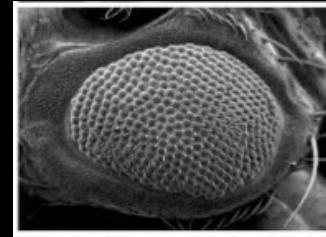




FlyBase

Linking Animal Models and Human Diseases



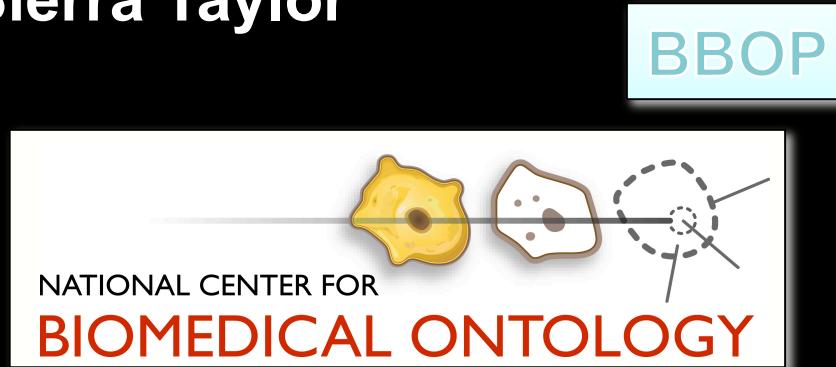
Supported by NIH P41 HG002659 and U54 HG004028
Cambridge University & the University of Oregon



Yvonne Bradford
Melissa Haendel
Kevin Schaper
Erik Segerdell
Amy Singer
Sierra Taylor

Michael Ashburner
Rachel Drysdale
George Gkoutos
David Sutherland

Mark Gibson
Suzi Lewis
Chris Mungall
Nicole Washington

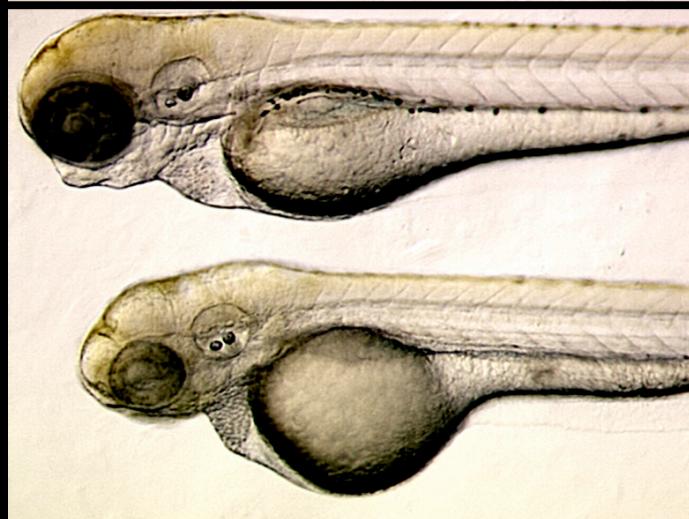


Linking Animal Models and Human Diseases

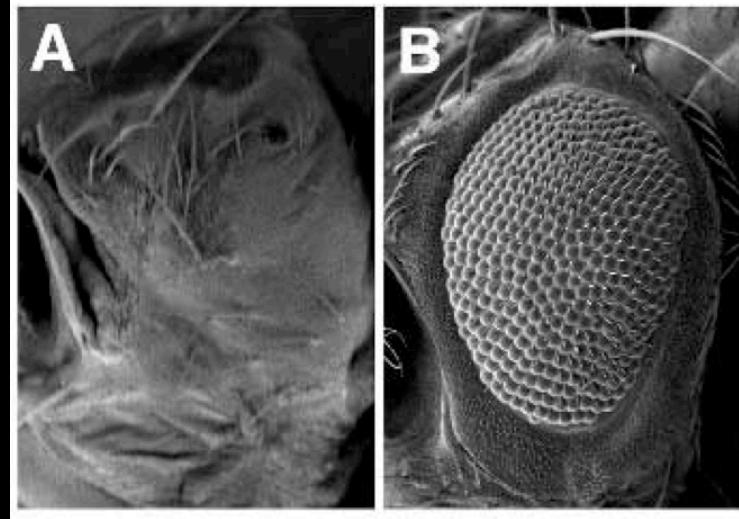
Develop methods to:

- Describe phenotypes
- Compare descriptions (annotations)
- Search phenotypes within and across species

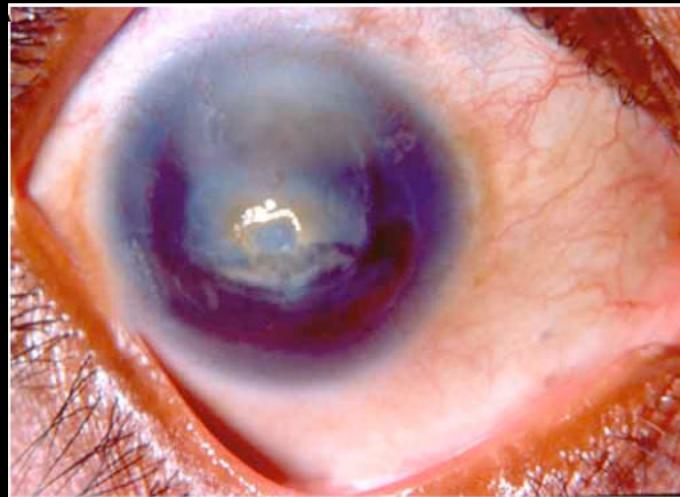
EYA gene mutants



zebrafish



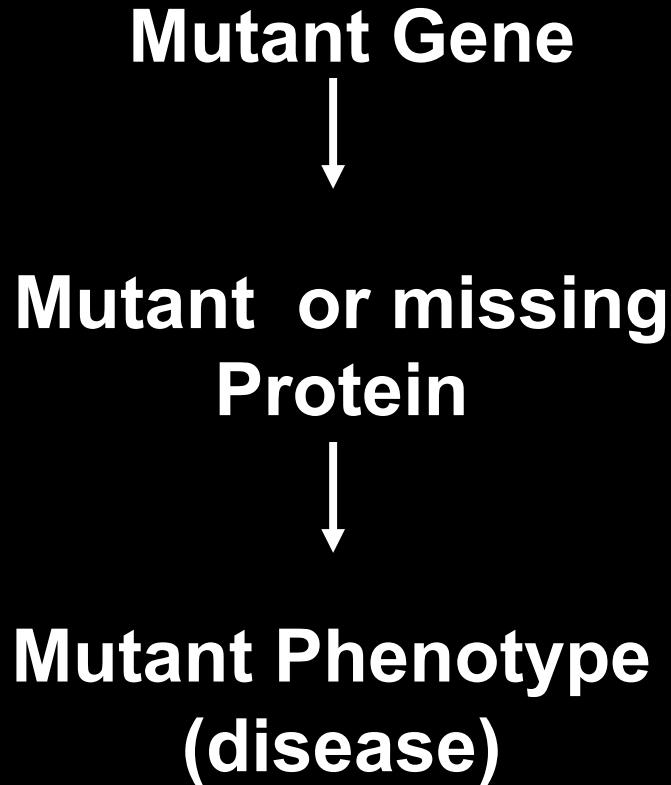
fly



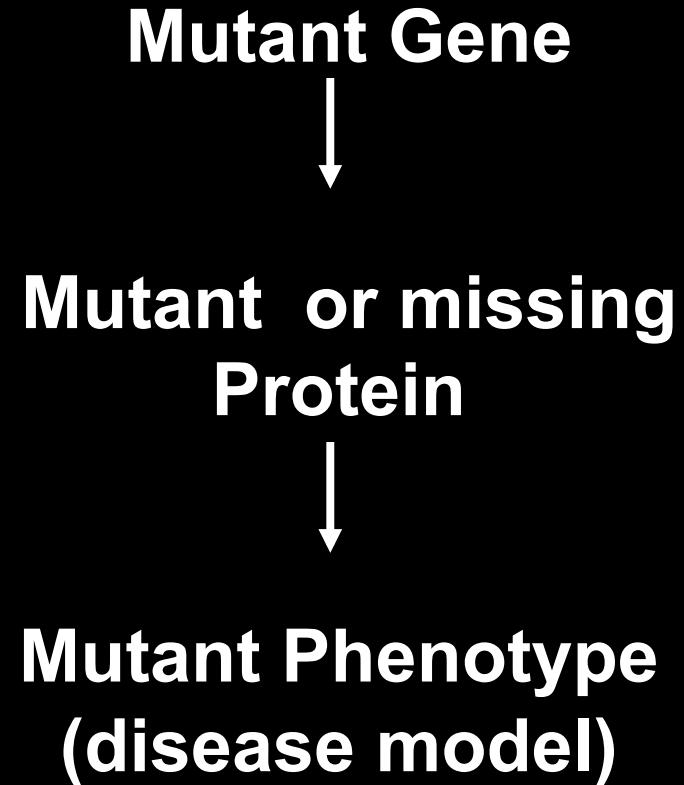
human

Animal disease models

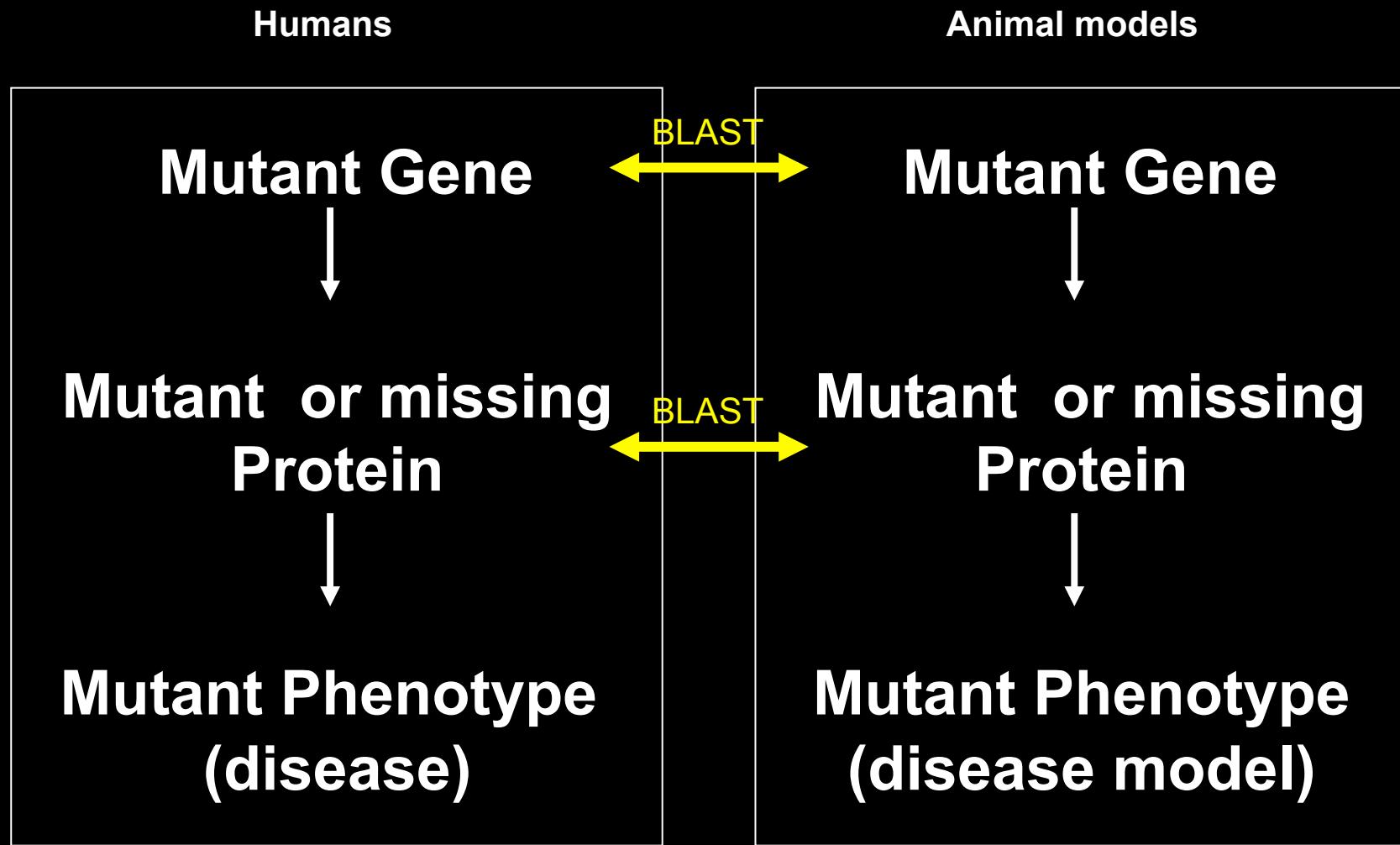
Humans



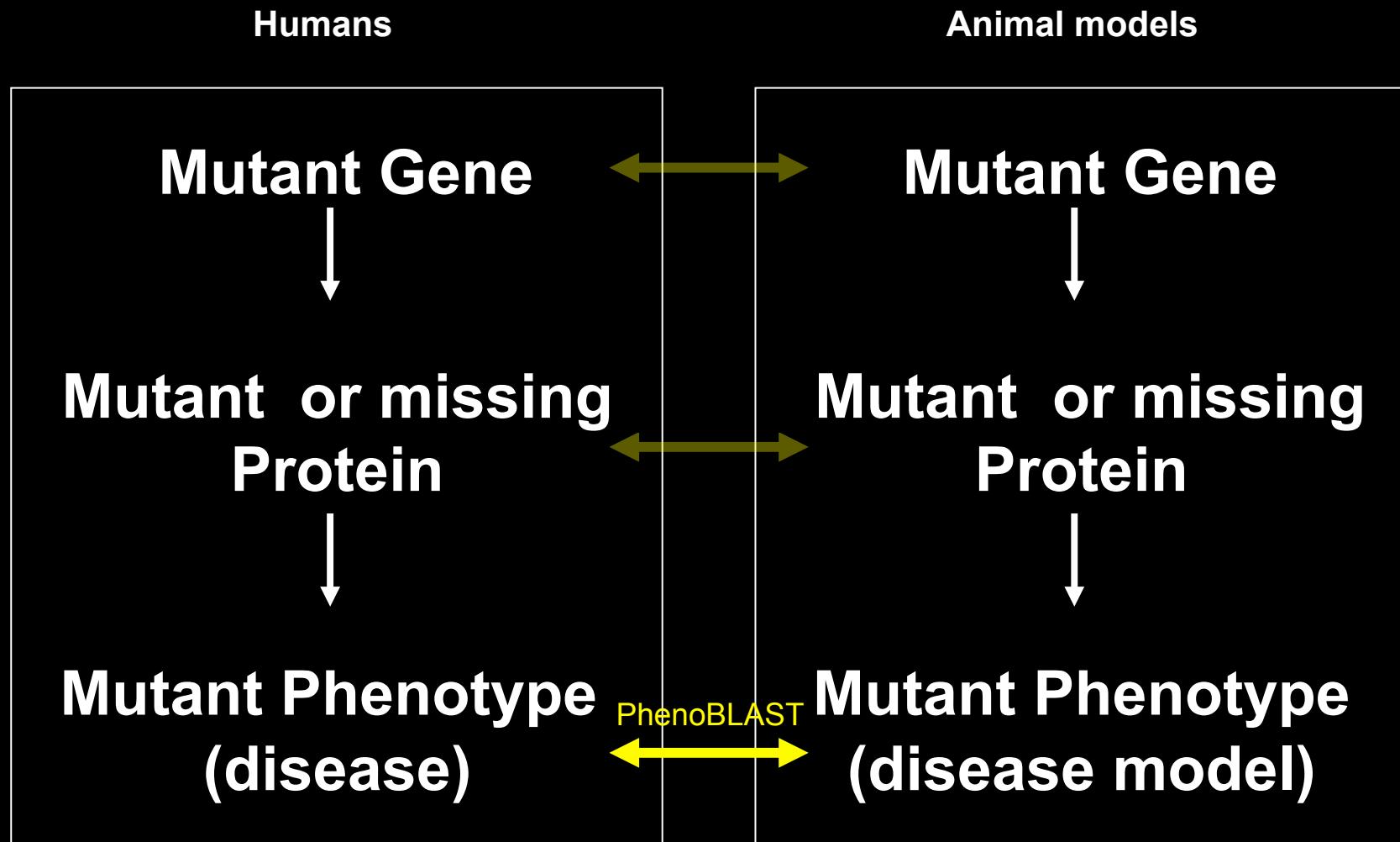
Animal models



Sequence analysis (BLAST) can connect animal genes to human genes



Shared ontologies and syntax can connect mutant phenotypes to candidate human disease genes



OMIM is a free-text disease description source

The screenshot shows the OMIM homepage. At the top is the OMIM logo and the Johns Hopkins University logo. A navigation bar includes links for All Databases, PubMed, Nucleotide, Protein, Genome, Structure, PMC, and OMIM. On the right, there's a "My NCBI" section with "Sign In" and "Register" buttons. Below the header is a search bar with dropdown menus for "Search" (set to "OMIM") and "for", and buttons for "Go" and "Clear". Underneath are tabs for "Limits", "Preview/Index", "History", "Clipboard", and "Details" (which is selected). Further down are "Display" options ("Detailed" dropdown set to "20", "Send to" dropdown), and "GeneTests, Links".

#113650

GeneTests, Links

BRANCHIOOTORENAL SYNDROME 1; BOR1

Alternative titles; symbols

BRANCHIOOTORENAL DYSPLASIA
MELNICK-FRASER SYNDROME

Gene map locus [8q13.3](#)

TEXT

A number sign (#) is used with this entry because of evidence that this form of the branchiootorenal syndrome (BOR1) is caused by mutation in the EYA1 gene ([601653](#)). Another form, BOR2 ([610896](#)), is caused by mutation in the SIX5 gene ([600963](#)).

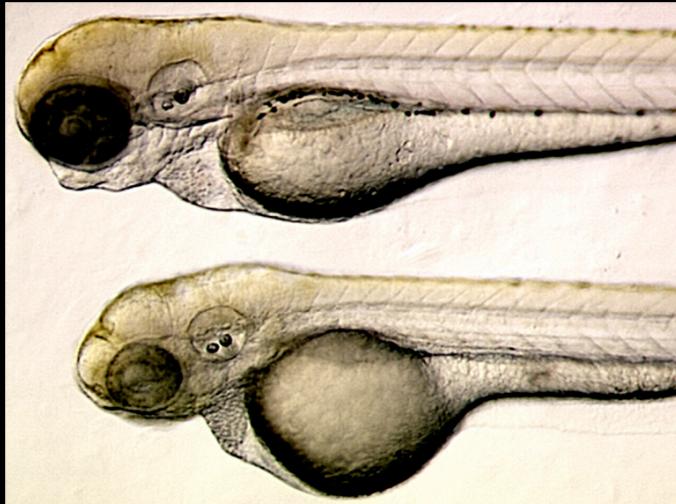
DESCRIPTION

Branchiootorenal syndrome is an autosomal dominant disorder characterized by sensorineural, conductive, or mixed hearing loss, structural defects of the outer, middle, and inner ear, branchial fistulas or cysts, and renal abnormalities ranging from mild hypoplasia to complete absence. Reduced penetrance and variable expressivity has been observed ([Fraser et al., 1978](#)). 

Information retrieval from text-based resources is difficult

| <u>OMIM Query</u> | <u># of records</u> |
|-------------------------|---------------------|
| "large bone" | 785 |
| "enlarged bone" | 156 |
| "big bones" | 16 |
| "huge bones" | 4 |
| "massive bones" | 28 |
| "hyperplastic bones" | 12 |
| "hyperplastic bone" | 40 |
| "bone hyperplasia" | 134 |
| "increased bone growth" | 612 |

Annotation of eya mutant phenotype using ontologies



Phenotype = Entity + Quality

EQ_1 = eye + small

EQ_2 = kidney + hypoplastic

Ontologies for Phenotype Annotation

Phenotype
(clinical sign) = Entity + Quality

Anatomical ontology

Cell & tissue ontology

Developmental ontology +

Gene ontology

PATO

biological process

molecular function

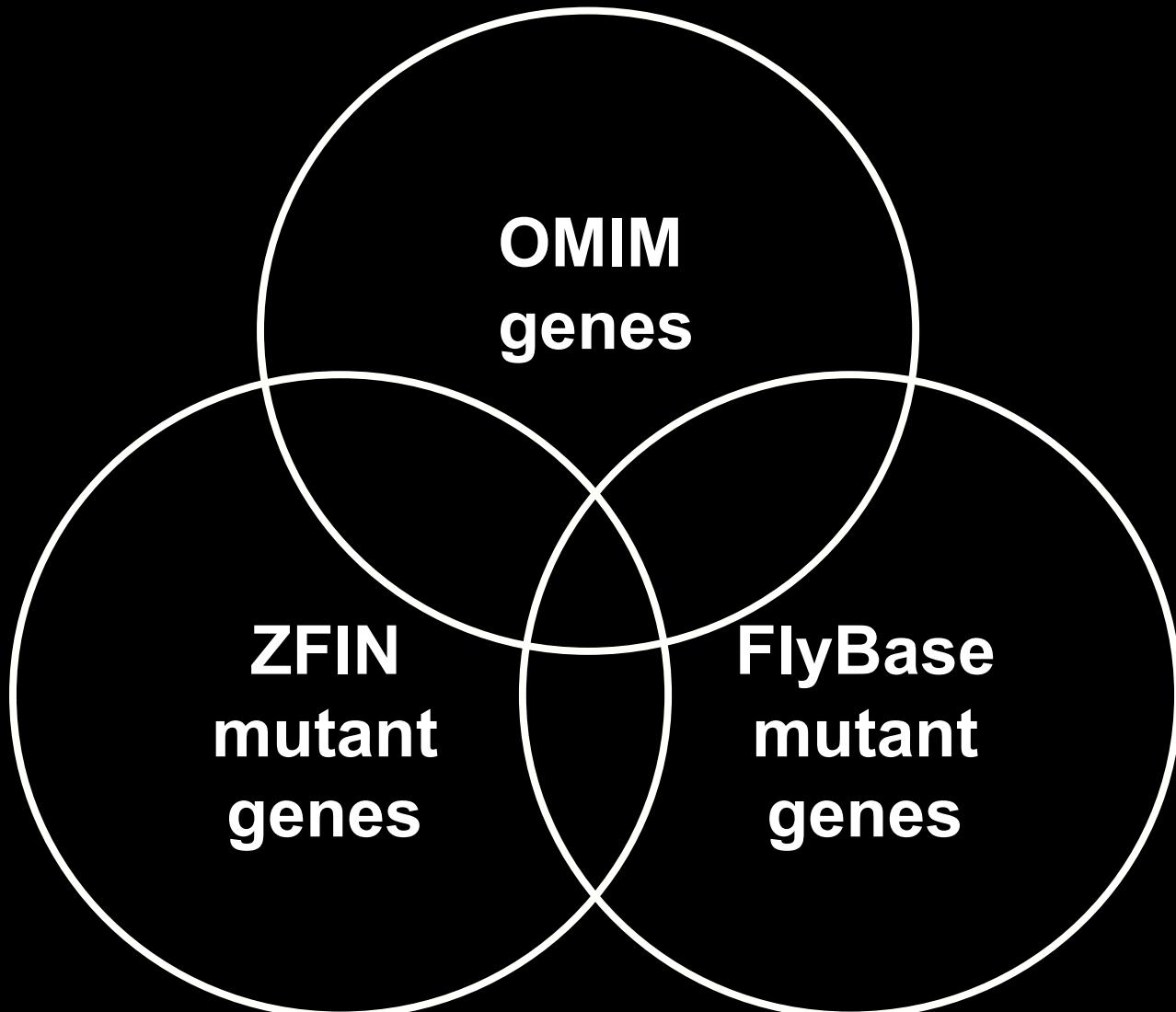
cellular component

Linking Animal Models and Human Diseases

Develop methods to:

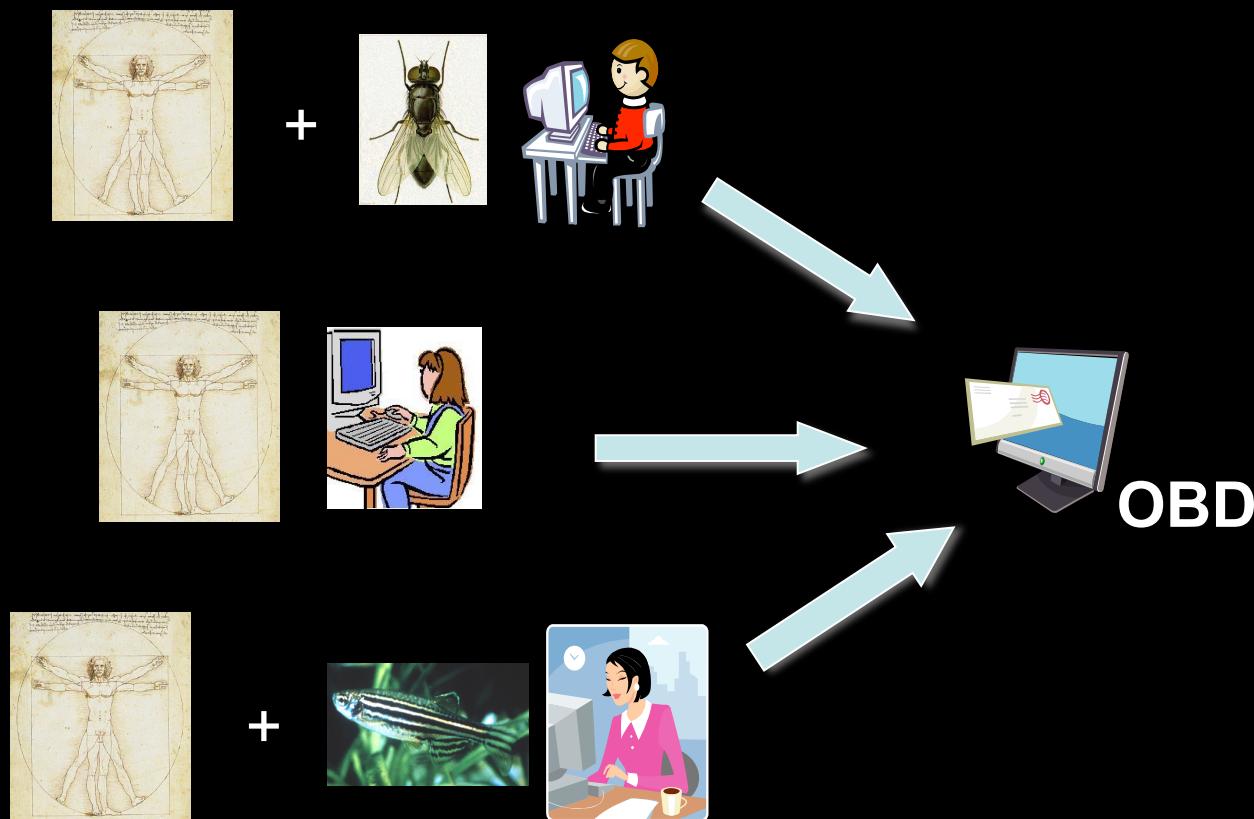
- Describe phenotypes
- Compare descriptions (annotations)
- Search phenotypes within and across species

Strategy: use shared genes as proof of principle



Experimental design

- Annotate phenotypes in human, zebrafish, and fly
- Annotate human phenotypes triple blind
- Compare annotations



Results: Number of annotations added to OBD

Human (from this project)

ATP2A1, EPB41, EXT2, EYA1, FECH, PAX2*, SHH, SOX9*,
SOX10*, TNNT2, TTN** (* annotated in triplicate)

268 genotypes

1669 annotations

Human (from NCBI:GAD)

2674 genes

23,744 annotations (using MP or DO)

Zebrafish (from ZFIN)

2911 genes and 4441 genotypes

17,494 annotations

Mouse (from MGI)

10,579 genes and 23,934 genotypes

116,609 annotations (using MP)

~10% of the annotations for 1 gen

~10% of the annotations for 1 gene

PUB=PMID:9087244 GT=eyo1[tm90b/tm90b] E=ZFA:0000940 /*neuromasts posterior*/ Q=PATO:0000419 /*decreased number*/ T=during(ZFS:0000037) /*during(Larval:Day 5)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:9087244 GT=eyo1[tm90b/tm90b] E=ZFA:0000034 /*lateral line*/ Q=PATO:0000001 /*quality*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:9087244 GT=eyo1[tm90b/tm90b] E=G0:0007626 /*locomotory behavior*/ Q=PATO:0000001 /*quality*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:9087244 GT=eyo1[tm90b/tm90b] E=ZFA:0001894 /*whole organism*/ Q=PATO:0000718 /*lethal*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:9087244 GT=eyo1[t015b/t015b] E=ZFA:0000431 /*semicircular canals*/ Q=PATO:0000937 /*disorganized*/ T=during(ZFS:0000036) /*during(Larval:Day 4)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:9087244 GT=eyo1[t015b/t015b] E=ZFA:0000139 /*immature otoliths*/ Q=PATO:0000587 /*small size*/ T=during(ZFS:0000036) /*during(Larval:Day 4)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:9087244 GT=eyo1[t015b/t015b] E=ZFA:0001227 /*pharyngeal arch 1 skeleton*/ Q=PATO:0000052 /*shape*/ T=during(ZFS:0000037) /*during(Larval:Day 5)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:9087244 GT=eyo1[t015b/t015b] E=ZFA:0000095 /*pharyngeal arch 3-7 skeleton*/ Q=PATO:0000587 /*small size*/ T=during(ZFS:0000037) /*during(Larval:Day 5)*/ Tag=PATO:0000460 /*abnormal*/
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PUB=PMID:9087244 GT=eyo1[t015b/t015b] E=G0:0007626 /*locomotory behavior*/ Q=PATO:0000001 /*quality*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:9087244 GT=eyo1[t015b/t015b] E=ZFA:0001894 /*whole organism*/ Q=PATO:0000718 /*lethal*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:9087244 GT=eyo1[t015b/t015b] E=G0:0048752 /*semicircular canal morphogenesis*/ Q=PATO:0000001 /*quality*/ T=during(ZFS:0000037) /*during(Larval:Day 5)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:9087244 GT=eyo1[t015b/t015b] E=ZFA:0000619 /*anterior cristae*/ Q=PATO:0001226 /*quantitative*/ T=during(ZFS:0000037) /*during(Larval:Day 5)*/ Tag=PATO:0000462 /*absent*/
PUB=PMID:9087244 GT=eyo1[t015b/t015b] E=ZFA:0000378 /*lateral cristae*/ Q=PATO:0001226 /*quantitative*/ T=during(ZFS:0000037) /*during(Larval:Day 5)*/ Tag=PATO:0000462 /*absent*/
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PUB=PMID:9087244 GT=eyo1[tp85b/tp85b] E=ZFA:0000431 /*semicircular canals*/ Q=PATO:0000937 /*disorganized*/ T=during(ZFS:0000036) /*during(Larval:Day 4)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:9087244 GT=eyo1[tp85b/tp85b] E=ZFA:0000139 /*immature otoliths*/ Q=PATO:0000587 /*small size*/ T=during(ZFS:0000036) /*during(Larval:Day 4)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:9087244 GT=eyo1[tp85b/tp85b] E=ZFA:0001227 /*pharyngeal arch 1 skeleton*/ Q=PATO:0000052 /*shape*/ T=during(ZFS:0000037) /*during(Larval:Day 5)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:9087244 GT=eyo1[tp85b/tp85b] E=ZFA:0000095 /*pharyngeal arch 3-7 skeleton*/ Q=PATO:0000587 /*small size*/ T=during(ZFS:0000037) /*during(Larval:Day 5)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:9087244 GT=eyo1[tp85b/tp85b] E=ZFA:0000040 /*neuromasts posterior*/ Q=PATO:0000419 /*decreased number*/ T=during(ZFS:0000037) /*during(Larval:Day 5)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:9087244 GT=eyo1[tp85b/tp85b] E=ZFA:0000034 /*lateral line*/ Q=PATO:0000001 /*quality*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:9087244 GT=eyo1[tp85b/tp85b] E=G0:0007626 /*locomotory behavior*/ Q=PATO:0000001 /*quality*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:9087244 GT=eyo1[tp85b/tp85b] E=ZFA:0001894 /*whole organism*/ Q=PATO:0000718 /*lethal*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:9087244 GT=eyo1[tp85b/tp85b] E=G0:0048752 /*semicircular canal morphogenesis*/ Q=PATO:0000001 /*quality*/ T=during(ZFS:0000037) /*during(Larval:Day 5)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:9087244 GT=eyo1[tp85b/tp85b] E=ZFA:0000619 /*anterior cristae*/ Q=PATO:0001226 /*quantitative*/ T=during(ZFS:0000037) /*during(Larval:Day 5)*/ Tag=PATO:0000462 /*absent*/
PUB=PMID:9087244 GT=eyo1[tp85b/tp85b] E=ZFA:0000378 /*lateral cristae*/ Q=PATO:0001226 /*quantitative*/ T=during(ZFS:0000037) /*during(Larval:Day 5)*/ Tag=PATO:0000462 /*absent*/
PUB=PMID:9087244 GT=eyo1[tp85b/tp85b] E=ZFA:0000566 /*posterior cristae*/ Q=PATO:0001226 /*quantitative*/ T=during(ZFS:0000037) /*during(Larval:Day 5)*/ Tag=PATO:0000462 /*absent*/
PUB=PMID:9087244 GT=eyo1[tp85b/tp85b] E=ZFA:0000055 /*sensory hair cells*/ Q=PATO:0000419 /*decreased number*/ T=during(ZFS:0000035) /*during(Larval:Protruding-mouth)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:9087244 GT=eyo1[tp85b/tp85b] E=ZFA:0000585 /*sensory hair cells*/ Q=PATO:0000419 /*decreased number*/ T=during(ZFS:0000037) /*during(Larval:Day 5)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:14752054 GT=eyo1[t22744/t22744] E=G0:0021984 /*adenohypophysis development*/ Q=PATO:0000064 /*pattern*/ T=during(ZFS:0000037) /*during(Larval:Day 5)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:14752054 GT=eyo1[t22744/t22744] E=CL:00000439 /*prolactin secreting cell*/ Q=PATO:0001226 /*quantitative*/ T=during(ZFS:0000030) /*during(Pharyngula:Prim-15)*/ Tag=PATO:0000467 /*present*/
PUB=PMID:14752054 GT=eyo1[t22744/t22744] E=CL:00000439 /*prolactin secreting cell*/ Q=PATO:0001226 /*quantitative*/ T=during(ZFS:0000037) /*during(Larval:Day 5)*/ Tag=PATO:0000467 /*present*/
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PUB=PMID:14752054 GT=eyo1[t22744/t22744] E=CL:00000440 /*melanocyte stimulating hormone secreting cell*/ Q=PATO:0001226 /*quantitative*/ T=during(ZFS:0000037) /*during(Larval:Day 5)*/ Tag=PATO:0000462 /*absent*/
PUB=PMID:14752054 GT=eyo1[t22744/t22744] E=CL:00000476 /*thyroid stimulating hormone secreting cell*/ Q=PATO:0001226 /*quantitative*/ T=during(ZFS:0000037) /*during(Larval:Day 5)*/ Tag=PATO:0000462 /*absent*/
PUB=PMID:14752054 GT=eyo1[t22744/t22744] E=CL:00000295 /*somatotrophin secreting cell*/ Q=PATO:0001226 /*quantitative*/ T=during(ZFS:0000037) /*during(Larval:Day 5)*/ Tag=PATO:0000462 /*absent*/
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PUB=PMID:15572137 GT=eyo1[tc257e/tc257e] E=ZFA:00000814 /*neuromasts opercular*/ Q=PATO:0001226 /*quantitative*/ T=during(ZFS:0000039) /*during(Larval:Days 7-13)*/ Tag=PATO:0000462 /*absent*/
PUB=PMID:15572137 GT=eyo1[tc257e/tc257e] E=ZFA:00001227 /*pharyngeal arch 1 skeleton*/ Q=PATO:0000411 /*round*/ T=during(ZFS:0000039) /*during(Larval:Days 7-13)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:15572137 GT=eyo1[tm90b/tm90b] E=G0:0030916 /*otic vesicle formation*/ Q=PATO:0000001 /*quality*/ T=during(Pharyngula:Prim-5)/* Tag=PATO:0000461 /*normal*/
PUB=PMID:15572137 GT=eyo1[tm90b/tm90b] E=ZFA:0000051 /*otic vesicle*/ Q=PATO:00000587 /*small size*/ T=during(ZFS:0000039) /*during(Hatching:Long-pec)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:15572137 GT=eyo1[tm90b/tm90b] E=ZFA:0000051 /*otic vesicle*/ Q=PATO:0000946 /*oblong*/ T=during(ZFS:0000033) /*during(Hatching:Long-pec)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:15572137 GT=eyo1[tm90b/tm90b] E=ZFA:0000051 /*otic vesicle*/ Q=PATO:0000587 /*small size*/ T=during(ZFS:0000036) /*during(Larval:Day 4)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:15572137 GT=eyo1[tm90b/tm90b] E=ZFA:0000051 /*otic vesicle*/ Q=PATO:0000599 /*narrow*/ T=during(ZFS:0000036) /*during(Larval:Day 4)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:15572137 GT=eyo1[tm90b/tm90b] E=G0:0048752 /*semicircular canal morphogenesis*/ Q=PATO:0000001 /*quality*/ T=during(ZFS:0000035) /*during(Larval:Protruding-mouth)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:15572137 GT=eyo1[tm90b/tm90b] E=G0:0048752 /*semicircular canal morphogenesis*/ Q=PATO:0000001 /*quality*/ T=during(ZFS:0000036) /*during(Larval:Day 4)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:15572137 GT=eyo1[tm90b/tm90b] E=ZFA:0000431 /*semicircular canals*/ Q=PATO:0000052 /*shape*/ T=during(ZFS:0000036) /*during(Larval:Day 4)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:15572137 GT=eyo1[tm90b/tm90b] E=ZFA:00000585 /*sensory hair cells*/ Q=PATO:0000419 /*decreased number*/ T=during(ZFS:0000037) /*during(Larval:Day 5)*/ Tag=PATO:0000460 /*abnormal*/
PUB=PMID:15572137 GT=eyo1[tm90b/tm90b] E=ZFA:0000386 /*maculae*/ Q=PATO:0000052 /*shape*/ T=during(ZFS:0000037) /*during(Larval:Day 5)*/ Tag=PATO:0000460 /*abnormal*/

Annotations vary among curators

Curator 1

E: Cornea
Q: Opaque

Curator 2

E: Middle layer of
corneal epithelium
Q: Opacity

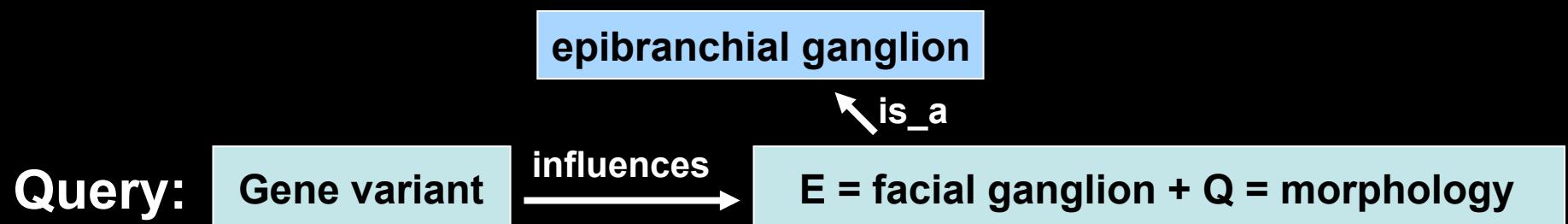
Curator 3

E: Lens quarter
Q: Opaque

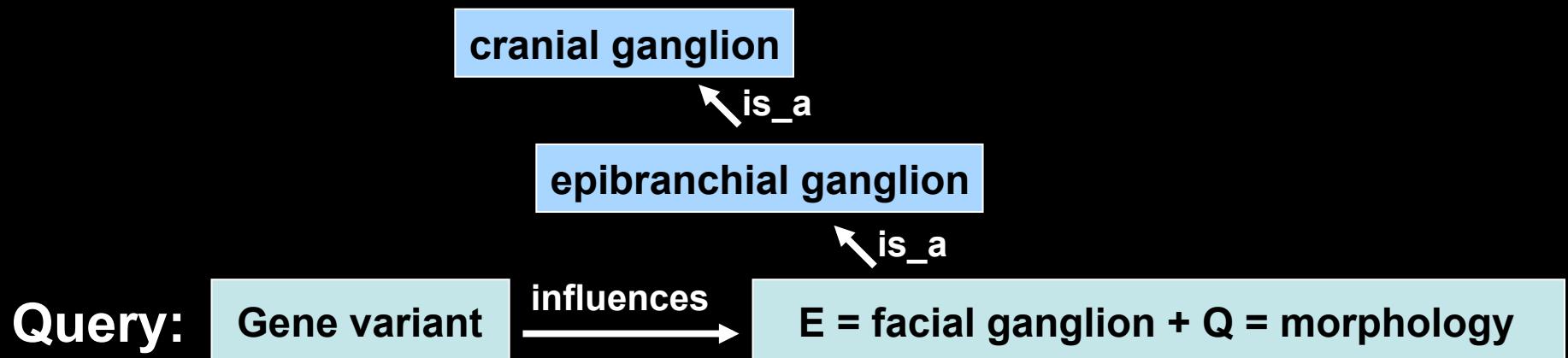
Example phenotype annotation

Query: Gene variant  E = facial ganglion + Q = morphology

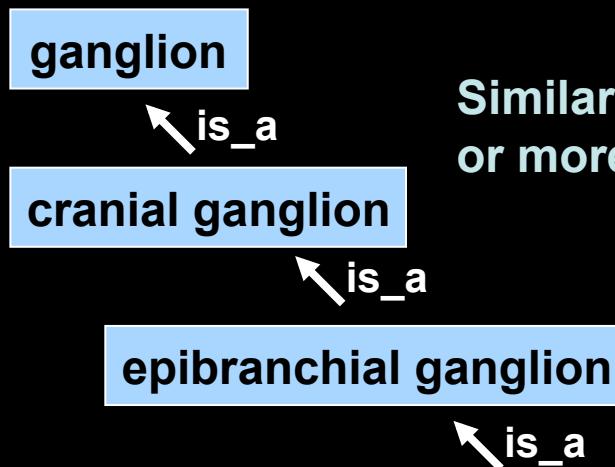
Terms are related by ontologies



Terms are related by ontologies



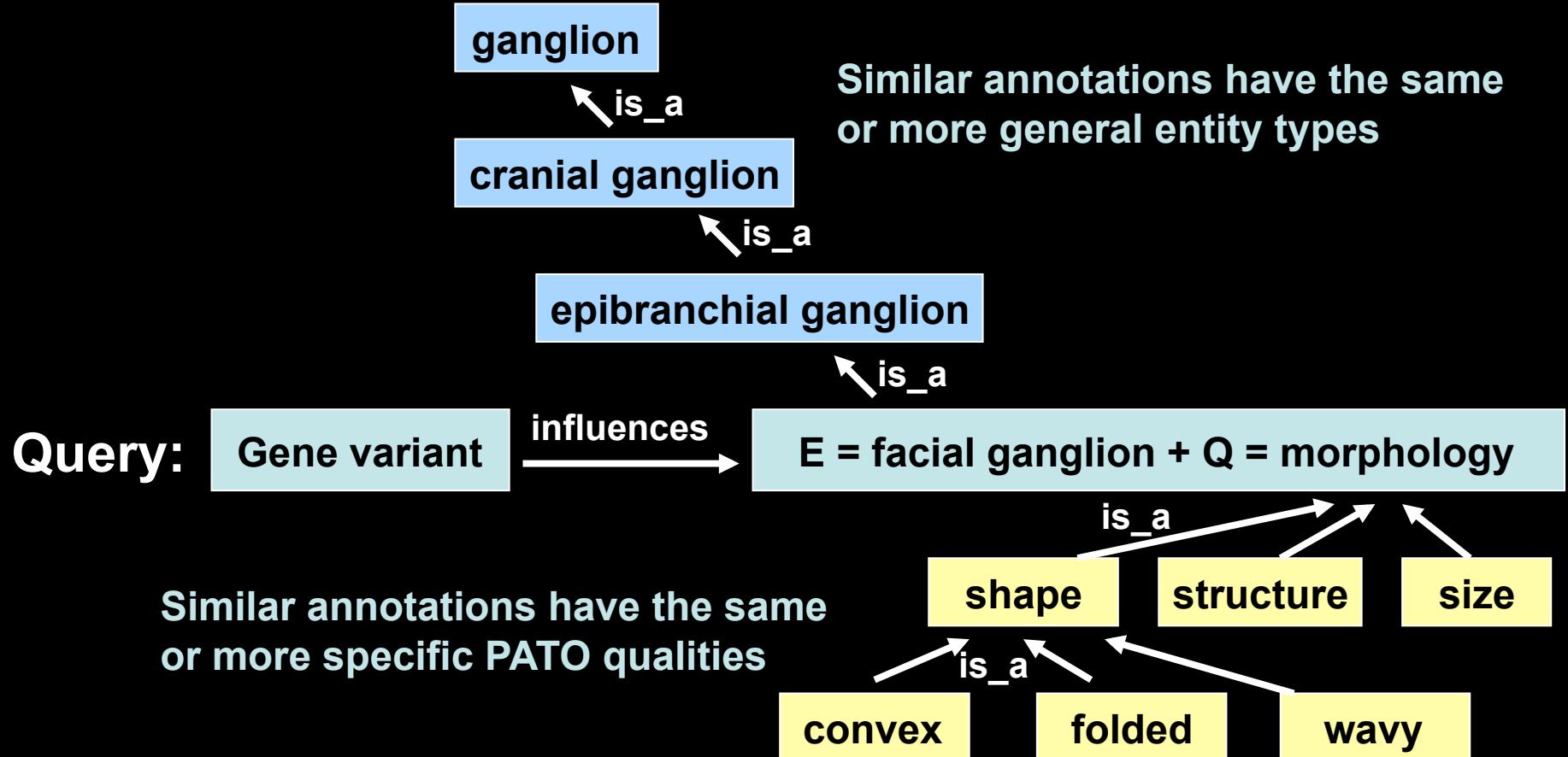
Terms are related by ontologies



Similar annotations have the same or more general entity types

Query: Gene variant $\xrightarrow{\text{influences}}$ E = facial ganglion + Q = morphology

Similarity calculated by reasoning across ontologies



Ontologies support comparisons

Curator 1

E: Cornea
Q: Opaque

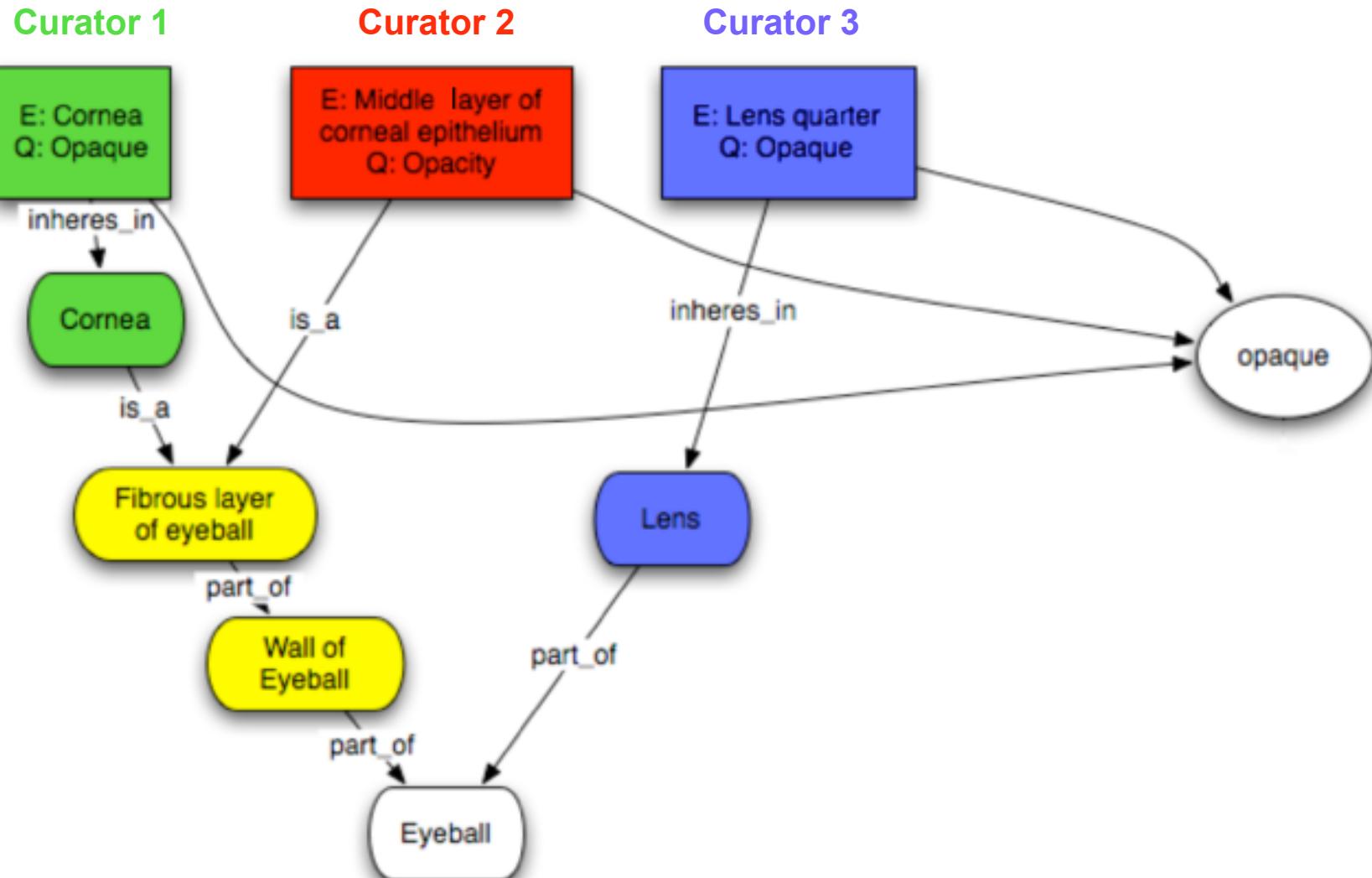
Curator 2

E: Middle layer of
corneal epithelium
Q: Opacity

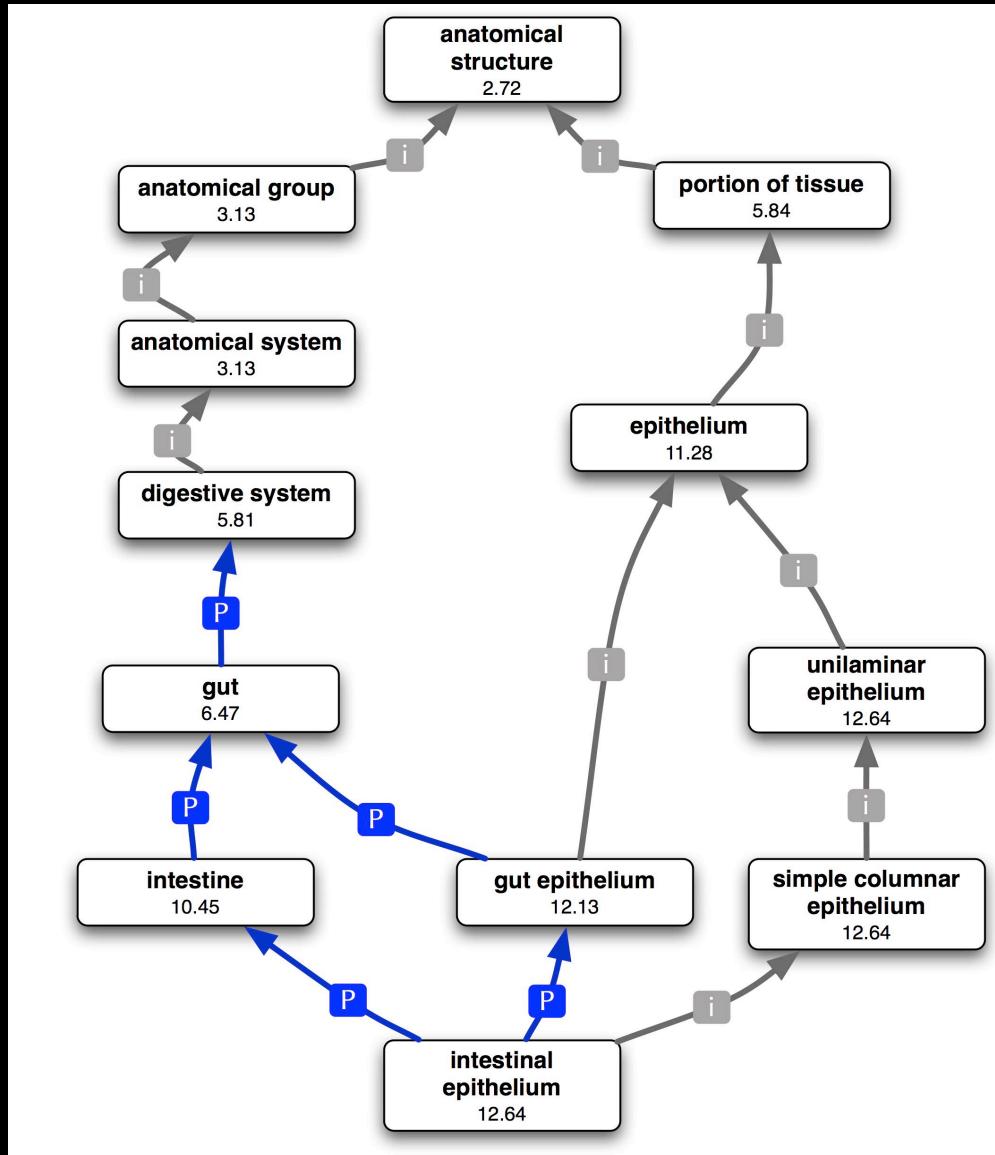
Curator 3

E: Lens quarter
Q: Opaque

Ontologies support comparisons

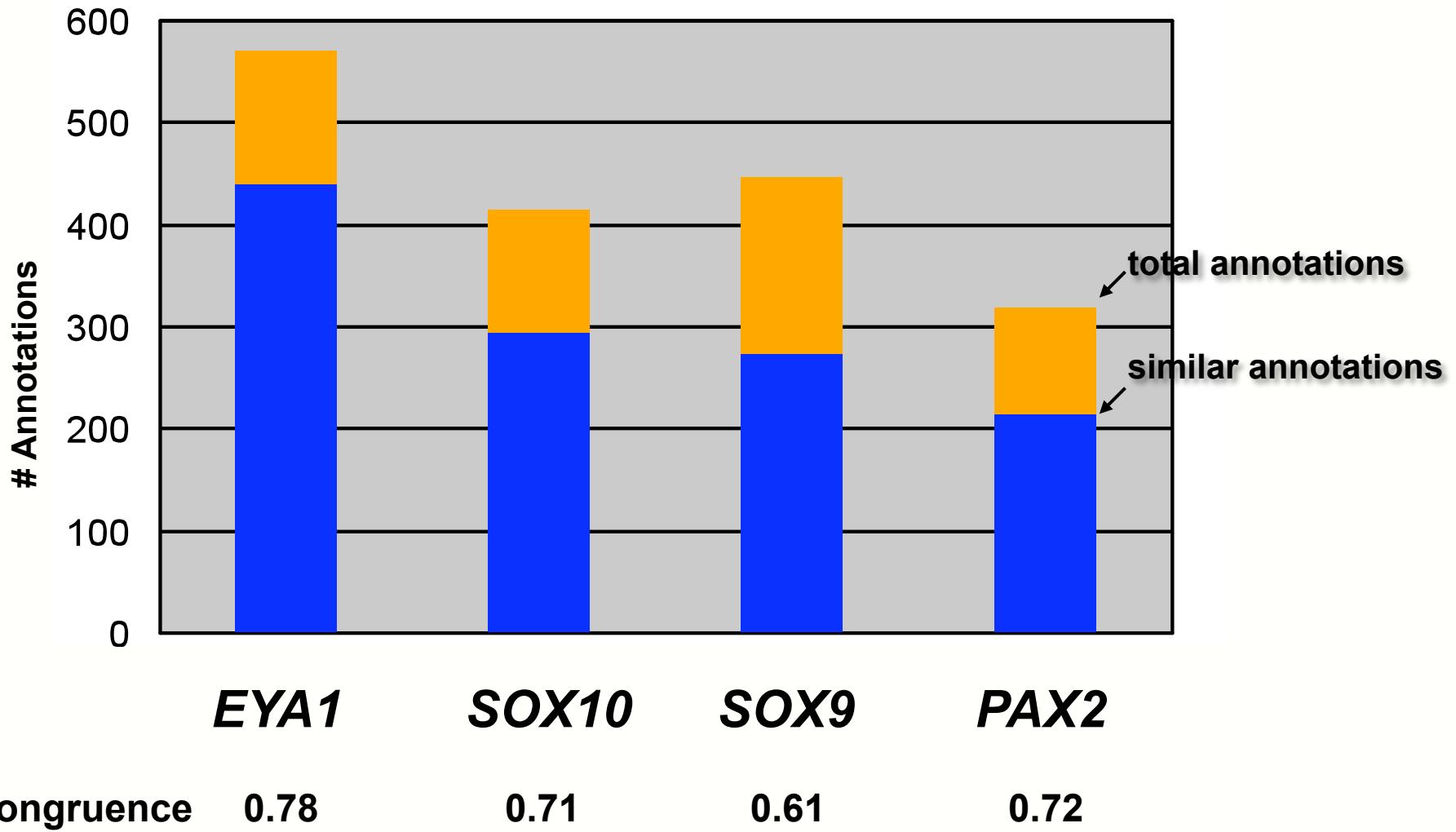


Subsumption reasoning for similarity scoring



Similarity is calculated based on depth within the ontology and annotation frequency

Average annotation consistency among curators

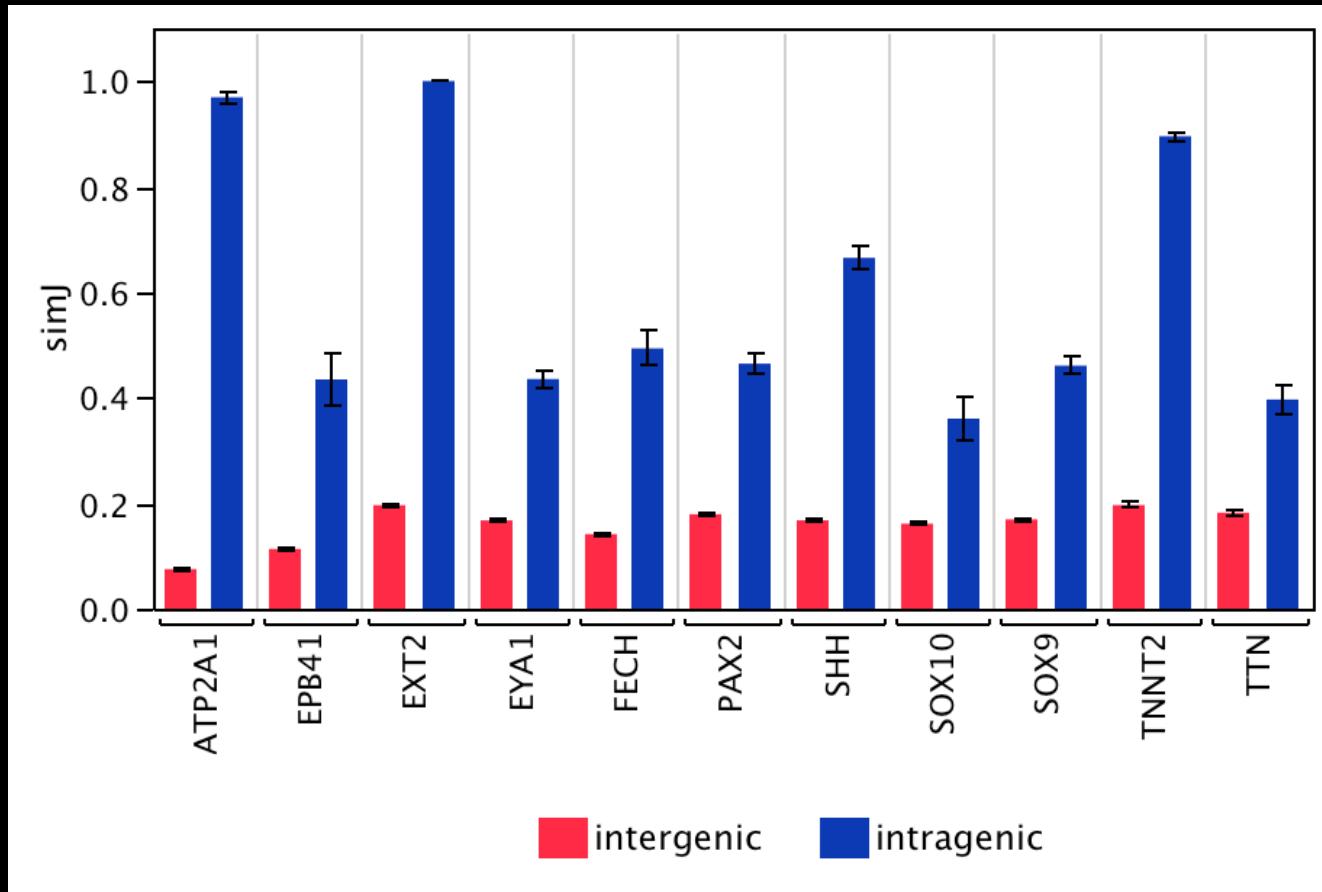


Linking Animal Models and Human Diseases

Develop methods to:

- Describe phenotypes
- Compare descriptions (annotations)
- Search phenotypes within and across species

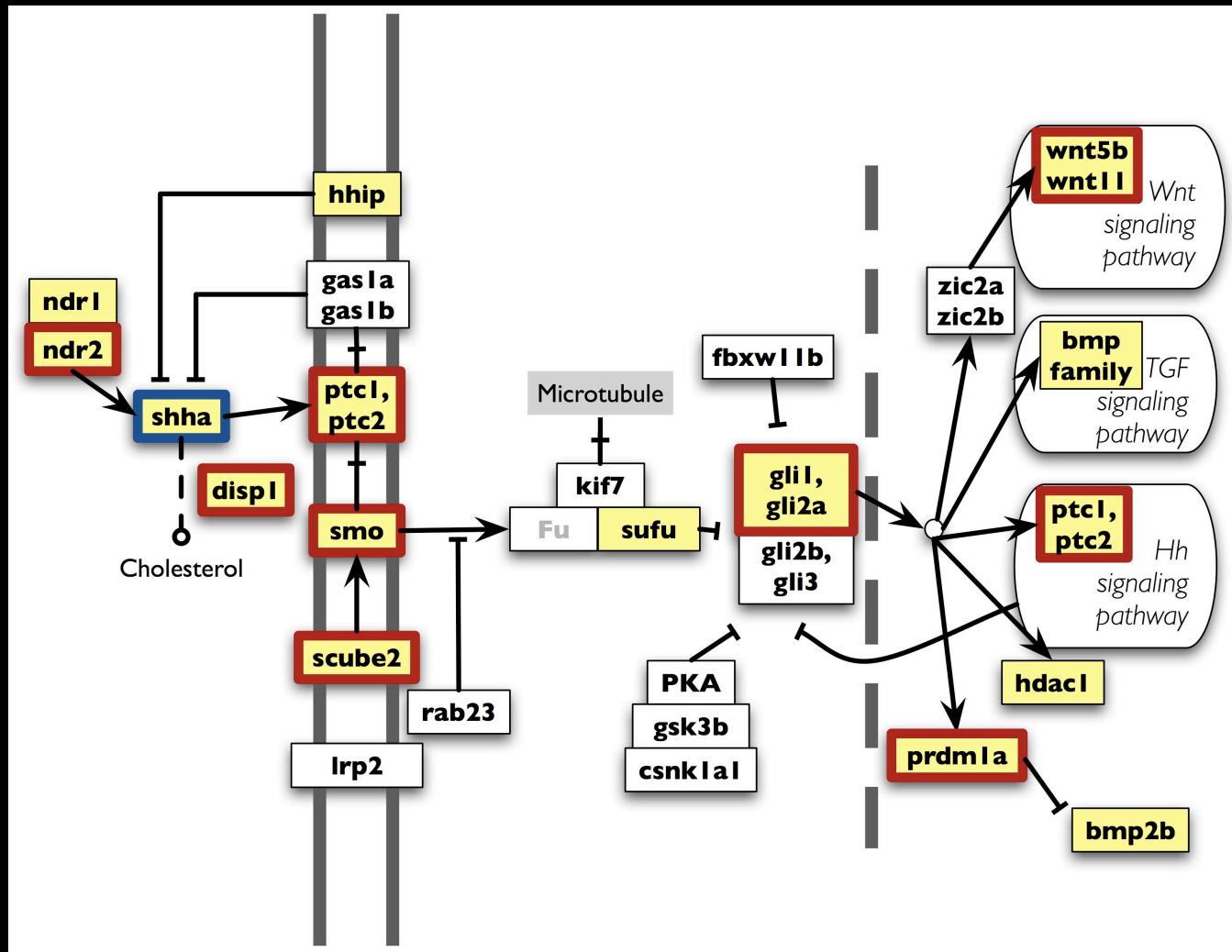
Phenotypes identify other alleles of the same gene



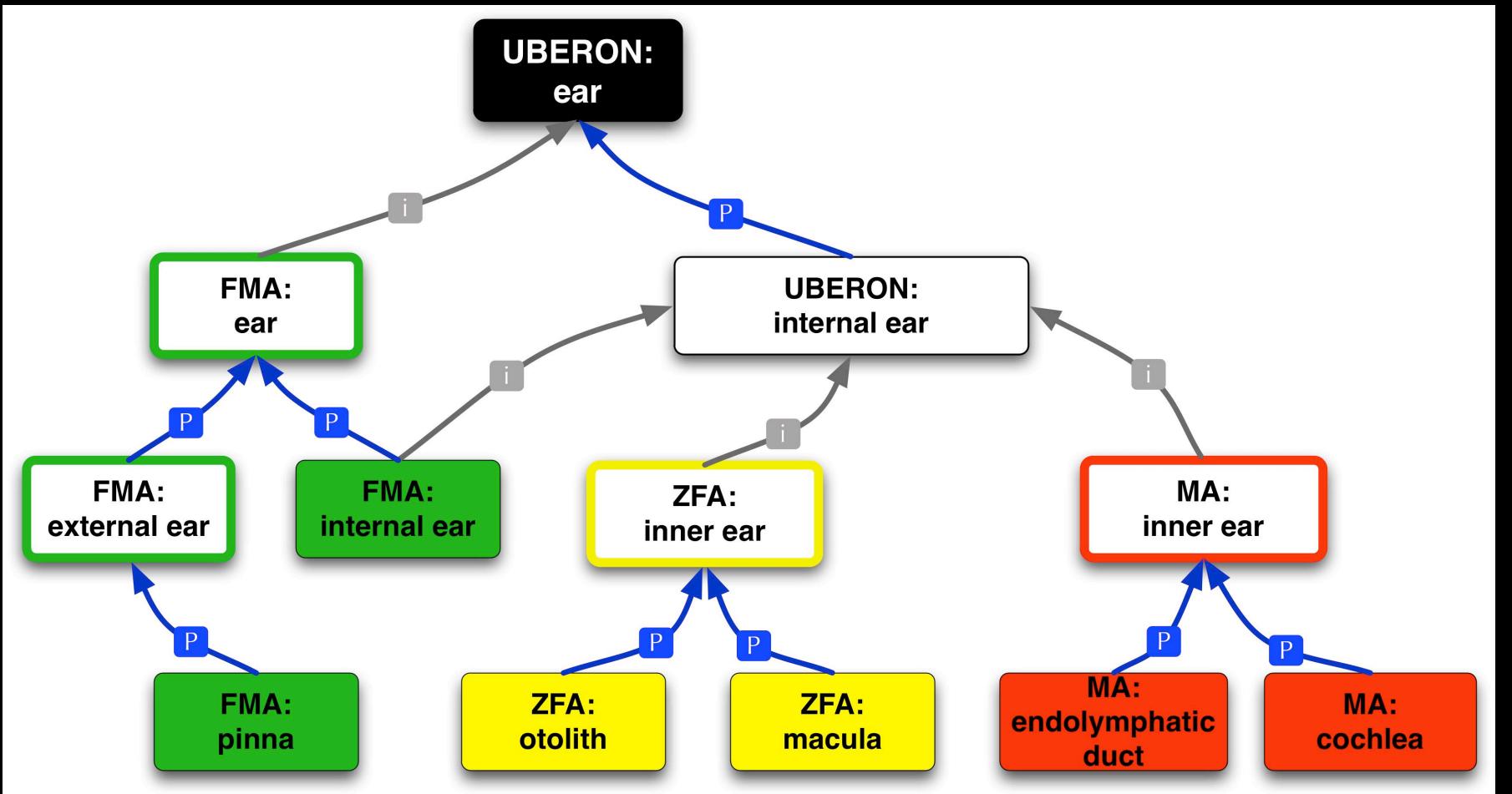
All alleles are significantly more similar to alleles of the same gene than to alleles of other genes $p<0.0001$

Annotations can identify other pathway members

Similarity search for zebrafish *shha^{t4/t4}* identifies pathway members



Cross-species comparisons require linking species-specific anatomy ontologies



Human phenotypes identify mutations in orthologous model organism genes

A search for phenotypes similar to:

Human *EYA1* variant OMIM:601653

MP:deafness = E = Sensory perception of sound Q = absent

Human phenotypes identify mutations in orthologous model organism genes

A search for phenotypes similar to:

Human *EYA1* variant OMIM:601653

MP:deafness = E = Sensory perception of sound Q = absent

returns:

Mouse *Eya1* *bor/bor* and *Eya1^{tm1Rilm/tm1Rilm}*

E = Sensory perception of sound Q = decreased

Annotations of animal phenotypes can identify candidate human disease genes

Human, SOX9
(Campomelic dysplasia)



Zebrafish, sox9a
(*jellyfish*)



| | | |
|-------------------------------|---|----------------------------------|
| Scapula: hypoplastic | ↔ | Scapulocoracoid: aplastic |
| Lower jaw: decreased size | ↔ | Cranial cartilage: hypoplastic |
| Heart: malformed or edematous | ↔ | Heart: edematous |
| Phalanges: decreased length | ↔ | Pectoral fin: decreased length |
| Long bones: bowed | ↔ | Cartilage development: disrupted |

Linking Animal Models and Human Diseases

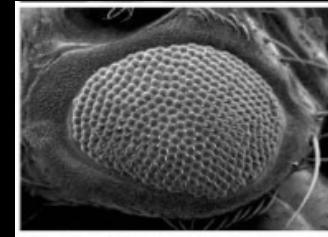
Develop methods to:

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FlyBase

Linking Animal Models and Human Diseases



Supported by NIH P41 HG002659 and U54 HG004028
Cambridge University & the University of Oregon

Vocabulary

Anatomical system

Cornea

Embryo

Eye

Nervous system

Visual system

Ontology

Embryo

- Anatomical system
- Nervous system
- Visual system
 - Eye
 - Cornea