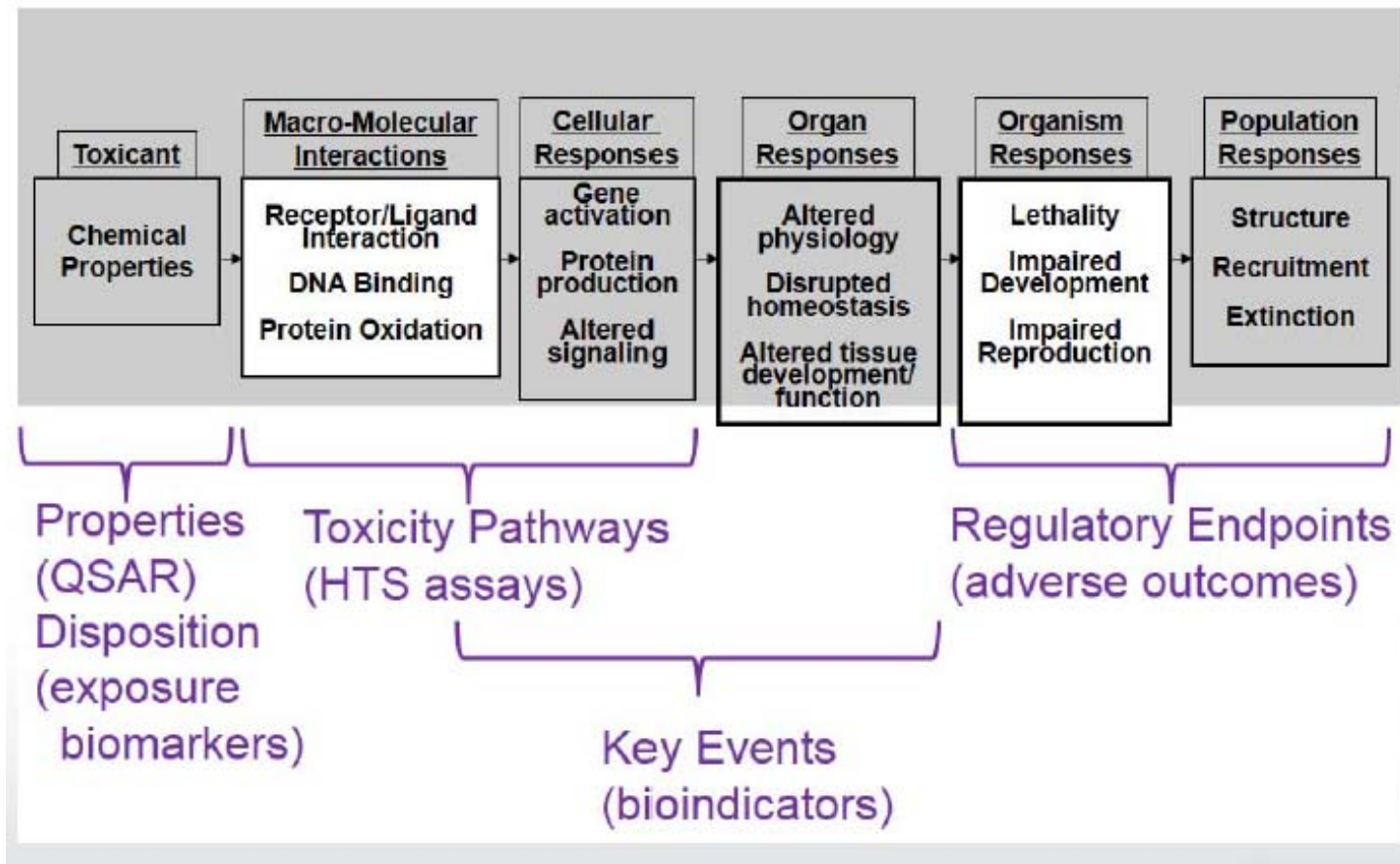
Ability of experimental systems to assess and predict neurodevelopmental toxicity across multiple levels of biological complexity



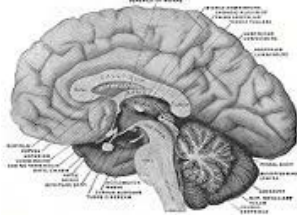
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|--|---|--|--|
| <ul style="list-style-type: none"> • Signaling pathways • Cell cycle kinetics • Viability including mechanism of cell death | <ul style="list-style-type: none"> • Signaling pathways • Cell cycle kinetics • Viability including mechanism of cell death • Differentiation • Neuronal phenotype | <ul style="list-style-type: none"> • Signaling pathways • Cell cycle kinetics • Viability including mechanism of cell death • Differentiation • Neuronal phenotype • Migration • Brain structure and morphology • Function • Behavior | <ul style="list-style-type: none"> • Signaling pathways • Cell cycle kinetics • Viability including mechanism of cell death • Differentiation • Neuronal phenotype • Migration • Brain structure and morphology • Function • Behavior |
|--|---|--|--|



AOP and biomarkers serve to link elements and describe disease pathogenesis



In Vitro Brain



Human neural progenitors cells (hNPCs)
Commercially available line derived from male human embryonic stem cells

In Vitro Testis



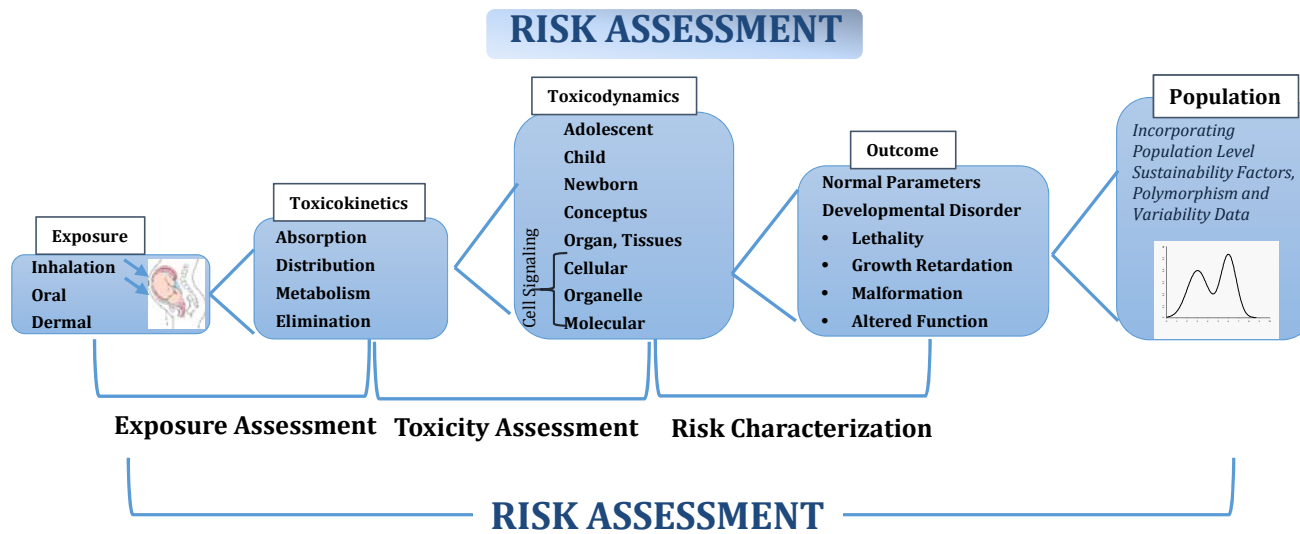
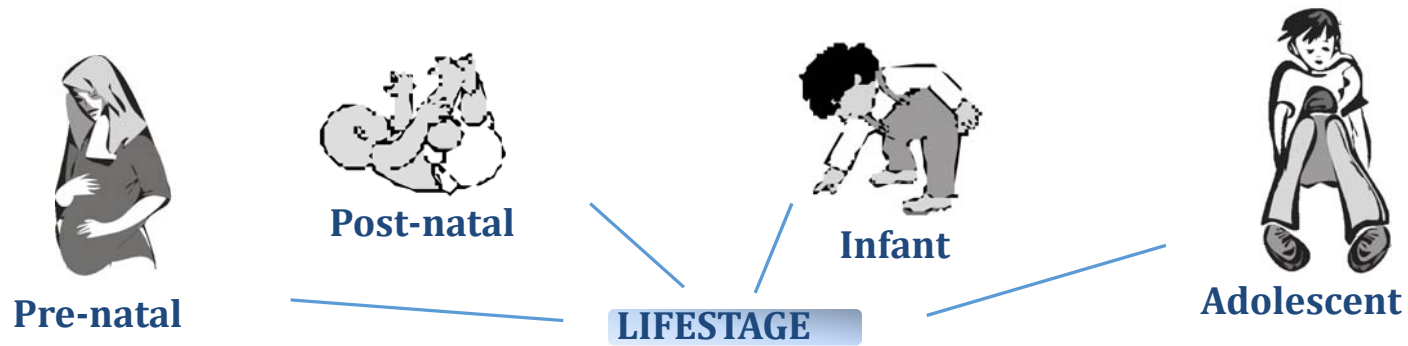
3D testicular co-culture
Primary co-culture derived from postnatal day 5 rat testis and cultured with a Matrigel overlay

Common Pathways of Response

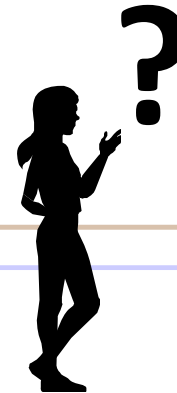
- Proliferation
- Differentiation
- Apoptosis
- Stress response
- Hormonal regulation
- Epigenetic regulation

Common Approaches

- Expression of key protein markers of specific cell types and developmental stages
- Quantification of normal pathway dynamics through time in culture (general assessment as well as targeted assessment of pathways of interest)
- Anchoring to *In Vivo* developmental pathway dynamics



How can we use new genomic information to inform our risk assessments?



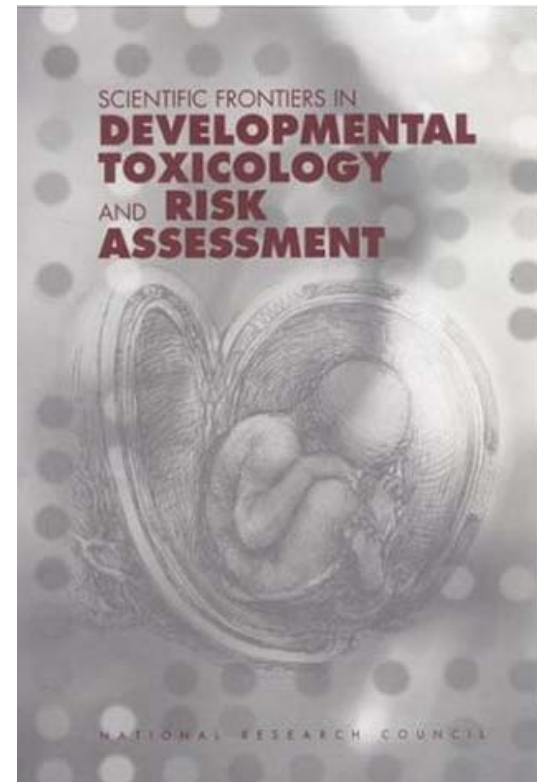
Scientific Frontiers in Developmental Toxicology and Risk Assessment

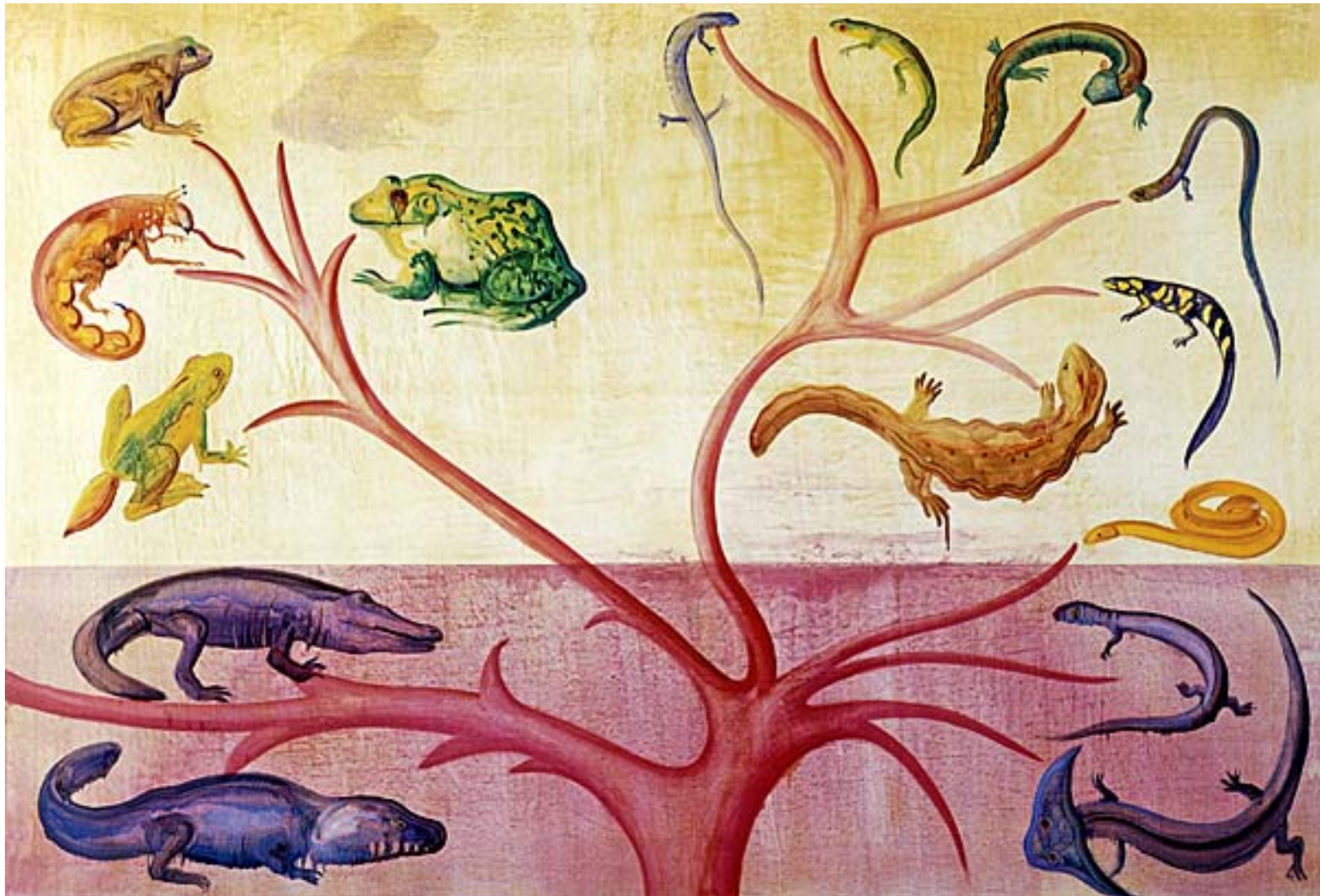
National Research Council

Chair: Elaine M. Faustman

Co-Chair: John C. Gerhart

www.books.nap.edu/catalog/9871.html





Alexis Rockman - *Amphibian Evolution*, 1987, oil & acrylic on canvas

Gene Ontology: Tool for the unification of biology.

The Gene Ontology Consortium

Ashburner M, Ball CA, Blake JA, Botstein D, Butler H, Cherry JM, Davis AP, Dolinski K, Dwight SS, Eppig JT, Harris MA, Hill DP, Issel-Tarver L, Kasarskis A, Lewis S, Matese JC, Richardson JE, Ringwald M, Rubin GM, Sherlock G.

Nat Genet. 2000 May;25(1):25-9.

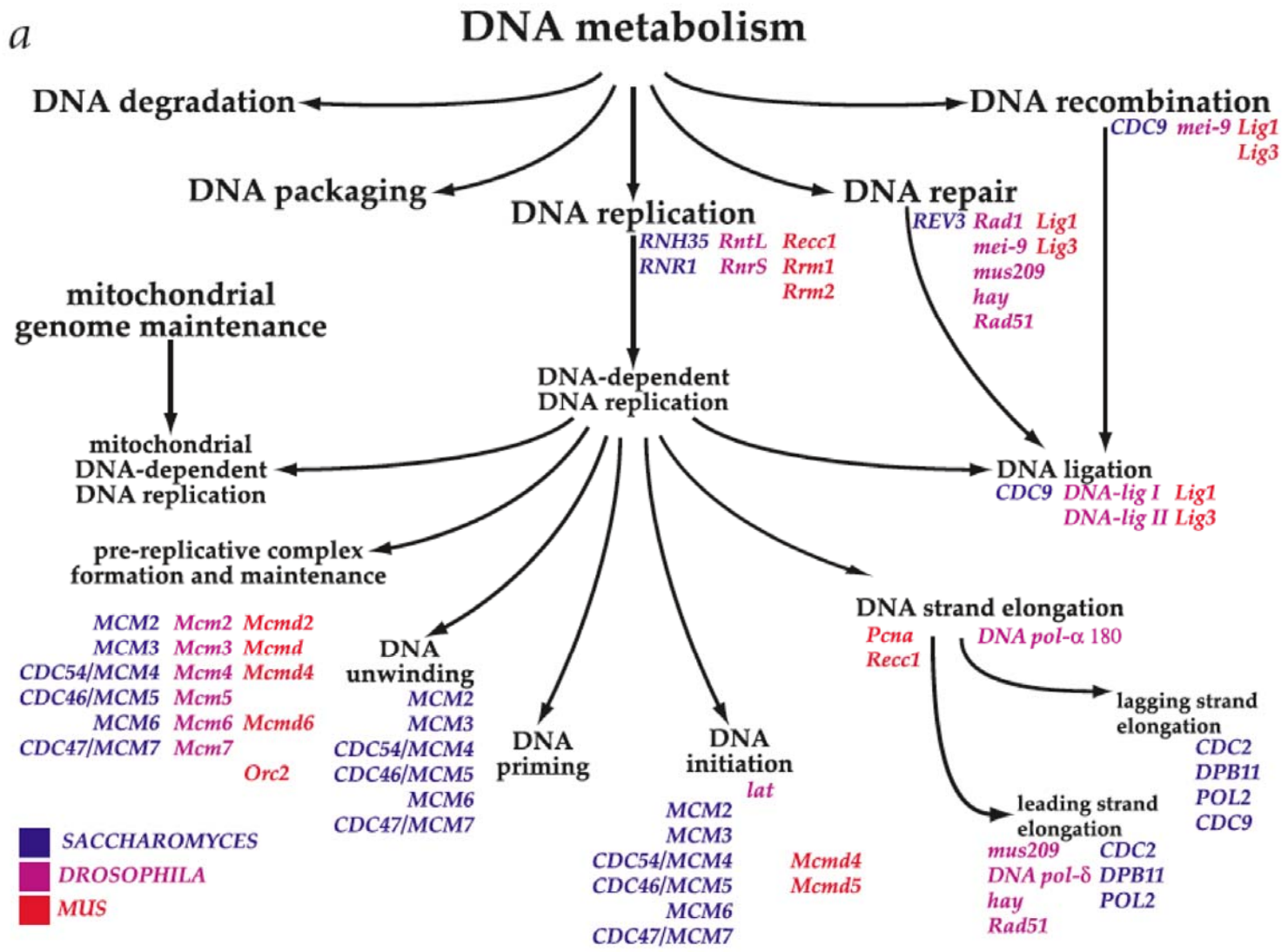
Gene Ontology Hierarchy: Based on the AmiGO, the GO Consortium's annotation and ontology toolkit

Carbon S, Ireland A, Mungall CJ, Shu S, Marshall B, Lewis S, AmiGO Hub, Web Presence Working Group.
AmiGO: online access to ontology and annotation data.

Bioinformatics. Jan 2009;25(2):288-9

<http://www.geneontology.org/>

Examples of Cross-Species Extrapolation within Gene Ontology Framework



Ashburner et al., 2000

Generalizations about cell-cell signaling in development

- Signaling is used in almost every developmental event, probably in all metazoa.
(E.g., in axis specification, morphogenesis, organogenesis, tissue renewal, cytodifferentiation...)
- There are approximately 17 pathways of cell-cell signaling.
(Perhaps a few more will be discovered.)
- The 17 pathways are highly conserved among metazoa. They were probably present in the last common ancestor of all modern bilateral animals.

The 17 Intercellular Signaling Pathways

Period During Development When Signaling Pathway Used

(The mammalian fetus uses all 17)

Early (axis specification, germ layer specification, left-right asymmetry) and continued in all later stages.

1. Wnt pathway
2. Hedgehog pathway
3. TGF β receptor (ser/thr kinase) pathway
4. Receptor tyrosine kinase (small G protein) pathway
5. Notch/Delta pathway
6. Cytokine receptor (cytoplasmic tyrosine kinases; JAK/STAT pathway)

Middle (during organogenesis and cytodifferentiation) and continued in all later stages.

7. IL1/Toll NF κ B pathway
8. Nuclear hormone receptor pathway
9. Apoptosis pathway
10. Integrin pathway
11. Receptor phosphotyrosine phosphatase pathway

Late (after cell types have differentiated). Used in Fetal/Larval/Adult Physiology.

12. Receptor guanylate cyclase pathway
13. Nitric oxide receptor pathway
14. G-protein coupled receptor (large G protein) pathway
15. Cadherin pathway
16. Gap junction pathway
17. Ligand-gated cation channel pathway

The 17 Intercellular Signaling Pathways

We now have new common languages and genomically conserved response pathways identified.

We are using our newly gained knowledge about genomic conservation to:

- Identify common pathways that are impacted across species and platforms?
- How and what toxicants impact these conserved pathways?
- At what levels and times of exposure are impacts observed?

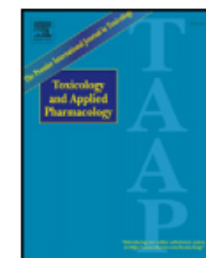


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Contents lists available at SciVerse ScienceDirect

Toxicology and Applied Pharmacology

journal homepage: www.elsevier.com/locate/ytaap



Identifying developmental toxicity pathways for a subset of ToxCast chemicals using human embryonic stem cells and metabolomics[☆]

N.C. Kleinstreuer^{b,*}, A.M. Smith^a, P.R. West^a, K.R. Conard^a, B.R. Fontaine^a, A.M. Weir-Hauptman^d, J.A. Palmer^a, T.B. Knudsen^b, D.J. Dix^b, E.L.R. Donley^a, G.G. Cezar^{a,c}

^a Stemina Biomarker Discovery, Inc., Madison, WI 53719, USA

^b NCCT, US EPA, RTP, NC 27711, USA

^c University of Wisconsin-Madison, Madison, WI 53706, USA

^d Covance, Inc., Madison, WI 53704, USA

Genomic Conservation

Challenges for *in vitro* to *in vivo* extrapolation.

- Cellular pathways information is used in a 3-D context at organ level.

Challenges for cross-species specific information.

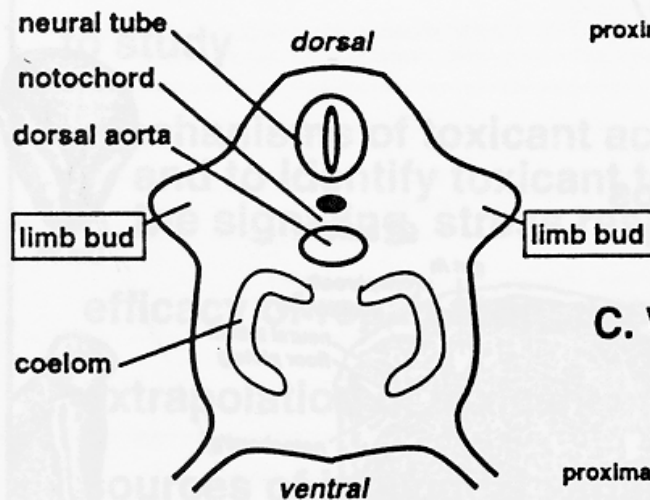
- Although cellular pathway conservation occurs, organ specific context is organism specific.

Challenges for cross-compound extrapolations.

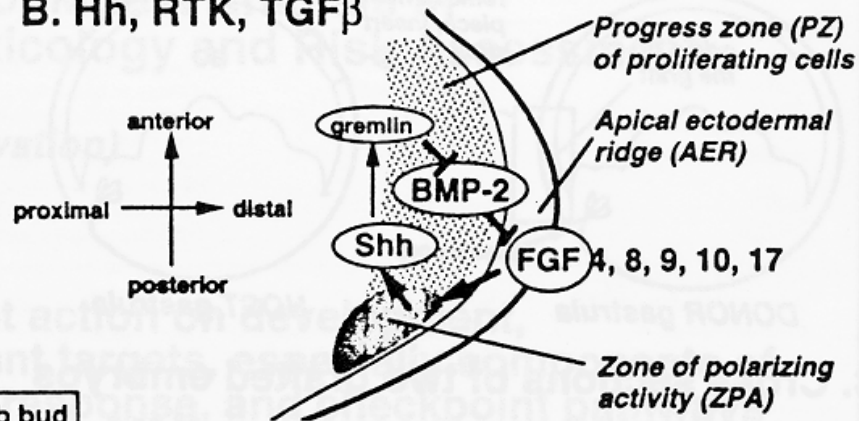
- Generation of toxicogenomic examples for toxicants are at the earliest stages.

Five signaling pathways in limb bud development

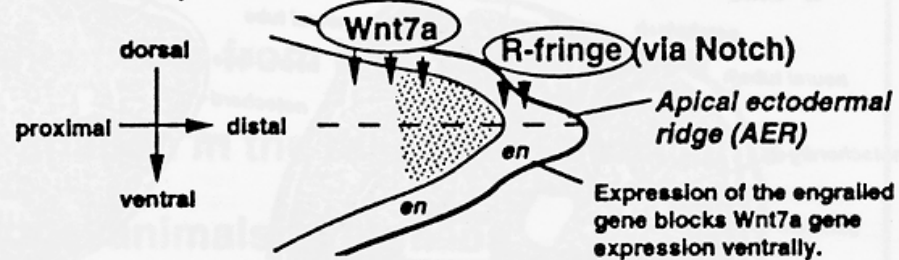
A. Location of the limb buds in the mouse or chick embryo



B. Hh, RTK, TGF β



C. Wnt, Notch



Roles of the Hedgehog Signaling Pathway

In vertebrate development:

- Induction of the floorplate of the neural tube by notochord
- Induction of the brain floorplate by prechordal mesoderm
- Induction of the sclerotome (from somite) by notochord left-right asymmetry
- Anteroposterior development of the fin/limb (via ZPA)
- Gut development, interactions with the visceral mesoderm
- Hair follicle development
- Break development
- Spermatogenesis

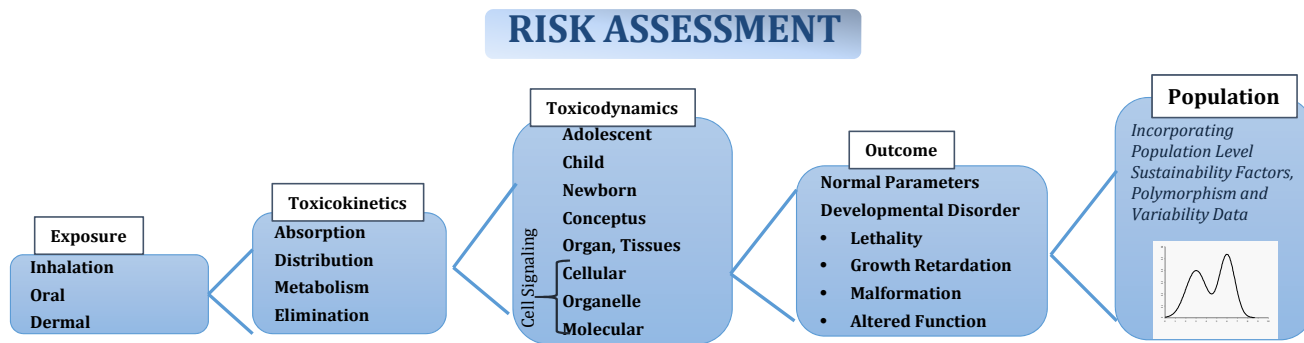
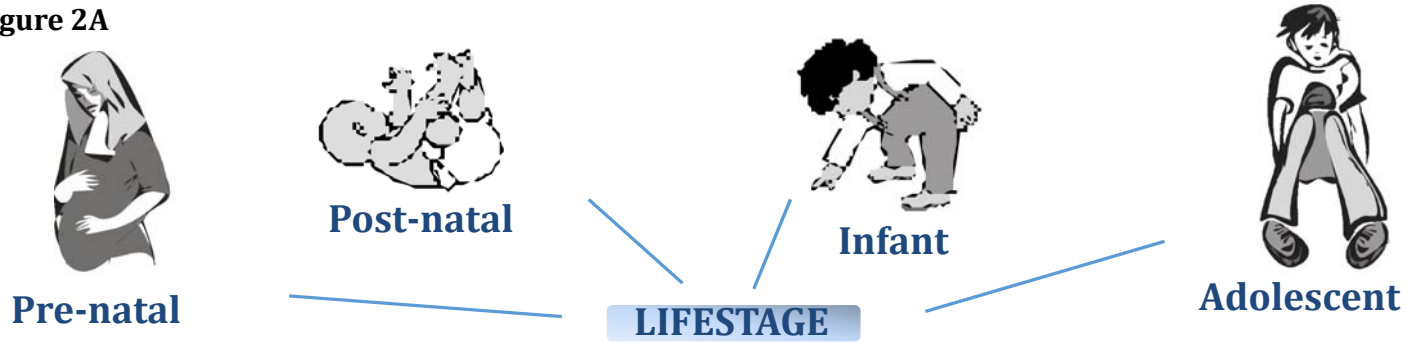
In Drosophila development:

- Segment formation, posterior compartment
- Appendage development
- Gut development, interactions with visceral mesoderm
- Eye/brain development
- Oogenesis

Challenges and Opportunities
*for using systems biology information and approaches for understanding
mechanisms of toxicity and dose-response*

- Intra- and cross-species extrapolation
- Facilitate use of model systems
- Characterize low dose and early temporal response
- Facilitate in vitro to in vivo extrapolation
- Extrapolation across levels of biological complexity
- Identify actual pathways of disease

Figure 2A



Computational Models of Neocortical Neuronogenesis and Programmed Cell Death in the Developing Mouse, Monkey, and Human

Julia M. Gohlke¹, William C. Griffith and Elaine M. Faustman

Department of Environmental and Occupational Health Sciences, University of Washington, Seattle, WA 98105, USA
¹Current address: Environmental Systems Biology Group, Laboratory of Molecular Toxicology, National Institute of Environmental Health Sciences, RTP, NC 27709, USA

A Computational Model for Neocortical Neuronogenesis Predicts Ethanol-Induced Neocortical Neuron Number Deficits

J.M. Gohlke^a W.C. Griffith^a S.M. Bartell^b T.A. Lewandowski^c
E.M. Faustman^a

A SYSTEMS-BASED COMPUTATIONAL MODEL OF ALCOHOL'S TOXIC EFFECTS ON BRAIN DEVELOPMENT

Julia M. Gohlke, Ph.D.; Susanne Hiller-Sturmböfel, Ph.D.; and Elaine M. Faustman, Ph.D., DABT

Wiley-Liss, Inc.

Birth Defects Research (Part B) 83:1–11 (2008)

Original Article

Computational Models of Ethanol-induced Neurodevelopmental Toxicity Across Species: Implications for Risk Assessment

Julia M. Gohlke, William C. Griffith, and Elaine M. Faustman*

Assessing the Health Benefits of Air Pollution Reduction for Children

Eva Y. Wong,¹ Julia Gohlke,¹ William C. Griffith,¹ Scott Farrow,^{2,3} and Elaine M. Faustman^{1,2}

Research report

The role of cell death during neocortical neurogenesis and synaptogenesis: implications from a computational model for the rat and mouse

Julia M. Gohlke, William C. Griffith, Elaine M. Faustman*

Modeling developmental processes in animals: applications in neurodevelopmental toxicology

Elaine M. Faustman^{a,b,c,*}, Julia Gohlke^{a,b,c}, Nancy L. Judd^{a,b,c},
Thomas A. Lewandowski^{a,b,c,d}, Scott M. Bartell^{a,b,c,e}, William C. Griffith^{a,b,c}

TOXICOLOGICAL SCIENCES 86(2), 470–484 (2005)
doi:10.1093/toxsci/kfi209
Advance Access publication May 25, 2005

A Systems-Based Computational Model for Dose-Response Comparisons of Two Mode of Action Hypotheses for Ethanol-Induced Neurodevelopmental Toxicity

J. M. Gohlke,¹ W. C. Griffith, and E. M. Faustman²

Summary Points

To extrapolate across organisms and biological levels of complexity (cell-free, *in vitro* to *in vivo*, rodent and human) risk assessors need...

- **KINETIC** and **DYNAMIC** information
- Framework to link information across biological systems/assay conditions
- Qualitative and quantitative information
- Systems biology allows for such considerations and provides a platform for examining mechanisms of action as well as extrapolation of results



Dr. Josef Warkany.



Mari Katayama



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Central Laboratory for Human Embryology



University of Washington

