

Executive Education

AI and Precision Medicine Around the World JOHN HALAMKA, MD, MS International Healthcare Innovation Professor, And Executive Director Of Healthcare Technology Exploration Center PAUL CERRATO, MA Former Editor, InformationWeek Healthcare; Contributing writer, Medscape March 12, 2019

Can AI and Precision Medicine Cure the Misdiagnosis Problem and Improve Clinical Outcomes?

How serious is the problem of diagnostic errors?

5% of U.S. adult outpatients experience diagnostic error each year

Autopsy data: dx errors contribute to about 10% of deaths

Medical record review: Dx errors cause 6-17% of hospital adverse effects

Dx errors affect about 12 million US adults annually.

National Academies of Sciences, Engineering, and Medicine. 2015. Improving diagnosis in health care. Washington, DC: The National Academies Pres Singh H et al. BMJ Quality Safety 2014;23:727-731.



Types of Dx errors

- Missed diagnosis
- Misdiagnosis, i.e, the wrong diagnosis
- Delayed diagnosis
- Overdiagnosis i.e., medicalization of everyday life



What's causing these mistakes?

- Cognitive errors: Clinicians' inadequate reasoning skills, biases, prejudices
- Information overload
- Poor handoff procedures
- Delayed or misplaced lab results
- Ignoring patients' input
- "The complexity of medicine now exceeds the capacity of the human mind."



Real-world examples of Personalized Medicine Solutions



Gene & Variation	rsID	Alleles	Result	
COMT V158M	rs4680	AG	+/-	
COMT H62H	rs4633	СТ	+/-	
COMT P199P	rs769224	GG	-/-	
VDR Bsm	rs1544410	сс	-/-	
VDR Taq	rs731236	AA	+/+	
MAO A R297R	rs6323	т	+/+	
ACAT1-02	rs3741049	AG	+/-	
MTHFR C677T	1133	AG	+/-	
MTHFR 03 P39 P	rs2066470	GG	-1-	
MTHFR A1298C	rs1801131	GT	+/-	

Profile: Methylation Profile Generated: 4/23/2014

- Jake needed 4 wisdom teeth pulled
- Talk about using Nitrous Oxide, laughing gas
- Forward thinking doc did gene sequencing years earlier

- MTHFR Methylenetetrahydrofolate reductase mutation
- 3 case reports of catastrophic neurologic complications when N2O given to patients with 2 MTHFR mutations



unknownnot reviewedevaluatedscore: 0 Polyphen 2: UnknownYP2C9-R144Chet unknown0.027UnknownModerate clinical importance, well- establishedThis variant, also called CYP2C9*2, is a pharmacogenetic variant that modulates sensitivity for Warfarin (due to reduced metabolism). This variant is associated with Caucasians. The FDA has approved reduced recommended Warfarin dosage based on the					
unknown pharmacogenetic clinical importance, well- established variant that modulates sensitivity for Warfarin (due to reduced metabolism). This variant is associated with Caucasians. The FDA has approved reduced recommended Warfarin dosage based on the	ITGAM-P1147S		0.141		score: 0 Polyphen 2:
variant.	<u>CYP2C9-R144C</u>	Contraction and a second second second	0.027	clinical importance, well-	called CYP2C9*2, is a pharmacogenetic variant that modulates sensitivity for Warfarin (due to reduced metabolism). This variant is associated with Caucasians. The FDA has approved reduced recommended Warfarin dosage based on the presence of this

Excerpt from John Halamka's gene sequencing report

- CYP2C9 gene \rightarrow protein --> metabolizes warfarin.
- John's mutation SLOWS warfarin breakdown \rightarrow lower dose requirement
- Normal dose → John bleeds out; w/o gene test: diagnostic error
- Pharmacogenomic testing individualizes care, reduces misdiagnoses.
- About 150 drugs now have FDA warning about possible genetic mutations that may influence drug metabolism.
- No national guidelines, almost no 3rd party reimbursement--despite good evidence that it reduces adverse effects.

JAMA. 2016;316(15):1533-1535. doi:10.1001/jama.2016.12103

Food and Drug Administration. Table of pharmacogenomic biomarkers in drug labeling. July 11, 2016.

http://www.fda.gov/Drugs/ScienceResearch/ResearchAreas/Pharmacogenetics/ucm083378.htm.



- Most chronic diseases are polygenic.
- Big data analytics → Polygenic risk score → For example: data from 6.6 million SNPs/ 400,000 persons → detects person at FOUR times the average risk of heart disease.(1)
- **BEWARE Marketing hype that gets ahead of the science.**

"Precision medicine" is a marketing term; the overarching belief that precision medicine is the future of medicine has led to what has been called an "arms race" or "gold rush" among academic medical centers to develop precision medicine initiatives." (2)

1. Khera AV, Chaffin M, Aragam KG, et al. Genome-wide polygenic score to identify a monogenic risk-equivalent for coronary disease. BioRxiv 2017. Available from: https://doi.org/10.1101/ 218388.

(2) David H. Gorski, MD, PhD, FACS, oncologist at the Barbara Ann Karmanos Cancer Institute



The High Cost of Precision Medicine

- Among 58 cancer drugs, many of which were precision med drugs
 - 1995: additional year of life cost \$54,000
 - 2005: \$139,000
 - 2013: \$207,000
 - ROI: Survival improved by only a few months
- Novartis CAR-T Gene Therapy, called Kymriah
 - The most precise form of cancer therapy yet
 - Price tag: \$475,000 for one time treatment

Howard DH, Bach PB, Brendt ER et al. Pricing in the Market for Anticancer Drugs. J Economic Perspectives. 2015; 29(1):139-162.

- Most cancer patients don't benefit from precision medicine.
- Checkpoint inhibitor drugs: Among all Americans who will die of cancer in one year, only 8% will benefit.(1)
- Personalized nutrition services—not ready for prime time
 - Habit.com and DNA Power claim gene variants dictate specific vitamin or mineral needs.
 - Associations between mutations and nutritional dysfunction don't establish cause and effect relationship.
 - Example: Variants of FTO gene linked to obesity; but clinical experiment found people lost weight just as well with and w/o the FTO mutation (2)

1. https://www.statnews.com/2017/03/08/immunotherapy-cancer-breakthrough/

2. Dow, D. Nutrition Action Health Letter, May 2018, pg 3.



Role of machine learning in Medicine

IBM Deep Blue Supercomputer vs Google's AlphaZero (Old school vs new school AI).





- Old school example: Encyclopedia-like CDS tools vs machine-learning based algorithms for diabetic retinopathy, melanoma, sepsis
- Use of deep learning, neural networks, and back propagation—giant step forward in digital world



Machine learning vs skin cancer

- Deep convolutional neural network
- Algorithm can distinguish melanoma from normal mole, initially trained using 129,000 clinical images
- As effective as trained dermatologists is accurately diagnosing skin cancer Esteva A. Kuprel B, Novoa RA et al. Dermatologist-level classification of skin cancer with deep neural networks. *Nature*. 2017;542:115-118.



• IDx-DR is FDA cleared system that uses fundus camera and machine learning based algorithms to analyze retinal images and help detect diabetic retinopathy

- Google research:
 - Trained on 128,175 retinal images
 - Compared computer analysis to analysis by 54 ophthalmologists
 - Computer-based results: 87% to 90% sensitivity, 98% specificity
 - As good as or better than human counterparts

Gulshan et al. Development and Validation of a Deep Learning Algorithm for Detection of Diabetic Retinopathy in Retinal Fundus Photographs. JAMA. 2016;316(22):2402-2410.





Watch the entire video below

AI Explained: What Is A Neural Net?

How Neural Networks Work lnput Output +2 Melanoma? -2 +1 +2 -7 -1 0 +4 -2 +3 -2 10,000s Not images of Melanoma? melanomas +4 and normal moles Layer Three Layer One Layer Two



- Research project by Cerrato and Halamka ٠
- A more in-depth look at mobile health, AI, • machine learning, and clinical decision support tools.

The Transformative Power of Mobile Medicine

Leveraging Innovation, Seizing Opportunities, and Overcoming Obstacles of mHealth



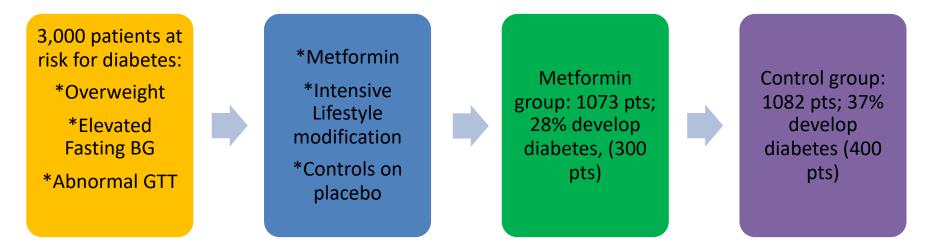
Paul Cerrato and John Halamka



https://www.elsevier.com/books/the-transformativepower-of-mobile-medicine/cerrato/978-0-12-814923-2. Discount Code HIMSS2019 valid until 3/31/2019

Big Data Analytics Applied to Type 2 Diabetes

Data from Diabetes Prevention Program (2002)



Diabetes Prevention Program Research Group; N Engl J Med 2002; 346:393-403

- Flaw in Diabetes Prevention Trial: Couldn't predict who would respond to Tx and who would not.
- Jeremy Sussman University of Michigan et al.
 - Data analysis that looked at 17 risk factors for diabetes
 - Used proportional hazards regression to make predictions
 - SEVEN risk factors helped pinpoint individuals most likely to develop type 2 diabetes—This is Personalized/Precision Medicine!

Sussman et al. BMJ 2015; Feb 19;350:h454



Sussman's Results: "Average reported benefit for metformin was distributed very unevenly across the study population, with the quarter of patients at the highest risk for developing diabetes receiving a dramatic benefit (21.5% absolute reduction in diabetes over three years of treatment) but the remainder of the study population receiving modest or no benefit."

Take home message: Data Analytics informed more detailed set of risk factors, allowing clinicians identify individuals more likely to benefit from treatment and those who would not.



Diabetes risk prediction tool

IMPORTANT NOTE: This is not a diagnostic tool. Talk to your doctor about your results.

INSTRUCTIONS

Measure or look up your value for each item below. Put your cursor or finger over your value on the number line for the first item. Then move your cursor or finger straight up to the Points line. Write down the number of points you earned for that item. Repeat for each of the seven items. Then, total up your score.

Points

What's your fasting blood sugar (in mg/dL)? What's your long-term blood sugar, or A1C (in %)? Family history of high blood sugar? (0 for no, 1 for yes) What's your blood triglyceride level (in mg/dL)? What's your waist measurement, in centimeters? (multiply inches by 2.54) How tall are you, in centimeters? (multiply inches by 2.54) What's your waist to hip ratio? (take your waist measurement at smallest point, and hip measurement at widest point. Divide the first number by the second.)

0	10		20	30	40	50	60	70	80	90	100	My Points
oe		10	o .	110	0	120	-	130	-	140		
3		1 4		5		6	÷		ė		9	
ò		_										
ò	20	bo Do	400	600	800	100	0					
60	90	120	150	180	210							
200	180	160	140	120								
0.5	0.7	15	i	1.25	1.5	1.75	2					-
										My	Total	

Total score of 146 or above: Talk to your doctor soon about your risk of diabetes, and what preventive steps you should take. Lower scores: At your next checkup, discuss with your doctor how you can keep your risk of diabetes from increasing.

If you haven't had a blood sugar test and you're over age 45 or you have a high body mass index (over 25), talk to your doctor about being tested. Also talk to your doctor if you haven't had your triglyceride levels measured in the last five years.

Model based on data from adults over age 25 who took part in the Diabetes Prevention Program. More information about the research behind this model: http://umhealth.me/diabpre

Used with permission, Univ of Michigan, Tufts University. Prediction tool is still undergoing clinical confirmation.



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Realizing the Promise of Precision Medicine

The role of patient data, mobile technology, and consumer engagement



Paul Cerrato and John Halamka

https://www.elsevier.com/books/realizing-thepromise-of-precision-medicine/cerrato/978-0-12-811635-7



What Big Data Analytics Can Do for Subgroup Analysis

Many clinical trials do subgroup analysis to look for smaller groups of patients who may respond to TX when main group didn't.

- Traditionally subgroup analyses consider ONE confounding variable or risk factor at a time.
 - Example: Clinical trial finds low fat diet for diabetic patients doesn't prevent heart disease, on average.
 - Factor in dietary intake of trans fats, which are atherogenic
 - Factor in extreme stress, e.g., death in family, divorce
- Many risk factors are synergistic, they only have effect on TX outcome in combination with others
- 10 risk factors can interact in 100s of ways not accounted for by single factor subgroup analysis
- Newer more sophisticated methods go beyond traditional subgroup analysis



Clinical Trial: Cardiovascular effects of intensive lifestyle intervention in type 2 diabetes.

About 5,000 overweight and obese pts with Type 2 diabetes divided into 2 groups: *Intensive lifestyle modification *Controls given basic education/support Goal: reduce cardiovascular deaths and heart disease events over 13.5 years

Trial stopped after 9.6 years. No benefits

N Engl J Med. 2013 Jul 11;369(2):145-54. Look AHEAD Research Group

- Aaron Baum et al reanalysis: A machine learning-based post-hoc analysis of heterogeneous treatment effects in the Look AHEAD trial
 - Causal Forest modelling to detect subgroups that benefited from the lifestyle mod program
 - Causal forest analysis identifies subgroups by building numerous decision trees from pre-specified covariates in a random subsample of the data
- Didn't look at one factor at a time but MANY combinations of factors
- Analyzing combinations of A, B, C, D might detect interlocking risk factors.

Baum A, et al. Lancet Diabetes Endocrinol. 2017 Oct;5(10):808-815.



Baum's results

- Intensive lifestyle modification averted cardiovascular events for these subgroups:
 - HbA1c 6.8% or higher (poorly managed diabetes)
 - Well controlled diabetes (Hba1c < 6.8%) and GOOD self reported health
- 85% of the study population benefitted
- 15% of population with controlled diabetes and POOR selfreported general health had NEGATIVE effects.
- One group cancelled out the other in original trial.



Take home messages:

- HbA1c and a short questionnaire on general health might identify people with type 2 diabetes likely to derive benefit from an intensive lifestyle intervention aimed at weight loss.
- Big Data analytics needed to make
 Precision/Personalized Medicine a reality



Advances in Clinical Decision Support Systems Move from Static Enclycopedic CDS tools to AI enhanced tools

- Medial EarlySign ColonFlag to detect high risk of colorectal cancer <u>https://earlysign.com</u>
- UpToDateAdvanced and Pathways <u>http://vid.uptodate.com/watch/scwKFikyHetLUoNLePokiH</u>
- Via Oncology, Elsevier http://viaoncology.com
- VisualDx <u>https://www.visualdx.com</u>

