Phenotype risk scores (PheRS) for risk prediction

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Case: What is wrong with this patient?



Various methods of testing for gene/disease associations

Looping through association tests

- GWAS/NGS one phenotype, many genotypes
- PheWAS one genotype, many phenotypes

Aggregation approaches

- GRS/PRS/GPS one phenotypes, many genotypes aggregated
- Phenotype risk scores (PheRS) one genotype, many phenotypes aggregated

Automating assessments of "phenotype patterns" in the EHR



Repeat this for any Mendelian diseases

Bastarache et al, Science 2018

CYSTIC FIBROSIS; CF

INHERITANCE

- Autosomal recessive

GROWTH	HPO		Phecodes			
Other						
- Failure to thrive	1508	>	264.2 H	Failure to thrive1.62		
CARDIOVASCULAR						
Heart						
- Cor pulmonale	1648	>	415.1 A	Acute pulmonary heart disease1.49		
RESPIRATORY						
Airways						
- Chronic bronchopulmonary infection	6538	>	483 A	Acute bronchitis & bronchiolitis1.00		
- Bronchiectasis	2110		496.3 I	Bronchiectasis1.80		
- Asthma	2099	>	495 /	Asthma0.98		
- Pulmonary blebs	-		-			
- Pseudomonas colonization	-		-			
ABDOMEN						
Pancreas						
- Pancreatic insufficiency in 80%	1738	>	577 I	Diseases of pancreas1.42		
Biliary Tract						
- Biliary cirrhosis	2613	>	571.6 J	Primary biliary cirrhosis2.06		



Many diseases have "phenotype patterns": consider Cystic Fibrosis





You can differentiate a group individuals diagnosed with a disease using **only the features** of the disease

Validating Phenotype Risk Scores on diagnosed individuals



Bastarache et al, Science 2018

RESEARCH ARTICLE

HUMAN GENOMICS

Phenotype risk scores identify patients with unrecognized Mendelian disease patterns

Gene	Vorient	relD	HOM/	Associated Mendelian Disease		Phenotype	Rota	Р	ClinVar	HCMD	ACMG
Gene	variant	rsiD	HEI	Associated Meridenan Disease	inheritance	categories in Fliens	Dela	Г	Clinvar	HGIMD	ACING
CFTR	c.1624G>1 p.Gly542Ter	rs113993959	1/27	Cystic fibrosis	AR		1.39	2.9×10 ⁻⁸	Р	Y	Р
CHRNA4	c.1448G>A p.Arg483Gln	rs55855125	1/21	Nocturnal frontal lobe epilepsy, 1	AD		0.58	9.0×10 ⁻⁸	U		U
DGKE	c.966G>A p.Trp322Ter	rs138924661	1/14	Nephrotic syndrome, type 7	AR		1.31	2.8×10 ⁻⁷	LP	Υ	LP→P
SUOX	c.228G>T p.Arg76Ser	rs202085145	0/24	Sulfocysteinuria	AR		0.82	1.7×10 ⁻⁶	U		U→P
CFTR	c.1657C>T p.Arg553Ter	rs74597325	0/12	Cystic fibrosis	AR		1.81	2.1×10 ⁻⁶	Р	Y	Р
KIF1B	c.2021C>T p.Thr674lle	rs41274468	0/21	Charcot-Marie-Tooth disease, 2A1	AD		0.79	5.3×10 ⁻⁶			U
VWF	c.5851A>G p.Thr1951Ala	rs144072210	0/21	Von Willebrand disease	AR*		0.53	8.6×10 ⁻⁶		Y	U
KIF1A	c.2676C>T p.Ala993=	rs116297894	1/25	Spastic paraplegia-30	AR		0.84	1.3×10 ⁻⁵	LB		LB→U
F10	c.872G>A p.Arg291Gln	rs149212700	0/15	Factor X deficiency	AR*		0.62	1.9×10 ⁻⁵			U
HFE	c.502G>C p.Glu168Gln	rs146519482	0/40	Hemochromatosis	AR		1.08	4.0×10 ⁻⁵	U	Y	U
TG	c.229G>A p.Gly77Ser	rs142698837	0/69	Thyroid dyshormonogenesis	AR		0.26	6.0×10 ⁻⁵		Y	U→P
SH2B3	c.1183G>A p.Glu395Lys	rs148636776	0/22	Familial erythrocytosis, 1	AD		1.48	6.1×10 ⁻⁵			U→P
SPTBN2	c.7109G>A p.Arg2370His	rs145522851	0/11	Spinocerebellar ataxia	AR*		0.75	9.0×10 ⁻⁵			U→LP
FAN1	c.1520G>A p.Arg507His	rs150393409	0/434	Interstitial nephritis, karyomegalic	AR		0.15	9.9×10 ⁻⁵			LB→U
PANK2	c.1561G>A p.Gly521Arg	rs137852959	0/26	HARP syndrome	AR		0.58	1.1×10 ⁻⁴	Ρ	Y	Р
SH2B3	c.1183G>A p.Glu395Lys	rs148636776	0/22	Essential thrombocythemia	AD		0.33	1.4×10 ⁻⁴			U→P
AGXT	c.883G>A p.Ala295Thr	rs13408961	1/35	Primary hyperoxaluria, type I	AR		0.82	1.7×10 ⁻⁴	U/LB		LB→U
PLCG2	c.751A>G p.lle251Val	rs190840748	0/10	Familial cold autoinflammatory syn. 3	AD		0.70	1.9×10 ⁻⁴			U

Tested

6644 variant/disease pairs

Found

18 significant associations (14 novel)

Neoplastic
Endocrine/Metabolic/Blood

Nervous/Psychiatric/Sensory Circulatory/Respiratory Digestive/Genitourinary
Musculoskeletal/Dermatologic

Other symptoms/Injuries

PheRS identifies novel pathogenic variants with clinical impact



Bastarache et al, Science 2018

PheWAS of a CF variant



Bastarache et al, Science 2018

A case of a rare disease



Dr. Christopher J. Richards: A 47-year-old woman was evaluated at the outpatient pulmonary clinic of this hospital because of recurrent sinusitis with progressive cough and bronchiectasis.

Since her mid-20s, the patient had had recurrent episodes of sinus congestion, with two or three sinus infections annually which had prompted treatment with

Mojica NEJM 2018, Bastarache NEJM 2019

1990 1992 1994 1996 1998 2000 2002 2004 2006 2008 2010 2012 2014 2016 2018 Year diagnosed



Premise

- ACMG59 variants are becoming increasingly returned (eMERGE, All of Us)
- Most rare variants are VUS

<u>eMERGEseq</u>

- 25,000 patients sequenced for 109 genes (including 58 ACMG "returnable" genes)
- 10 clinical sites
- All linked to EHR data

PheRS for high-throughput variant interpretation using EHRs: *FBN1* (Marfan Syndrome)

Known pathogenic variants



eme

netwo

Known benign variants

p.L2815L	p.Q2296Q	p.D2285D	p.A2025S	p.N1282S	p.P1148A	p.D964D	p.C685C	p.A52A
0.2	0	0	0	0.4	0 1	0.4	0 1	0 1
-0.2		0	0	0.4	0.1	0.4	0.1	0.1

What about FBN1 Variants of Uncertain Significance



p.D2860G	p.K2851E	p.K2848T	p.V2771I	p.N2767S	p.R2730Q	p.G2727S	p.R2726Q	p.A2714V	p.G2691S
3.7	2.3	0.6	-0.4	-0.1	0.2	-0.7	-0.8	0	-0.5
p.P2676L	p.G2618R	p.I2616M	p.I2616V	p.T2520M	p.K2510R	p.Q2477R	p.Q2467R	p.K2460R	p.R2414Q
0.3	-0.2	1.9	0	-0.1	1.1	0	-1	-0.6	-0.8
p.G2367R	p.S2361W	p.G2351S	p.C2339Y	p.R2311H	p.M2273I	p.E2193K	p.V2165L	p.N1975N	p.P1837S
0.5	2.5	0.7	1.7	1	-1.4	-0.1	-0.5	-0.4	0.7
p.R1832H	p.G1780G	p.V1667I	p.R1644Q	p.M1576T	p.I1498V	p.G1482S	p.P1453L	p.D1448N	p.G1441R
-0.8	0.4	-0.2	-0.5	0.4	0.2	-0.5	0.1	0.5	0.2
p.A1439G	p.S1438N	p.P1424A	p.L1405R	p.M1384V	p.I1359V	p.G1334D	p.Y1266F	p.N1168S	p.I1154I
-0.1	-0.3	-0.1	0.7	1.9	0.1	-0.3	0.4	0	0.1
p.G1143G	p.H1130R	p.G1126S	p.I1076L	p.R1066T	p.G1049S	p.P1009R	p.E1005K	p.V984V	p.V984I
0.4	0.4	-1.2	-0.2	-0.1	-0.1	-0.2	0.4	-1	0.5
p.M977R	p.E965K	p.E965Q	p.L925V	p.V916M	p.E915K	p.N867S	p.1849M	p.E812K	p.P698L
0	-0.4	-0.8	1.7	0.3	-0.2	0.2	-0.1	-0.6	0.8
p.A686T	p.P673S	p.T524M	p.V449I	p.P430L	p.G422E	p.M393V	p.R327T	p.D288G	p.N156S
-0.2	0.2	0	0.2	0.5	0.3	-0.3	-0.1	0	0.1
p.Q117R	p.N28S								
5.6	0.5								

Case: A diagnosis – riboflavin deficiency



PheRS may help diagnose people earlier, but it will be hard

Polycythemia vera due to a JAK2 mutation



EHRs provides dense resource for efficient discovery: BioVU's example





The power of a data biosphere of common semantics and APIs



Sources for genetic data

Research cohorts

- Clinical testing will explode
 - Cancer testing
 - Increasing rare disease and expanding indications (UHC, BCBS Evidence Street)
 - Yet another reason to store genetic data not as PDFs...
 - Genomics as the tool to really move the Learning Healthcare System into standard practice?



Birney et al. biorXiv 2017. https://doi.org/10.1101/203554

A small sampling of the VUMC Team



emerge network

+many others!





