Andreas Laner Sebastian Köhler Peter Robinson (MGZ München; laner@mgz-muenchen.de) (Charité – Universitätsmedizin Berlin; drseb.github.io.) (Jackson Lab; peter.robinson@jax.org)

- History of HPO
- Current status
- Applications
- Workshop/ Demonstration



Why phenotypes matter ?

- Phenotypic abnormality = clinical feature
- Constellation / Pattern of phenotypes / clinical features defines a disease:

... is a rare developmental disorder defined by the combination of **aplasia cutis congenita of the scalp vertex** and **terminal transverse limb defects**. In addition, **vascular anomalies** such as **cutis marmorata telangiectatica** ... are recurrently seen.

OMIM

WILLIAMS-BEUREN SYNDROME; WBS

Alternative titles; symbols

CHROMOSOME 7q11.23 DELETION SYNDROME, 1.5- TO 1.8-MB WILLIAMS SYNDROME; WMS; WS

Cytogenetic location: 7q11.23 Genomic coordinates (GRCh38): 7:72,700,000-77,900,000

Gene-Phenotype Relationships

Location	Phenotype	Phenotype MIM number	Inheritance	Phenotype mapping key	
7q11.23	Williams-Beuren syndrome	194050	AD	4	

Clinical Synopsis

▼ TEXT

A number sign (\ddagger) is used with this entry because Williams-Beuren syndrome (WBS) is a contiguous gene deletion syndrome resulting from the hemizygous deletion of 1.5 to 1.8 Mb on chromosome 7q11.23.

For a discussion of the genes deleted in this syndrome and possible genotype/phenotype correlations, see below.

Description

Williams-Beuren syndrome is a multisystem disorder caused by hemizygous deletion of 1.5 to 1.8 Mb on chromosome 7q11.23, which contains approximately 28 genes. Pober (2010) reviewed the clinical features of Williams-Beuren syndrome as well as the genomic and genetic basis and clinical management.

See also the distal chromosome 7q11.23 deletion syndrome (613729), which occurs between the WBS region and the MAGI2 gene (606382).

Clinical Features

Williams et al. (1961) described a syndrome characterized by supravalvular aortic stenosis (SVAS), mental retardation, and distinctive facial features. Beuren et al. (1962) described a similar syndrome with the additional features of dental anomalies and peripheral pulmonary artery stenosis. Two features of the syndrome had been described as distinct entities: supravalvular aortic stenosis

- Free text phenotypic description
- Very expressive

OMIM

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Clinical Synposis (CS) section

INHERITANCE Autosomal dominant GROWTH Height Short stature Weight - Abnormal weight gain Other Intrauterine growth retardation (IUGR) HEAD & NECK Face Medial eyebrow flare - Flat midface - Periorbital fullness (puffy eyes) - Epicanthal folds - Long philtrum 👤 Ears - Sensorineural hearing loss, mild to moderate - Hyperacusis Phonophobia - Abnormal brain auditory evoked responses (BAER) - Decreased or absent ipsilateral acoustic reflex response to maximum stimulation Eyes - Stellate pattern of iris - Strabismus Altered visual acuity Nose - Depressed nasal bridge 👤 - Anteverted nares 👤 Mouth - Thick lips Teeth - Hypodontia - Microdontia 💄 CARDIOVASCULAR Heart Supravalvular aortic stenosis

- Non-standardized method for describing phenotypes
- Not designed to be machine interpretable

• Spelling problems

- Non-standardized method for describing phenotypes
- Not designed to be machine interpretable

• Spelling problems

Incomplete: Fulltext contains phenotype information; absent in **CS**

Inconsistent: No handling of synonyms

`Height: short stature'
 `Reduced adult height'
 `Final adult height, 84-128cm'

- Non-standardized method for describing phenotypes
- Not designed to be machine interpretable

• Spelling problems

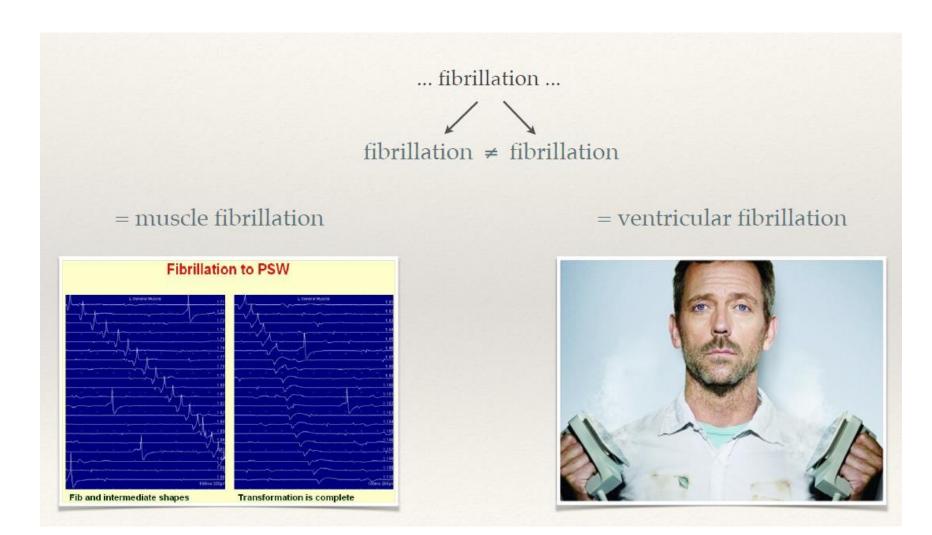
CS contains symptoms such as: 'Heart: Prolonged QTc interval' or 'T-wave abnormalities' Imagine query for 'ECG Abnormalities' , how to ensure the examples above are found?

- Non-standardized method for describing phenotypes
- Not designed to be machine interpretable

hypereflexia - hyperreflexia congential - congenital defeciency - deficiency

• Spelling problems

Homonyms



Motivation for HPO Development

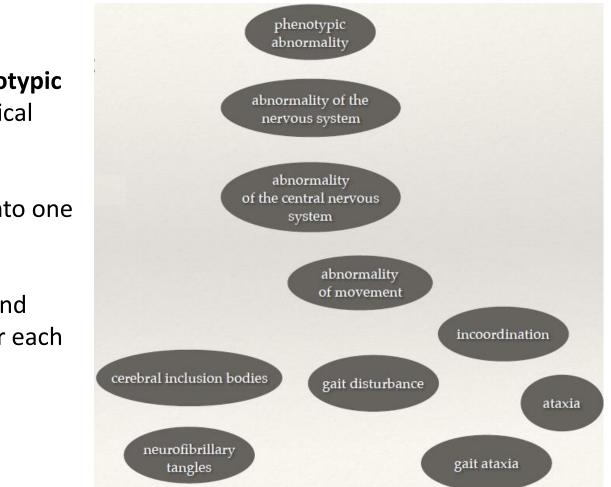
OMIM Query	Number of Results
large bones	264
large bone	785
enlarged bones	87
enlarged bone	156
big bones	16
huge bones	4
massive bones	28
hyperplastic bones	12
hyperplastic bone	40
bone hyperplasia	134
increased bone growth	612

Washington et al. *PLoS Biology (2009)* Linking human diseases to animal models using ontology-based phenotype annotation

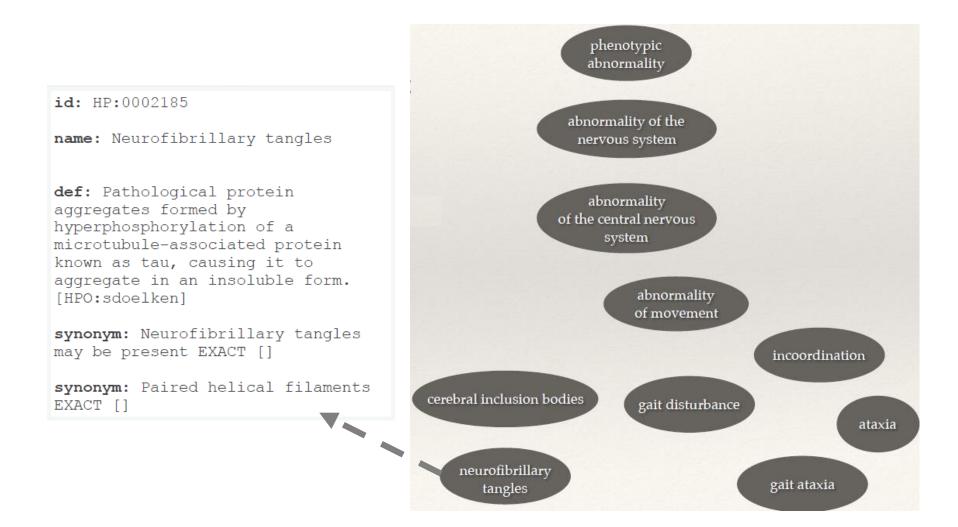
Goal of HPO

- Computer-interpretable clinical features
 - Compare diseases based on clinical features
 - Compare patients based on clinical features
 - Compare patients with diseases based on clinical features
 -
 - Prioritization of variants in high troughput sequencing assays

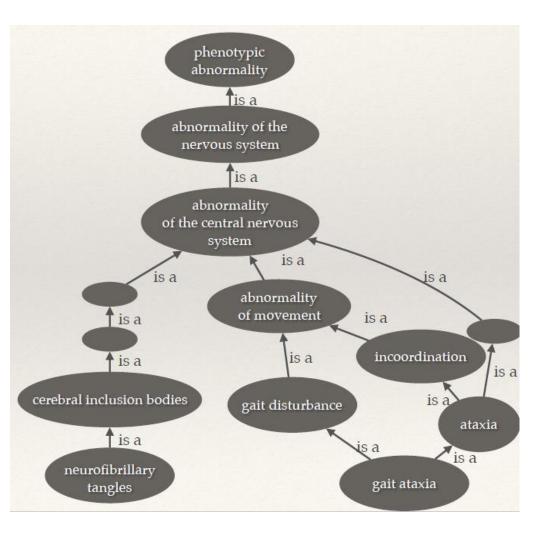
• Easy to use and freely available



- Description of phenotypic abnormalities (=clinical features) in humans
- Synonyms merged into one term
- Creation of textual and logical definitions for each term

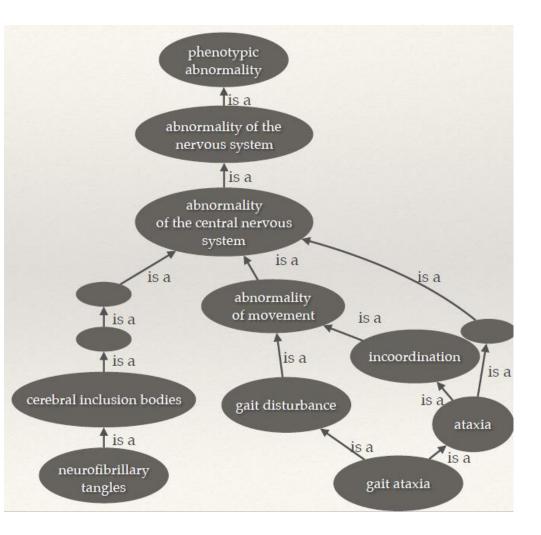


- Semantic relations (is a sublass of)
- From top to bottom terms get more specific



Annotation of diseases

- HPO terms are used to annotate (describe) diseases
 - E.g. *neurofibrillary tangles* is used to annotate Alzheimer Disease
- Note: Annotation with neurofibrillary tangles induces annotation to all ancestor terms



Köhler et al.

The Human Phenotype Ontology project: linking molecular biology and disease through phenotype data; NAR (2014)

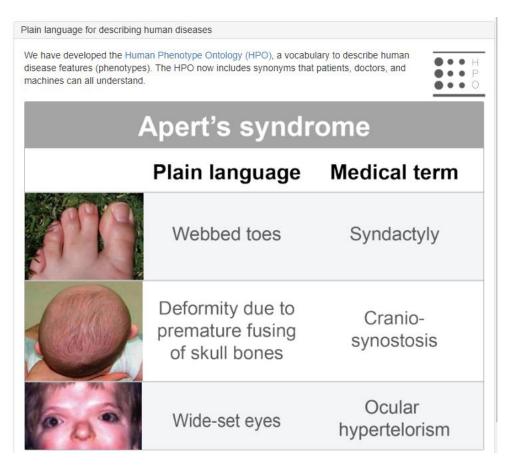
Current Status

♦ 4 root classes

- Phenotypic abnormality
- Mode of Inheritance
- Clinical modifier
- Mortality/ Aging
- ♦ Over 13.000 terms in HPO
- Over 156.000 annotations of > 7.700 rare diseases (OMIM, Orphanet, DECIPHER)
- ➡ Over 133.000 annotations of > 3.100 common diseases

Recent projects

Translations of labels, synonyms and textual definitions (crowdsourcing)



Recent projects

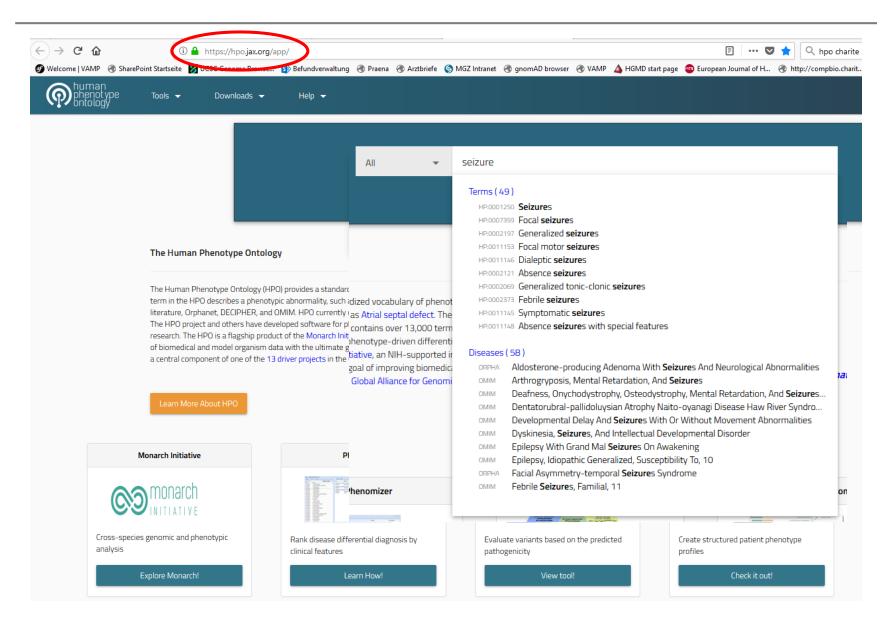
Translations of labels, synonyms and textual definitions (crowdsourcing)



Numbers from 2017

The HPO team needs help to get HPO available in our language as well

Sebastian Köhler (Charité – Universitätsmedizin Berlin; drseb.github.io)



Enter search terms			
Enter Search terms			
Infopage for HPO class	Seizures		
Primary ID HP:0001250 Alternative IDs HP:0002306, HP:0002182, HP:0002348, HP:0 HP:0002466, HP:0002125, HP:0002417, HP:0 HP:0006997, HP:0002391, HP:0002437, HP:0 HP:0001303, HP:0002479, HP:0002432, HP:0 HP:0002430, HP:0002431, HP:0002794 PURL http://purl.obolibrary.org/obo/HP_0001250	010520, 002434,		Textual definition Seizures are an intermittent abnormality of the central nervous system due to a sudden, excessive, disorderly discharge of cerebral neurons and characterized clinically by some combination of disturbance of sensation, loss of consciousness, impairment of psychic function, or convulsive movements. The term epilepsy is used to describe chronic, recurrent seizures. Logical definition Currently we do not have logical definition for this class. Feel free to suggest a logical definition at our <u>github tracker</u> .
Superclasses Abnormality of nervous system physiology	S	ubclasses <u>Multifocal seizures</u> <u>Focal seizures</u> <u>Epileptic spasms</u> <u>Dialeptic seizures</u> Symptomatic seizures	

Disease id Disease name							
ORPHA:2930 Cronkhite-Canada syndrome							
ORPHA:127 Borjeson-Forssman-Lehmann syndrome							
ORPHA:1951 Epilepsy-telangiectasia syndrome							
OMIM:6125	82 CHROMOSOME 6PTER-P24 DELETION SYNDROME						
ORPHA:5	Long chain 3-hydroxyacyl-CoA dehydrogenase deficiency						
OMIM:311400 PAINE SYNDROME							
	Export to Excel 🗷 Export to CSV 📟						
174 associat	ted genes						
Gene							
	ted genes						
Gene CLPP	ted genes Associated diseases						
Gene CLPP (8192) NHLRC1	ted genes Associated diseases PERRAULT SYNDROME 3 (OMIM:614129) MYOCLONIC EPILEPSY OF LAFORA (OMIM:254780)						
Gene CLPP (8192) NHLRC1 (378884) GPHN	Associated diseases PERRAULT SYNDROME 3 (OMIM:614129)						
Gene CLPP (8192) NHLRC1 (378884) GPHN (10243) TACO1	Associated diseases PERRAULT SYNDROME 3 (OMIM:614129) MYOCLONIC EPILEPSY OF LAFORA (OMIM:254780) Hereditary hyperekplexia (ORPHA:3197), HYPEREKPLEXIA, HEREDITARY (OMIM:149400), MOLYBDENUM COFACTOR DEFICIENCY, COMPLEME (OMIM:615501)	32)					

Export to Excel 🔳 🛛 Export to CSV 📟

/mseqdr.org/search_pher		es & Tools - C	😹 Breast Cancer In	forma 🔥 PIC	BASE product logi	View all genes - Intern	···· 💟 🏠	Q ontobee	
About GBrowse	MSeqDR-LSD		Phenome	Collaboration	Submission	MSeqDR PhenoTips		Please Login or Re	
MSeqDR			Genomic	Search 🔻 Ente	er search term here.	Mouse-over for examples.	Q		
			Hu	man Dise	ase and Ph	enotype Searc	h		
			Sear	ch term, sir	ngle or multipl	e lines	44		
				Ba	tch Search: OMIN	1 HPO			
1	SEIZURES	Term ID	HPO Disord	er Detail				Matche Field	d Top Match
1:1	SEIZURES	HP:0001250	Seizures	Synon Defini Seizur exces combi functi seizur	es are an intermitter sive, disorderly disch nation of disturbanc on, or convulsive mo	arge of cerebral neurons an e of sensation, loss of consc	i nervous system due to a su d characterized clinically by ousness, impairment of psyc is used to describe chronic,	some Synonyr	
1:2	SEIZURES	HP:0001327	Photomyoc seizures	lonic Synon Definit		oclonic seizures		Name o Synonyr	
1:3	SEIZURES	HP:0002069	<u>Generalizec</u> <u>clonic seizu</u>	I tonic- rres auton	ym: Generalised toni tion: alized tonic-clonic s	eizures are generalized seizu	res with bilateral symmetrica tic muscles usually associate		
1:4	SEIZURES	HP:0002121	Absence se	izures consc	tion: rent absence seizure		nd are characterized by a los	Name o s of Synonyr	
1:5	SEIZURES	HP:0002123	Generalized myoclonic s	Synon Definitiseizures muscle	ym: Myoclonic epile; tion: es with sudden, brie		gle or multiple contraction(: al, proximal limb, distal).	s) of Synonyr	
1:6	SEIZURES	HP:0002173	<u>Hypoglycen</u> seizures	Synon		emic seizures		Name of Synonyr	

Name	URL
PhenomeCentral	phenomecentral.org
DDD (Deciphering Developmental Disorders)	www.ddduk.org
DECIPHER (DatabasE of genomiC variation and	decipher.sanger.ac.uk
Phenotype in Humans using Ensembl Resources)	
ECARUCA (European Cytogeneticists Association	http://umcecaruca01.extern.umcn.nl:
Register of Unbalanced Chromosome Aberrations)	8080/ecaruca/ecaruca.jsp
The 100 000 Genomes Project	https://www.genomicsengland.co.uk/
Geno2MP (Exome sequencing data linked to phenotypic	http://geno2mp.gs.washington.edu
information from a wide variety of Mendelian gene	
discovery projects)	
NIH UDP (Undiagnosed Diseases Program)	available via phenomecentral.org
NIH UDN (Undiagnosed Diseases Network)	available via phenomecentral.org
HDG (Human Disease Gene Website series)	www.humandiseasegenes.com
Phenopolis(anopen platform for harmonization and	https://phenopolis.github.io
analysis of sequencing and phenotype data)	
GenomeConnect (Patient portal developed by ClinGen	www.genomeconnect.org
(67)	
FORGE Canada & Care4Rare Consortium	available via phenomecentral.org
RD-Connect	platform.rd-connect.eu
Genesis	thegenesisprojectfoundation.org

Table 2. Tools and applications using HPO

Tool

Phenotype-driven differential diagnosis Phenomizer BOQA FACE2GENE Phenolvzer Phenotype-driven exome/genome analysis Exomiser PhenIX Phevor PhenoVar eXtasy OMIMExplorer Phen-Gen Geno2MP Genomiser SimReg ontologySimilarity Functional and network analysis TopGene/ToppFunn WebGestalt SUPERFAMILY GREAT Random walk on heterogeneous network PANDA PREDICT Clinical data management and analysis Phenotips Patient Archive GENESIS (GEM.app)

Cross-species phenotype analysis PhenoDigm MouseFinder Monarch PhenomeNet UberPheno MORPHIN PhenogramViz Phenotype knowledge resources and databases Orphanet MalaCards NIH genetic testing registry OMIM dcGO ClinVar GeneSetDB **MSeqDR** DIDA (digenic diseases database) Genetic and Rare Diseases (GARD) Information Center Visualization PhenoStacks PhenoBlocks **DECIPHER** (phenogram) phenogrid ontologyPlot

Köhler et al.; The human phenotype ontology in 2017. NAR (2016)

Table 2. Tools and applications using HPO

Tool

Phenotype-driven differential diagnosis
Phenomizer
BOQA
FACE2GENE
Phenolyzer
Phenotype-driven exome/genome analysis
Exomiser
PhenIX
Phevor
PhenoVar
eXtasy
OMIMExplorer
Phen-Gen
Geno2MP
Genomiser
SimReg
ontologySimilarity
Functional and network analysis
TopGene/ToppFunn
WebGestalt
SUPERFAMILY
GREAT
Random walk on heterogeneous network
PANDA
PREDICT
Clinical data management and analysis
Phenotips
Patient Archive
GENESIS (GEM.app)

Cross-species phenotype analysis PhenoDigm MouseFinder Monarch PhenomeNet UberPheno MORPHIN PhenogramViz Phenotype knowledge resources and databases Orphanet MalaCards NIH genetic testing registry OMIM dcGO ClinVar GeneSetDB MSeqDR DIDA (digenic diseases database) Genetic and Rare Diseases (GARD) Information Center Visualization PhenoStacks PhenoBlocks **DECIPHER** (phenogram) phenogrid ontologyPlot

Phenotyp-driven Differential Diagnosis

Phenomizer: Search for diseases or differential diagnosis with HPO terms

JCSC Genome B	rowse 🚯 Befundverwaltung 🛞 Praena 🛞 Arztbrief	e 🌀 MGZ Intranet	🛞 gnomAD browser 🛛 🛞 VAMP 🔺 HGMD	start page 🛛 👜 European Journal of H 🤅	🕽 http://compbio.charit 🗧 ClinVar
lenu. • Support f	the Phenomizer. Help.				The Phenomize
Features. D	Diseases. Ontology.	Patient's Fe	atures.		
Enter feature	search. reset.	HPO.	Feature. 🔺	Modifier.	Num diseases.
HPO id.	Feature.				
HP:0010704	1-2 finger syndactyly				
HP:0005767	1-2 toe complete cutaneous syndactyly				
HP:0010711	1-2 toe syndactyly				
HP:0010706	1-3 finger syndactyly				
HP:0001459	1-3 toe syndactyly				
HP:0010707	1-4 finger syndactyly				
HP:0010712	1-4 toe syndactyly				
HP:0006088	1-5 finger complete cutaneous syndactyly				
HP:0010708	1-5 finger syndactyly				
HP:0010713	1-5 toe syndactyly				
HP:0030300	10 pairs of ribs				
HP:0000878	11 pairs of ribs				
HP:0030306	11 thoracic vertebrae	News		×	
HP:0001233	2-3 finger syndactyly				
HP:0005709	2-3 toe cutaneous syndactyly	Info			
HP:0004691	2-3 toe syndactyly	- The Phen	omizer is developed and maintained by Sebastian Köh	hler (see	
HP:0010709	2-4 finger syndactyly	group webs	site for more info).		
HP:0005768	2-4 toe cutaneous syndactyly		omizer Orphanet uses the latest Orphanet date and or ranking the differential diagnoses.	a different	
HP:0010714	2-4 toe syndactyly	-			
HP:0010692	2-5 finger syndactyly		e the following papers when you use this too	I/HPO in	
HP:0010715	2-5 toe syndactyly	your publ	icativits.		
HP:0008083	2nd-5th toe middle phalangeal hypoplasia		., <u>Clinical diagnostics in human genetics with semanti</u>	i <u>c similarity</u>	
HP:0011939	3-4 finger cutaneous syndactyly		<u>i ontologies.</u> Senet (2009) vol. 85 (4) pp. 457-64		
HP:0006097	3-4 finger syndactyly				
HP:0009779	3-4 toe syndactyly		I., The Human Phenotype Ontology in 2017.	/shu1030	
HP:0010710	3-5 finger syndactyly	INUCIEIC ACIO	ds Research (2017) doi: https://doi.org/10.1093/nar/	10km 1029	
HP:0010716	3-5 toe syndactyly				

Phenotyp-driven Differential Diagnosis

Phenomizer: Search for diseases or differential diagnosis with HPO terms

Menu. • Support the	e Phenomizer,Help,					The Phenomiz
Features. Dis	eases. Ontology.		Patient's Features	Diagnosis. 🕱		
Foot deformity		search. reset.	HPO.	Feature. 🔺	Modifier.	Num diseases.
HPO id.	Feature.		□ category.: Abnorm	ality of limbs (1 Item)		
HP:0001760	Abnormality of the foot		HP:0001760	Abnormality of the foot	observed.	1200 of 7994
HP:0001776	Bilateral talipes equinovarus			-		
HP:0005656	Positional foot deformity			ality of the eye (1 Item)		
HP:0001839	Split foot		HP:0000648	Optic atrophy	observed.	358 of 7994
HP:0010219	Structural foot deformity		🛛 🖃 category.: Abnorm	ality of the integument (1 Item)		
HP:0001884	Talipes calcaneovalgus		HP:0001000	Abnormality of skin pigmentation	observed.	463 of 7994
HP:0008081	Valgus foot deformity		□ category.: Abnorm	ality of the nervous system (3 Items)		
			HP:0001251	Ataxia	observed.	467 of 7994
			HP:0001249	Intellectual disability	observed.	1242 of 7994
			HP:0012675	Iron accumulation in brain	observed.	0 of 7994
N Page 1	of 1 🕨 🕅 🛟	Features 1 - 7 of 7	Clear.		Mode of inheritance.	✓ Get diagnosis.

Phenotyp-driven Differential Diagnosis

Phenomizer: Search for diseases or differential diagnosis with HPO terms

Features. D	iseases. Ontology.	F	Patient's Fea	tures. Diagnos	is. 🗵 Diagnosis. 🗵	
Enter feature	. search. reset.	Algo	rithm: resnik	(Unsymmetric).	6 Features.	
HPO id.	Feature.		p-value. 🔺	Disease Id.	Disease name.	Genes.
HP:0010704	1-2 finger syndactyly		0.2535	OMIM:136600	FRIEDREICH ATAXIA, SO-CALLED, WITH OPTIC ATROPHY AND SENSORINEURALDEAFNESS	
HP:0005767	1-2 toe complete cutaneous syndactyly		0.2535	OMIM:614499	#614499 MENTAL RETARDATION, AUTOSOMAL RECESSIVE 34; MRT34	METTL23 (124512
HP:0010711	1-2 toe syndactyly		0.2535	OMIM:614329	%614329 MENTAL RETARDATION, AUTOSOMAL RECESSIVE 31; MRT31	METTL23 (12451)
IP:0010706	1-3 finger syndactyly		0.2535	OMIM:614254	#614254 MENTAL RETARDATION, AUTOSOMAL DOMINANT 8; MRD8	MBD5 (55777), C
IP:0001459	1-3 toe syndactyly		0.2535	OMIM:300387	#300387 MENTAL RETARDATION, X-LINKED 63; MRX63;;MENTAL RETARDATION, X-LINKED 68; MRX68	ZNF711 (7552), II
HP:0010707	1-4 finger syndactyly		0.2535	OMIM:136610	#136610 FRAGILE SITE 2Q11	
IP:0010712	1-4 toe syndactyly		0.2535	OMIM:614256	#614256 MENTAL RETARDATION, AUTOSOMAL DOMINANT 10; MRD10	CACNG2 (10369
IP:0006088	1-5 finger complete cutaneous syndactyly		0.2535	OMIM:300849	#300849 MENTAL RETARDATION, X-LINKED 41; MRX41;;MENTAL RETARDATION, X-LINKED 48; MRX48	ZNF711 (7552), I
IP:0010708	1-5 finger syndactyly		0.2535	OMIM:611090	#611090 MENTAL RETARDATION, AUTOSOMAL RECESSIVE 12; MRT12	METTL23 (12451
IP:0010713	1-5 toe syndactyly		0.2535	OMIM:300046	MENTAL RETARDATION, X-LINKED 23	ZNF711 (7552),
P:0030300	10 pairs of ribs		0.2535	OMIM:611095	MENTAL RETARDATION, AUTOSOMAL RECESSIVE 9; MRT9	METTL23 (1245
P:0000878	11 pairs of ribs		0.2535	OMIM:612581	#612581 MENTAL RETARDATION, AUTOSOMAL DOMINANT 4; MRD4	MBD5 (55777), (
P:0030306	11 thoracic vertebrae		0.2535	OMIM:300419	#300419 MENTAL RETARDATION, X-LINKED, WITH OR WITHOUT SEIZURES, ARX-RELATED; MRXARX;; ME	ZNF711 (7552),
P:0001233	2-3 finger syndactyly		0.2535	OMIM:612580	#612580 MENTAL RETARDATION, AUTOSOMAL DOMINANT 3; MRD3	MBD5 (55777), (
P:0005709	2-3 toe cutaneous syndactyly		0.2535	OMIM:300803	#300803 MENTAL RETARDATION, X-LINKED 97; MRX97;;MRXZ	ZNF711 (7552),
P:0004691	2-3 toe syndactyly		0.2535	OMIM:309530	MENTAL RETARDATION, X-LINKED 1	ZNF711 (7552),
P:0010709	2-4 finger syndactyly		0.2535	OMIM:614257	#614257 MENTAL RETARDATION, AUTOSOMAL DOMINANT 11; MRD11	MBD5 (55777), (
P:0005768	2-4 toe cutaneous syndactyly		0.2535	OMIM:300047	MENTAL RETARDATION, X-LINKED 20	ZNF711 (7552),
P:0010714	2-4 toe syndactyly		0.2535	OMIM:136630	MENTAL RETARDATION, FRA12A TYPE	DIP2B (57609)
IP:0010692	2-5 finger syndactyly		0.2535	OMIM:614249	#614249 MENTAL RETARDATION, AUTOSOMAL RECESSIVE 18; MRT18	METTL23 (12451
IP:0010715	2-5 toe syndactyly		0.2535	OMIM:611093	#611093 MENTAL RETARDATION, AUTOSOMAL RECESSIVE 7; MRT7;;MENTAL RETARDATION, AUTOSOM	METTL23 (12451
IP:0008083	2nd-5th toe middle phalangeal hypoplasia		0.2535	OMIM:614020	#614020 MENTAL RETARDATION, AUTOSOMAL RECESSIVE 14; MRT14	METTL23 (12451
IP:0011939	3-4 finger cutaneous syndactyly		0.2766	OMIM:311050	OPTIC ATROPHY 2	
P:0006097	3-4 finger syndactyly		0.3300	OMIM:300210	#300210 MENTAL RETARDATION, X-LINKED 58; MRX58	ZNF711 (7552), I
P:0009779	3-4 toe syndactyly		0.3300	OMIM:300355	%300355 MENTAL RETARDATION, X-LINKED 73; MRX73	ZNF711 (7552),
P:0010710	3-5 finger syndactyly		0.3300	OMIM:300115	%300115 MENTAL RETARDATION, X-LINKED 50; MRX50	ZNF711 (7552), I
IP:0010716	3-5 toe syndactyly		0.0000			

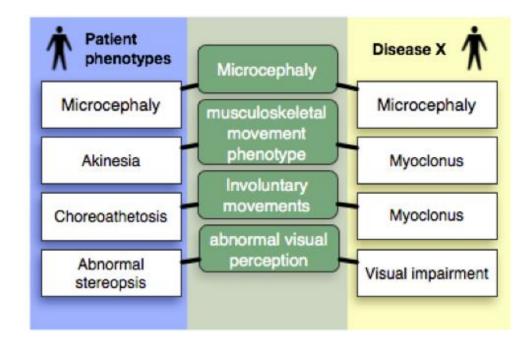
Clinical Data Management and Analysis



PhenoTips® is a software tool for collecting and analyzing phenotypic information of patients with genetic disorders.

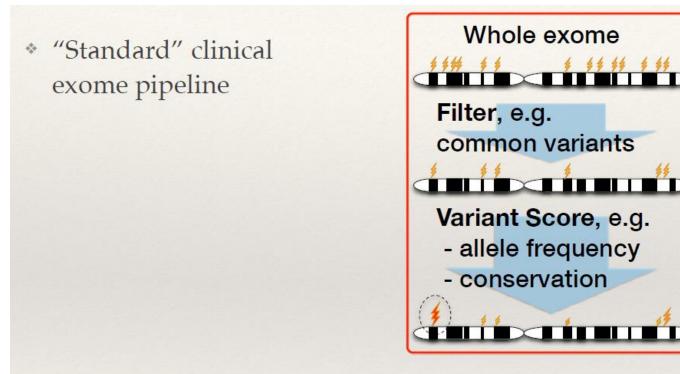
- Free and open source
- Web-based application
- Easy to customize
- Standardized phenotyping using the Human Phenotype Ontology (HPO)
- · Error-tolerant, predictive search of the ontology
- Real-time evaluation of the informational value of the phenotypic description via the Monarch Phenotype Profile Analysis
- Powerful built-in pedigree editor
- Measurements and growth curves
- Diagnosis assistance based on the entered data

Quick pher. type search:	Related terms
siezur	
Y N Seizures 0	V IX Y N HP-0002121 Absence seizures 6
Y N Focal seizures O (also known as: Seizures, partial, afebrile)	V N PP-001148 Absence seizures with special features () V N PP-001148 Absence seizures with special features () N V N PP-001148 N V N PP-001148 N V N PP-001148
Y N Hypocalcemic seizures O (also known as: Seizures due to hypocalcemia)	V V V N PP-contrast Obtraction absence seizures
Y N Atonic seizures 0	V NA V N (HP:0011147) Typical absence seizures 6
Y N Hemiclonic seizures Also known as Y N Febrile seizures Generalized seizures, recurs (also known as: Seizures) Infrequent generalized seizures, and recurs	rement of both cerebral hemisphe Image: Provide and Provide
Y N Absence seizures Seizures Y N Gelastic seizures Is a type of Seizures Y N Maternal seizures BROWSE RELATED TERMS	V N HP:0002069] Generalized tonic-clonic seizures N Y N HP:0007193] N Y N N Y N HP:0007297] Photosensitive tonic-clonic seizures



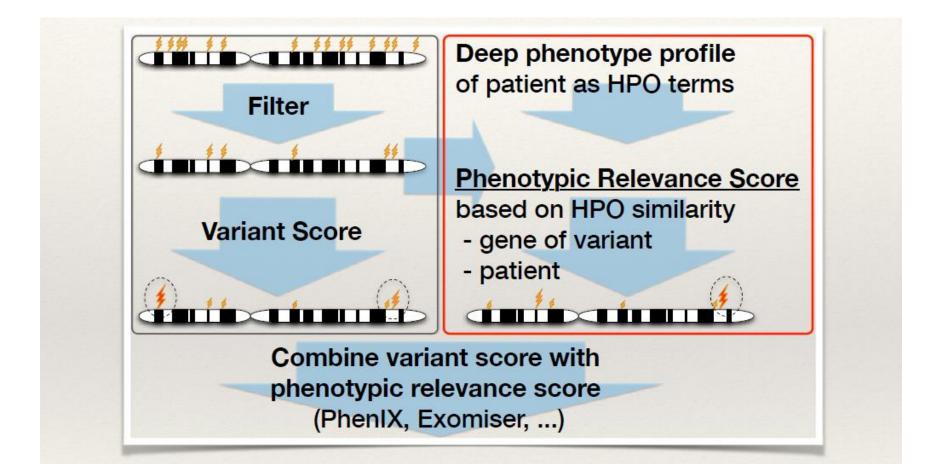
- Basic idea of ontological search: Do not need exact match! But semantically similar diseases score well.
- Image a BLAST-search for sets of clinical features. (Phenomizer)

Clinical Genomics



- Predicts causative variant based on information in genome of patient and background genomic data
- Each human genome harbors about 100 genuine loss-of-function SNVs with ~20 genes completely inactivated (3) and around 50-100 CNVs. (DG MacArthur et al., Science 2012)

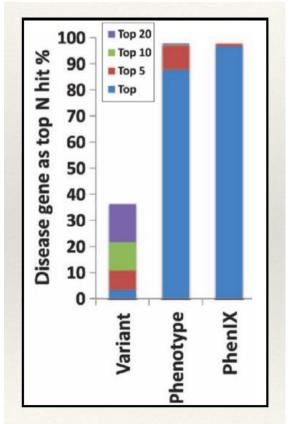
Clinical Genomics



Robinson, Köhler, et al. Improved exome prioritization of disease genes through crossspecies phenotype comparison Genome Research (2013) Zemojtel , Köhler et al. Effective diagnosis of genetic disease by computational phenotype analysis of the disease-associated genome Science Translational Medicine (2014)

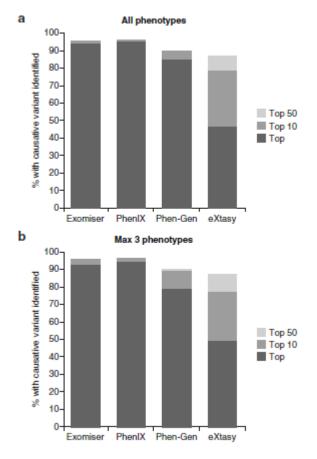
Clinical Genomics

Performance



Combination of variant score and phenotype score is key

Other tools



Smedley and Robinson Genome Medicine (2015) 7:81 DOI 10.1186/s13073-015-0199-2

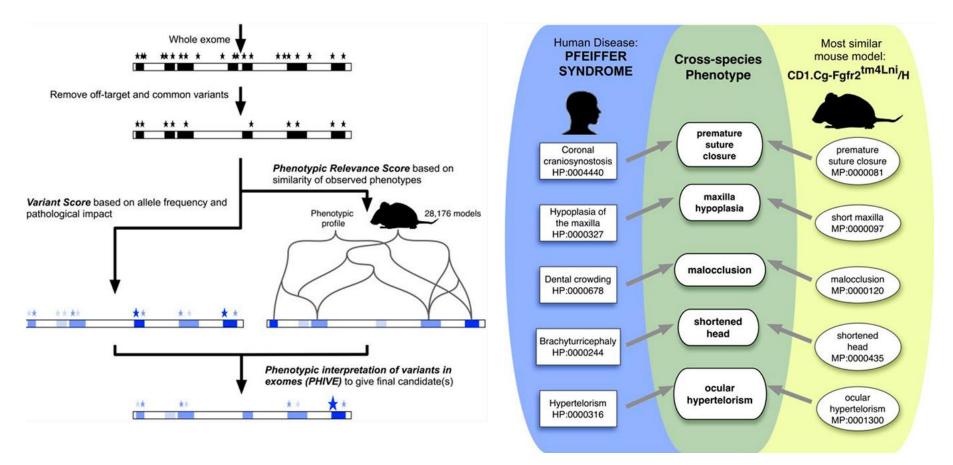
Phenotyp-driven Exome/Genome Analysis

mpbio.charite.de/PhenIX/		🗉 🚥 💟 🚖 🔍 mobile
CESE Schome Browse 🔇 MGZ NGL	🚶 Resources & Tools - C 🔀 Breast Cancer Informa 🛕 BIOBASE product log	ji 🚺 View all genes - Intern 🚺 View user account #00 ז Google
	PhenI	CHARITÉ UNIVERSITÄTSMEDIZIN BERLIN
	How does PhenIX work?	What input does PhenIX require?
	PhenIX, Phenotypic Interpretation of eXomes, is a pipeline for ranking (prioritizing) candidate generation where at NGC papels with comprehens countered of human Mendelian disease genes. It ranks genes based on predicted variant pathogenicity as well as phenotypic similarity of disease: associated with the genes harboring these variants to the phenotypic profile the individual being investigated, based on analysis powered by the Hump Phenotype on set (HEO).	the patient. The PhenIX server is designed to work with single sample VCF files, but locally installable versions are available le of on a collaborative basis that offer additional functionality for
	Run PhenIX online: HPO term (s): VCF file: Durchsuchen Keine I Mode of inheritance: Frequency cutoff: Number of candidates to show: Submit	Datei ausgewählt.

© 2014, Exomiser team: Charité Universitätsmedizin Berlin, Institute for Medical Genetics and Human Genetics, <u>Computational Biology and</u> Bioinformatics Group and Sanger Mouse Informatics Group at the <u>Sanger Institute</u>.

Phenotyp-driven Exome/Genome Analysis

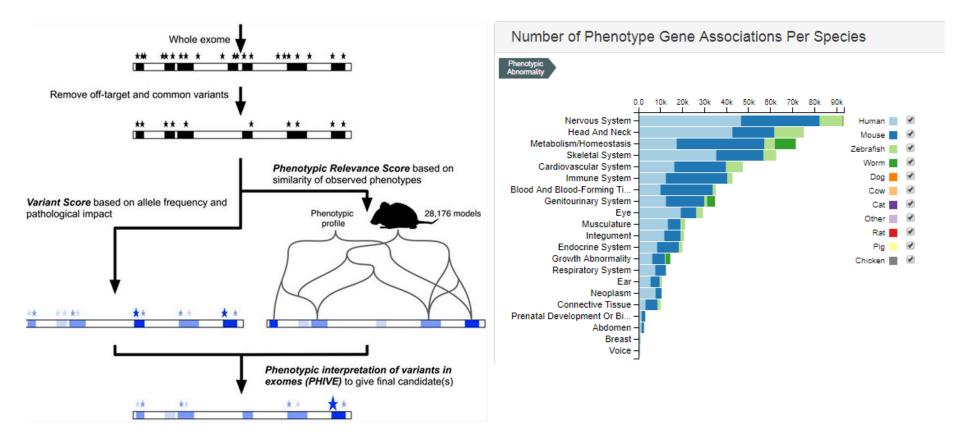
Exomiser – filtered genes assigned a phenotypic relevance score based on comparison with mouse and zebrafish models with mutations in orthologous genes



Genes with variants that survive the initial filtering steps are screened for mouse models with phenotypic to the human disease

Phenotyp-driven Exome/Genome Analysis

Exomiser – filtered genes assigned a phenotypic relevance score based on comparison with mouse and zebrafish models with mutations in orthologous genes



genes with variants that survive the initial filtering steps are then screened for mouse models with phenotypic to the human disease

Summary

HPO – a controlled vocabulary of phenotypic abnormalities for human genetics

- Freely available
- Open source

Novel approaches towards:

- Differential diagnosis tools (e.g. Phenomizer)
- Variant prioritization tools (e.g. Exomiser)
- Standard patient description in projects world-wide

Caveat: Phenotyp-driven variant prioritization

- Phenotypes in your patient (may) change over time
- Phenotypes are not always expressed / observed or described properly (two diseases)
- Phenotypes are not determined for (very) rare diseases (OMIM updates)
- Phenotypes are not very selective for e.g. mental retardation (Phenomizer; e.g. "intellectual disability" + "seizures" + "developmental delay")

... Challenges to (H)WPO



The famous Bavarian "Wolpertinger"