

Harmonizing and sharing phenotypes across organisms for diagnostics and mechanism discovery

The Monarch Initiative

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3 August, 2021

These slides bit.ly/mi-risk-s3

CURRENT DISCRETE
CLINICAL DATA

EMERGING
HIGH-THROUGHPUT
DATA

PHENOTYPIC FEATURES

ENVIRONMENT

GENETICS

Family
History
Pedigree



Clinical
notes



Clinical
labs



Diagnostic
imaging



Drugs
prescribed



Survey
instruments



Single
genes



Pedigree
analysis



Exercise



Wearables



Biomonitoring



Drug
Adherence
(PBM)



Microbiome

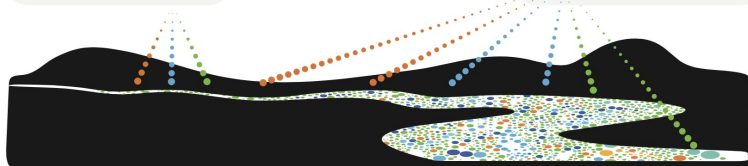


Diet



Metabolomics
Epigenomics
Gene panels
Exomes (WES)
Genomes (WGS)

Clinical Phenotyping & Diagnostics





Monarch Initiative

monarchinitiative.org

Unified Human Data

Development of ontologies and design patterns

Tools, web services, visual widgets

E.g.: Phenopackets

A bridge to the clinic

Data

Ontologies

Tools

Standards

Clinical delivery



Genomics

Proteomics

Metabolic Pathways

Molecular Modeling

Molecular Simulation

Cellular Models

Molecular Assays



Genomic Testing

Biospecimens

Lab Data

Trials Data

Disease & Syndrome

Medical Imaging

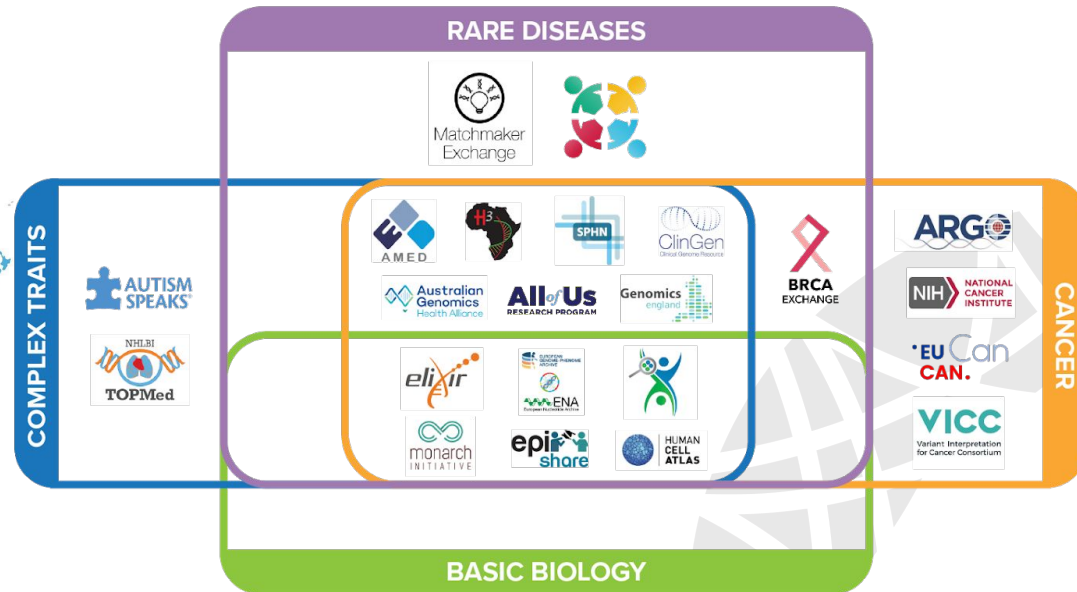
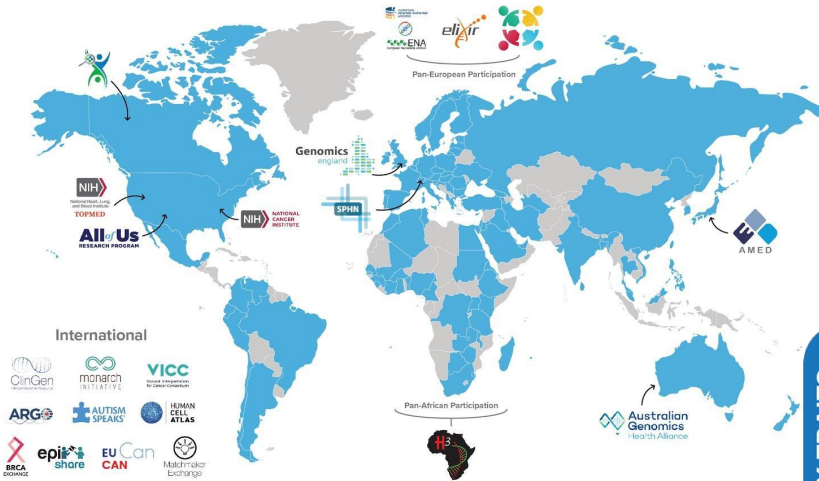
EHR Structures

Patient Record Data

Global Alliance for Genomics & Health (GA4GH)

www.ga4gh.org

GA4GH aims to accelerate progress in genomic science and human health by developing standards and framing policy for responsible genomic and health-related data sharing.



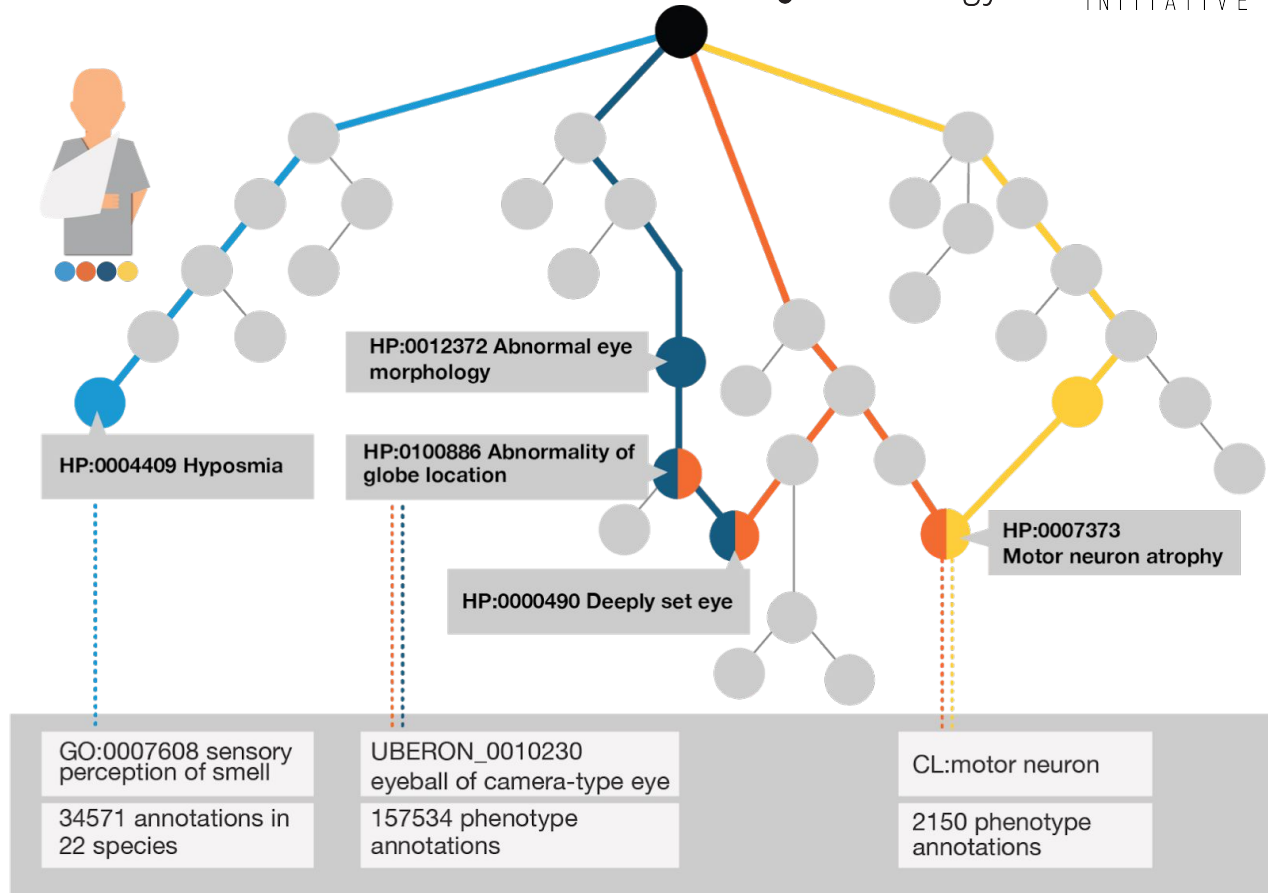
Global Alliance
for Genomics & Health

Collaborate. Innovate. Accelerate.

Human Phenotype Ontology (HPO)

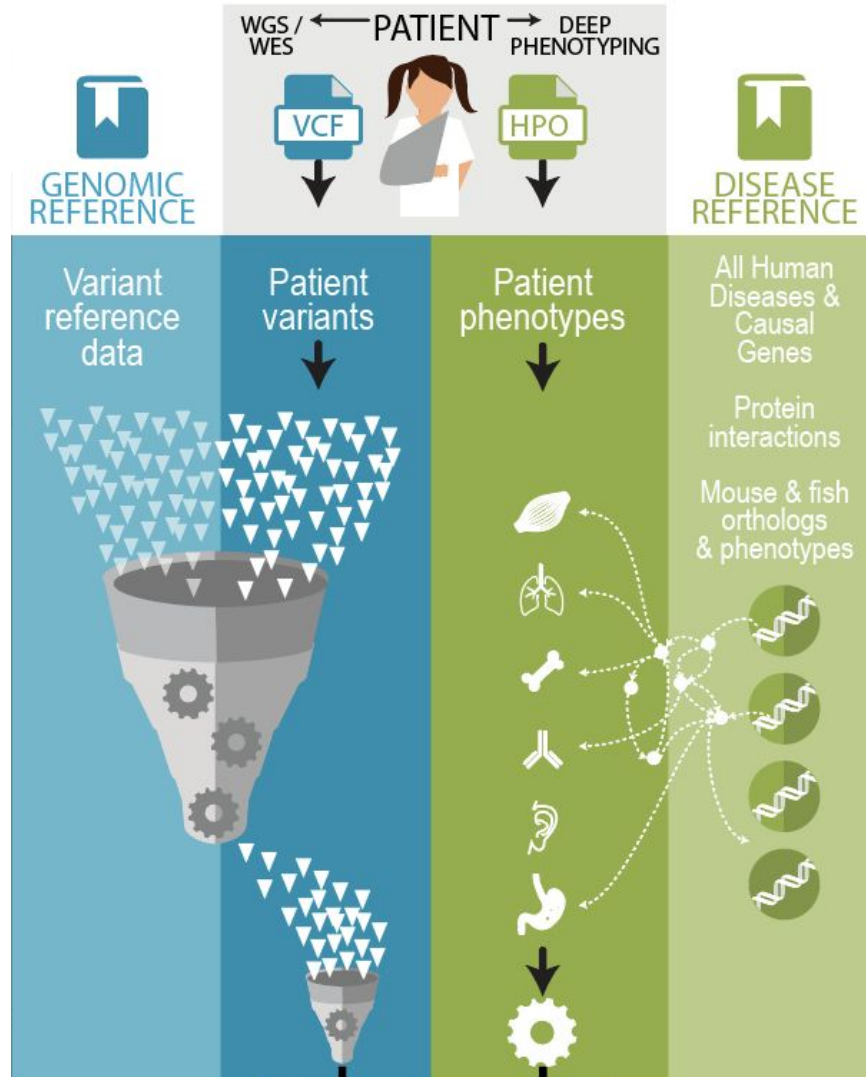
- **Phenotyping terminology**
>14,500 terms
- **Computational disease models**
>190,000 disease-phenotype annotations (associations)
- **Widely adopted in rare disease genomic diagnostic tools**
100,000 Genomes Project, SOLVE-RD, NIH-UDP, etc.

hpo.jax.org

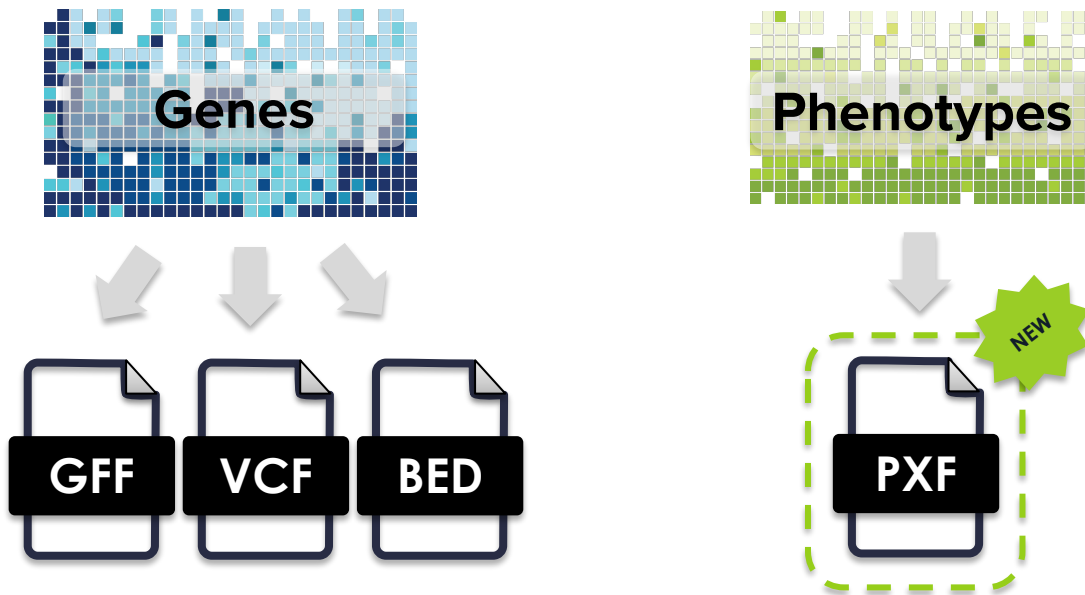


Combining genomic and phenomic data improves variant prioritization for diagnosis

doi: [10.1038/qim.2015.137](https://doi.org/10.1038/qim.2015.137)



Standard exchange formats exist for sequence/genomes but not for phenotypes

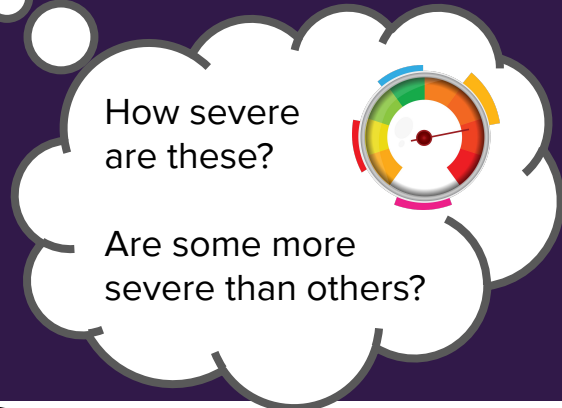
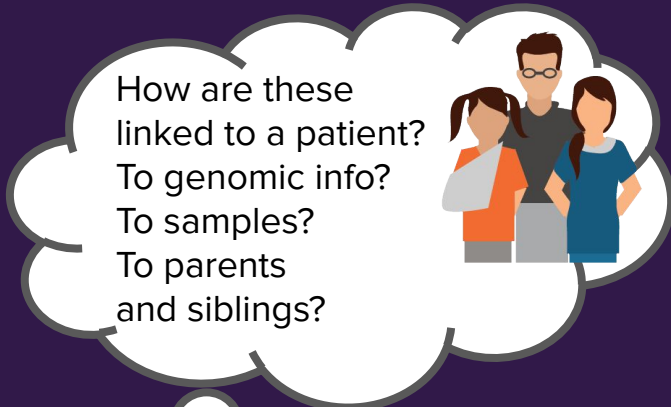
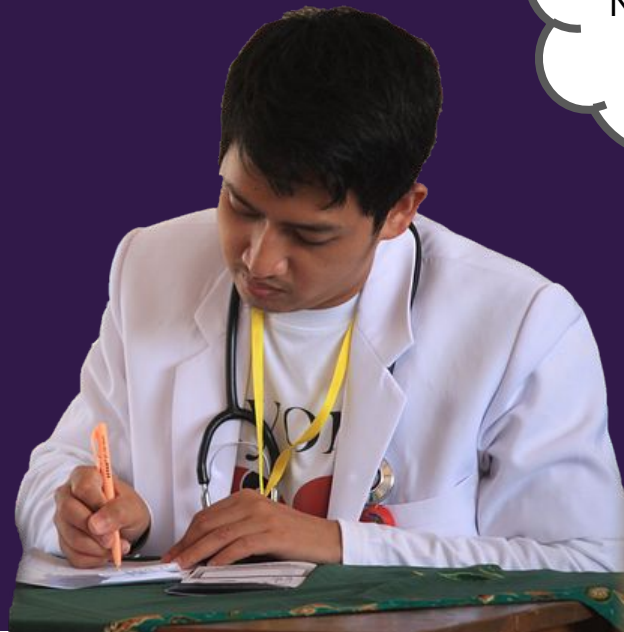


We need a standard way to share case-level phenotypic information that is not free text, a candidate diagnosis proxy, nor full EHR data exported via PDF



Phenopackets can help us do better

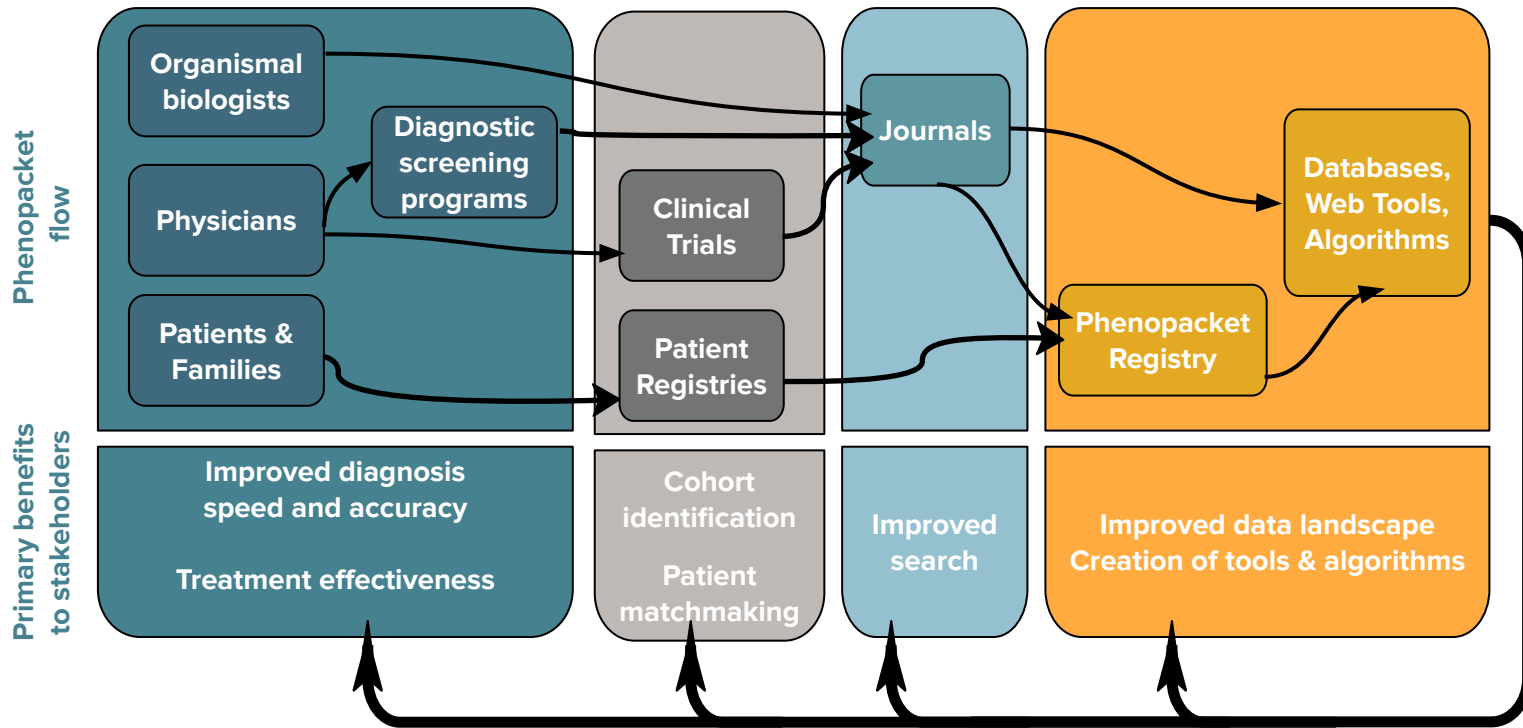
Craniosynostosis
Brachydactyly
Proptosis
Broad thumb...

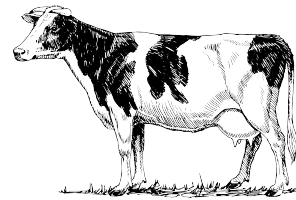
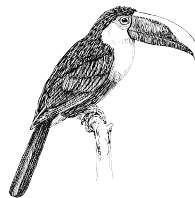
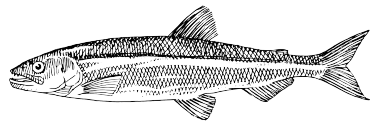
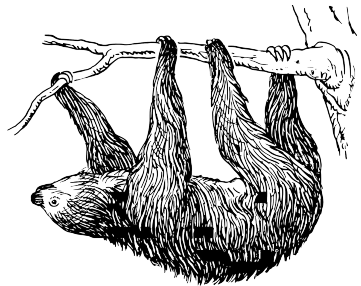


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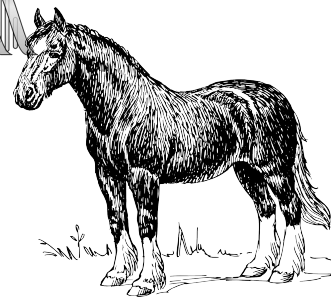
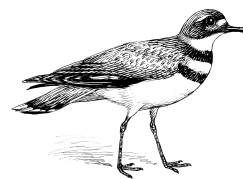
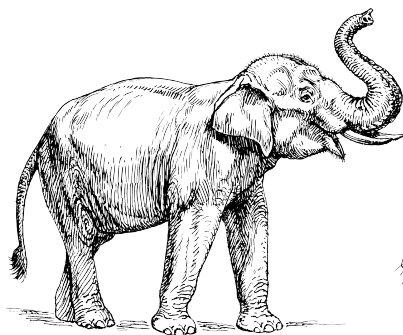
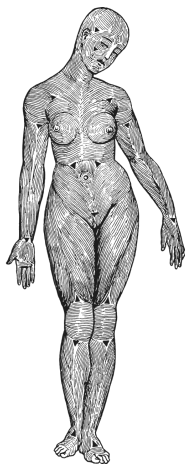
The Phenopacket Ecosystem

users and use cases





The Value of Cross-Species Research



Other species aren't just relevant; each has unique phenotypes



- The dog's retina has area centralis (analogous to the human macula) & fovea-like region, similar to humans; useful to study naturally occurring cone diseases



- Aged cats are natural models of Alzheimer's Disease: they form Abeta oligomers, neurofibrillary tangles, and have neuronal loss



- Naked Mole Rats don't get cancer



- Armadillos are a natural host of *M. leprae*, the mycobacterium that causes leprosy (only one besides humans)



- Tree shrews' glioblastomas are morphologically & genetically similar to humans (& more similar than mouse models)

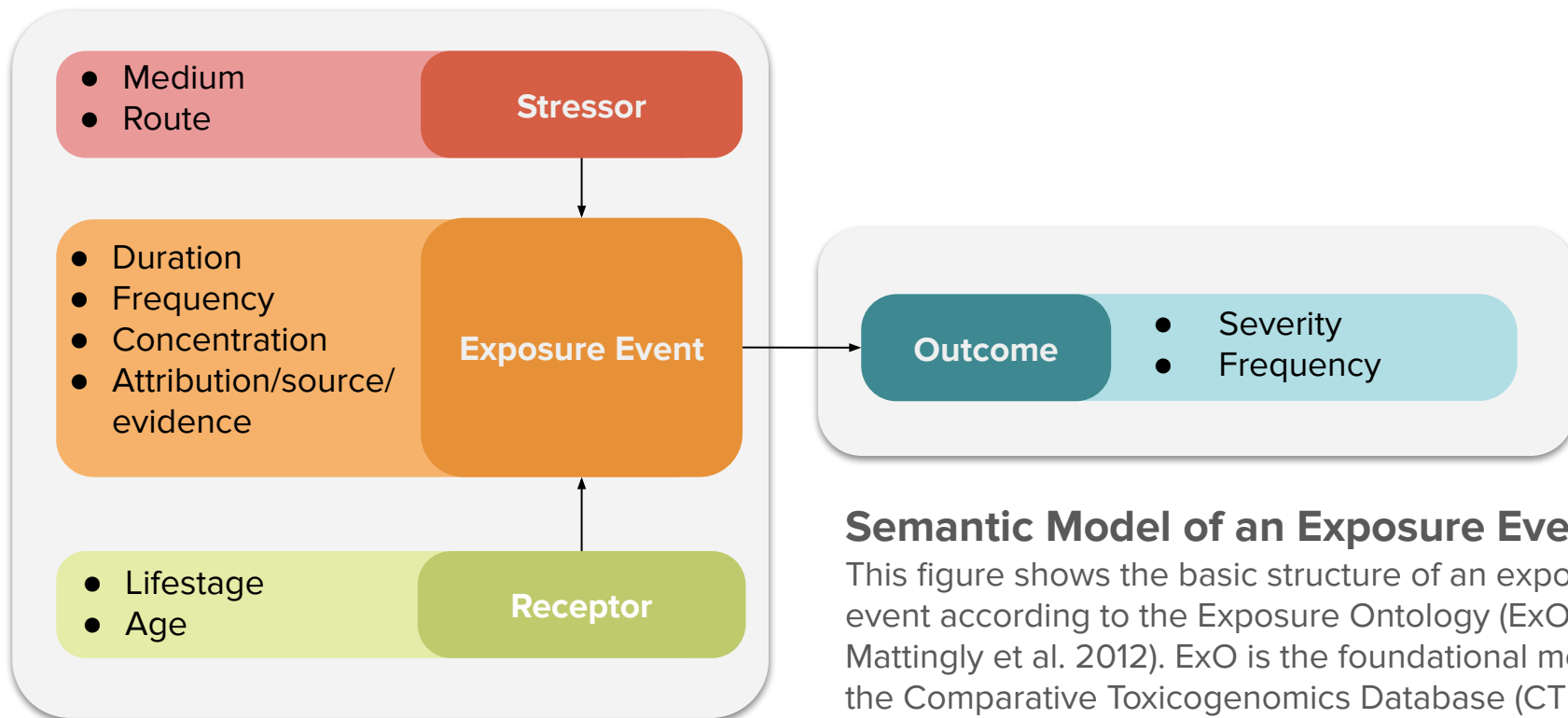


- Great pond snails are models of inflammation-mediated memory dysfunction, and show evidence of spontaneous neural tissue regeneration after injury



- Silkworms are a model for uric acid metabolism. Decreases in plasma uric acid are correlated with clinical progression of Parkinson's Disease

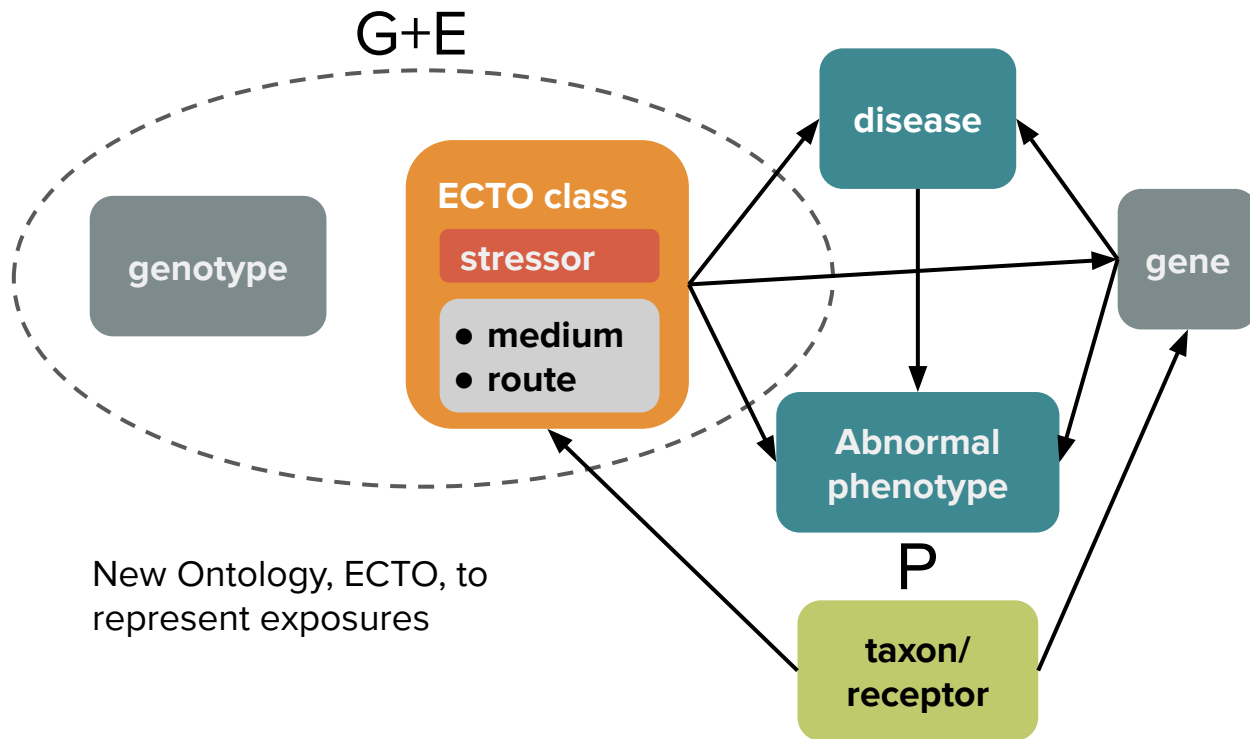
Environmental Exposures Modeling with ExO



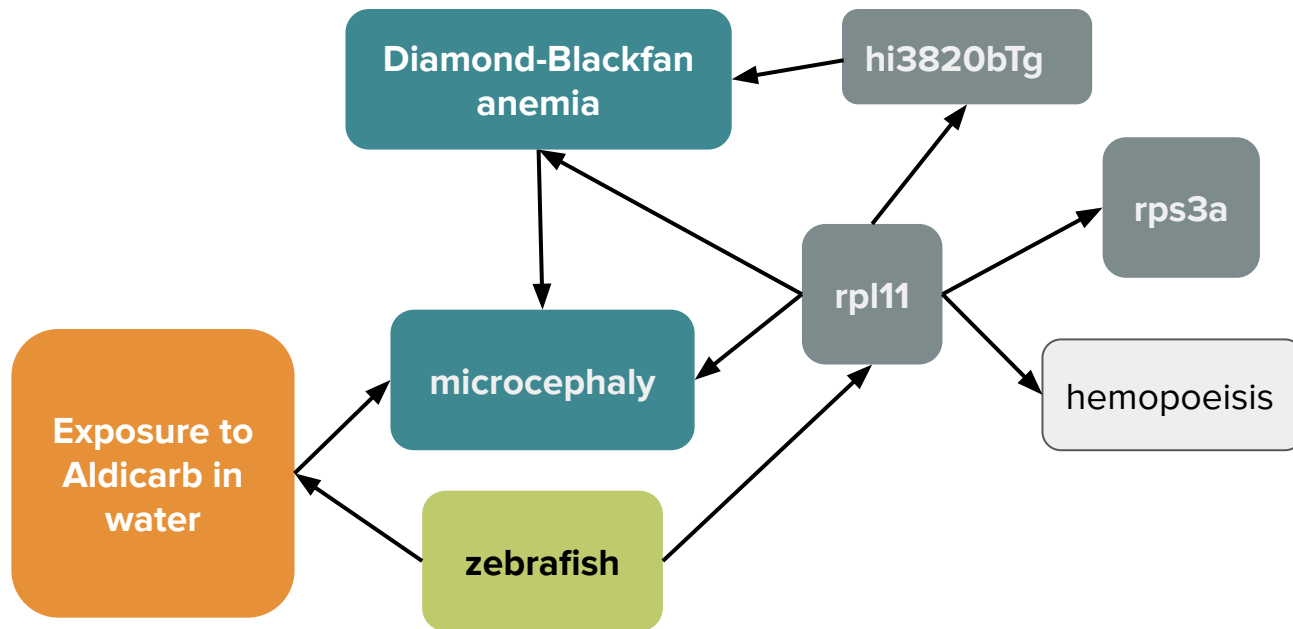
Semantic Model of an Exposure Event.

This figure shows the basic structure of an exposure event according to the Exposure Ontology (ExO; Mattingly et al. 2012). ExO is the foundational model for the Comparative Toxicogenomics Database (CTD; Mattingly et al. 2006).

Integration with the Monarch Knowledge Graph

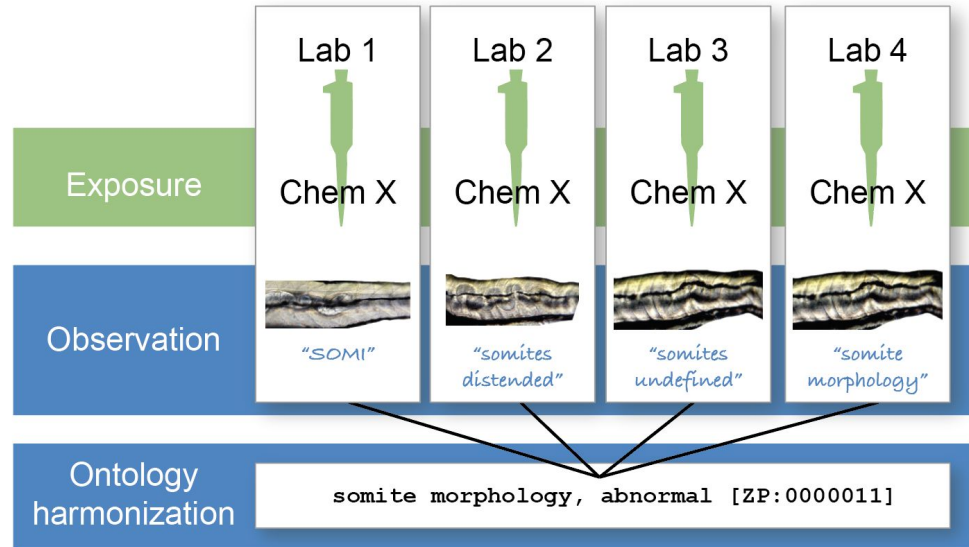


Integration with the Monarch Knowledge Graph



High Throughput Zebrafish Studies

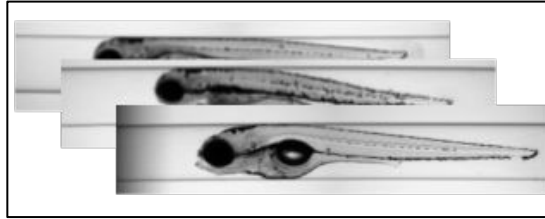
- High-throughput zebrafish studies
- Quickly finding endpoints
- Labs use their own vocabulary
- Hinders data integration
- Ontologies are a potential solution
- Can we standardize endpoint reporting in a useful way?



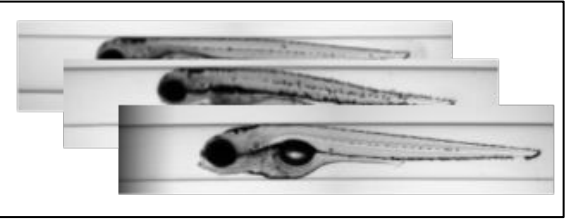
High Throughput Zebrafish Studies

- Annotators used 1,748 unique terms to describe 48 ZPO phenotypes
- Abnormalities of the gut, pectoral fin, and otic vesicles were most heterogeneously described
- Abnormalities of the heart and yolk were most consistently identified

Survey 1



Survey 2



RESULTS:

- Does everyone mean the same thing when they use the same term? **NO**
For example, the term 'heart edema' often lumped many heart deformities.
- Is everyone scoring the same images with the same endpoints? **NO**
In survey 1, annotators did not even agree on which embryos were normal
- Does using the ontology improve consistency across labs? **YES**
Agreement between annotators was better when ontology terms were provided (Fleiss' Kappa for Survey 1 = 0.07 and Survey 2 = 0.11)

Thank you

monarchinitiative.org

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