

Cancer Surveillance, Data, and FHIR

Warren A. Kibbe, Ph.D.

Professor, Biostats & Bioinformatics

Chief Data Officer, Duke Cancer Institute

warren.kibbe@duke.edu



@wakibbe

#PrecisionOncology

#DataSharing

#CancerSurveillance

#DataHarmonization

Take homes

- Data generation is no longer the bottleneck – **data management, analysis, reasoning** are
- **Data science** is everywhere
- Understanding the patient context, the **patient trajectory**, is key
- **Well-structured data** can be easily exchanged, **is highly fluid**, transformational

Understanding Cancer


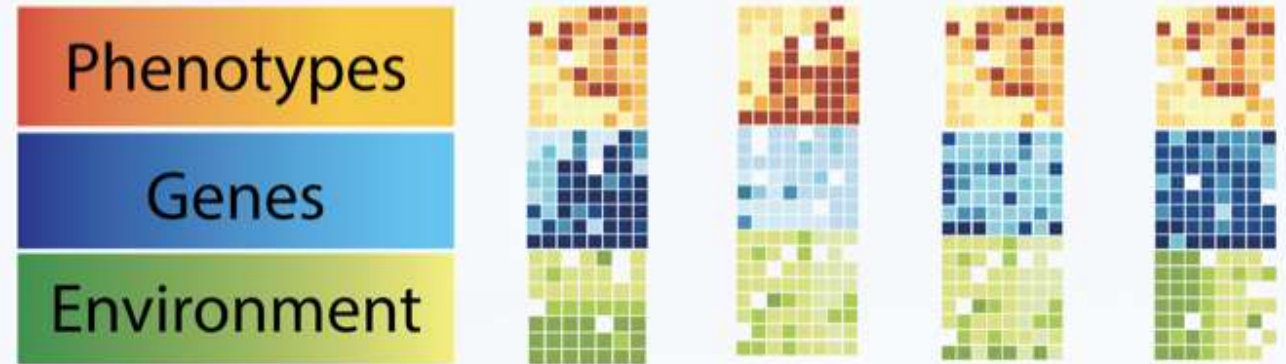
- **Precision medicine** will lead to **fundamental understanding** of the complex interplay between genetics, epigenetics, nutrition, environment and clinical presentation and **direct effective, evidence-based prevention and treatment.**



Ramifications across many aspects of health care

The promise of precision medicine:

How can we meaningfully group patients?



signs and
symptoms,
demographics,
exposure, diet,
traits, etc.



Current sources of data

molecular



genome



pathology



imaging



labs



notes



sensors



Our ability to generate biomedical data continues to grow in terms of variety and volume

molecular



genome



pathology



imaging



EHR



behavior

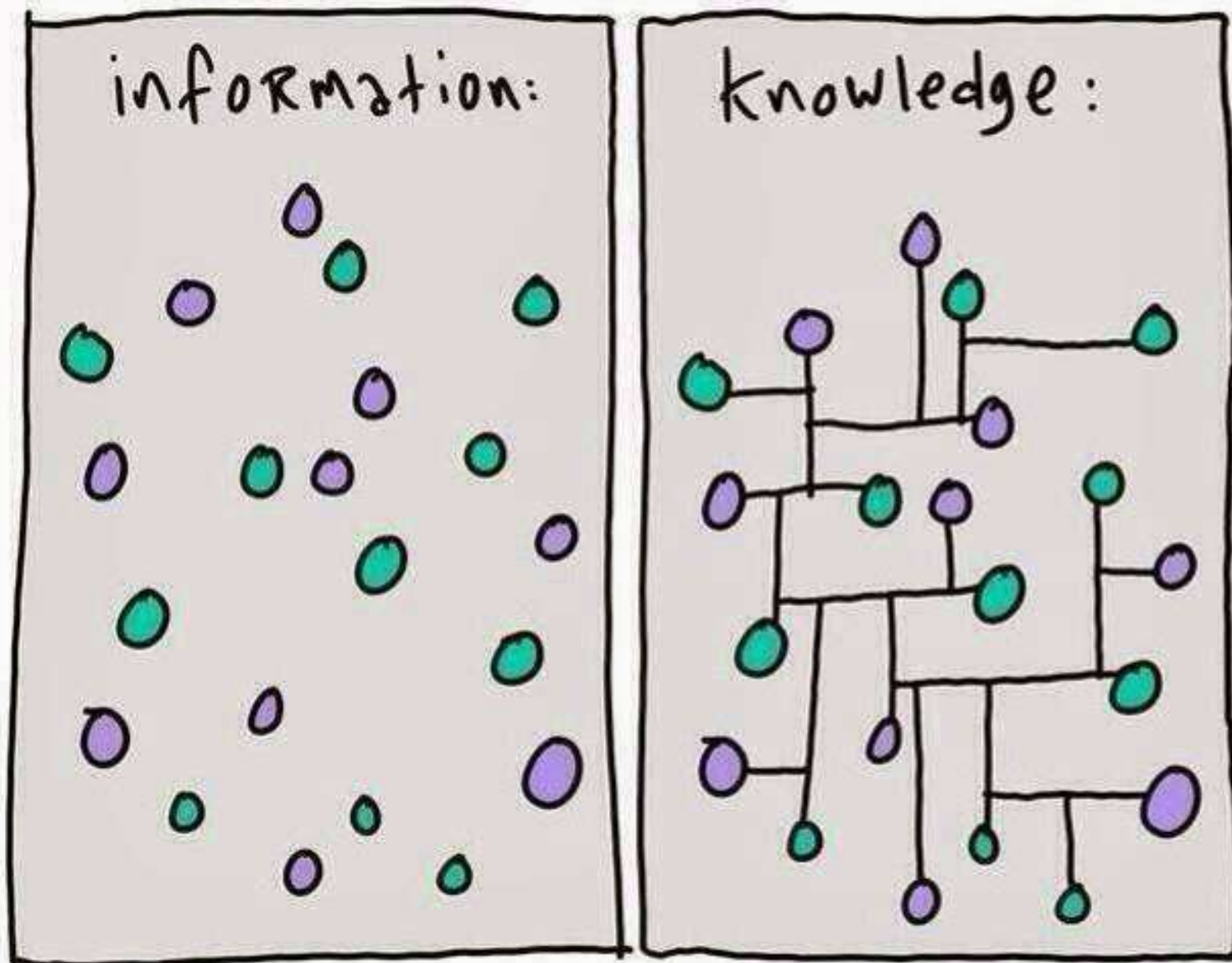


population



Multi-scalar, multi-modal,
temporal data analysis is in its
infancy

Managing Data

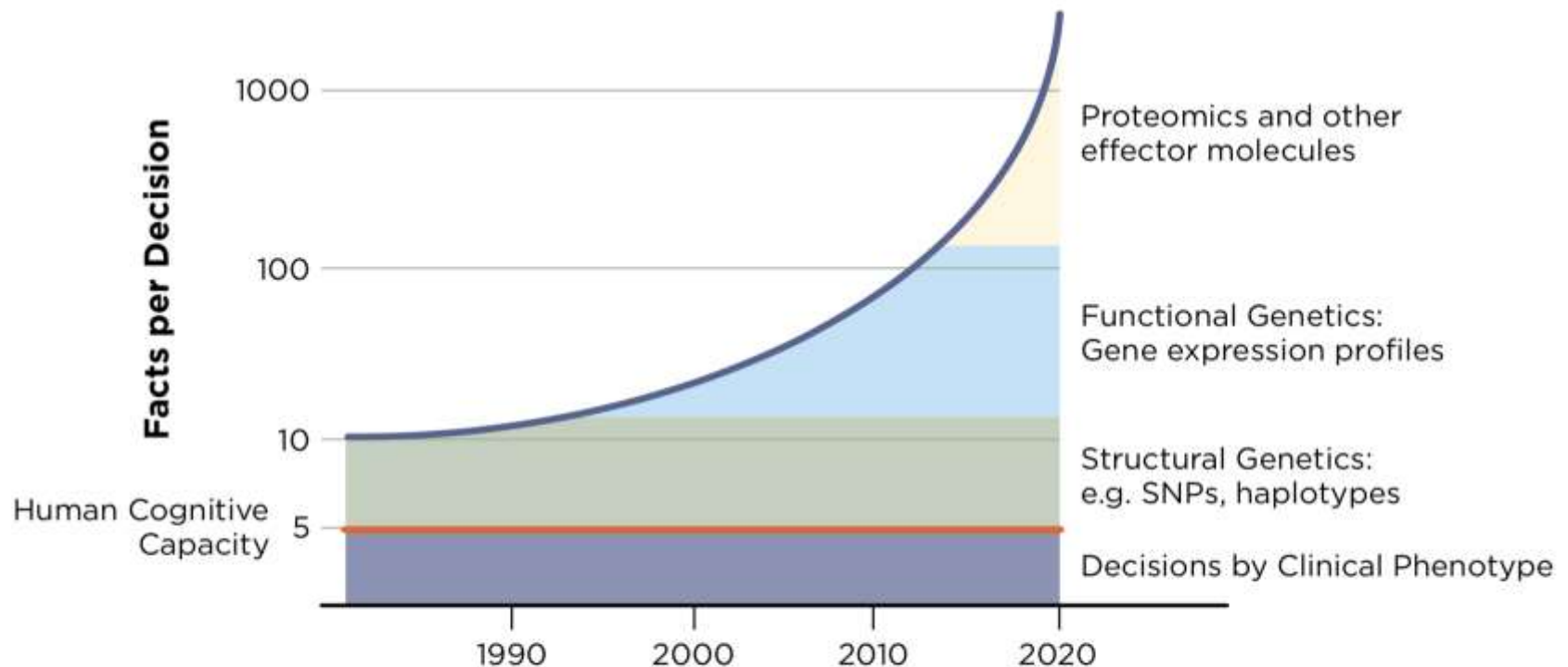


@gapingvoid

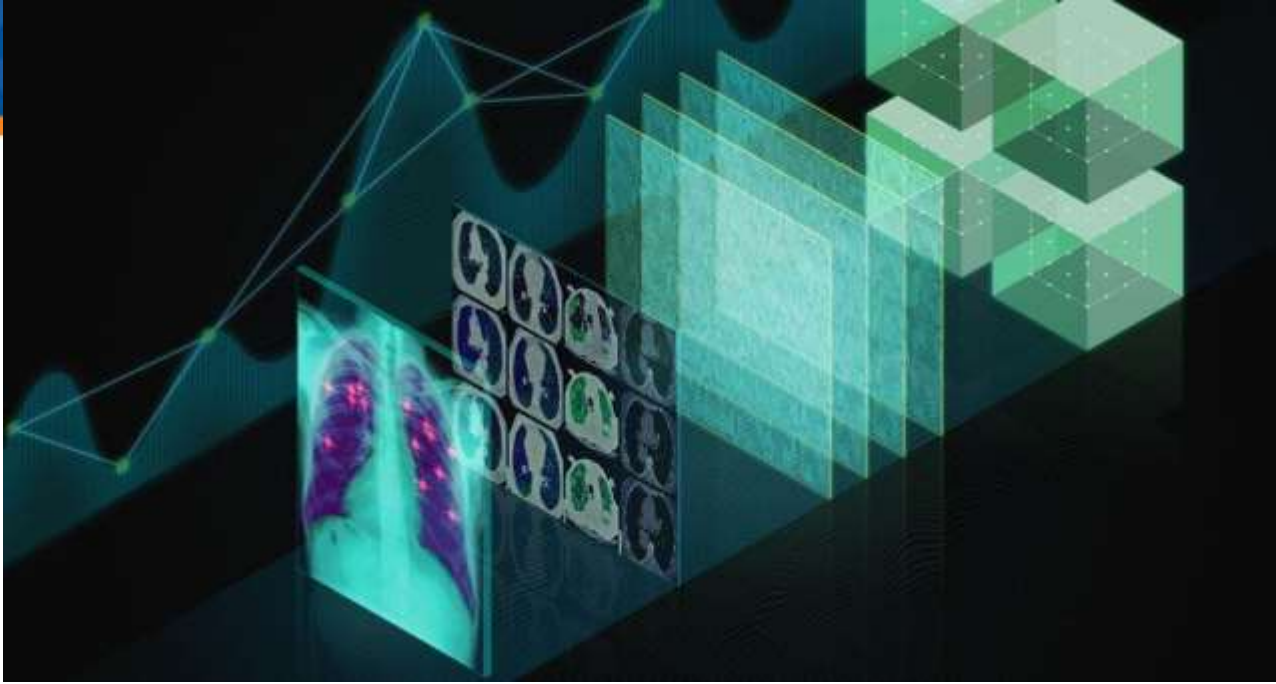
Human cognitive capacity is constant

The Learning Health System

Medical decisions becoming more complex



William Stead, IOM Meeting, 8 October 2007. Growth in facts affecting provider decisions versus human cognitive capacity.



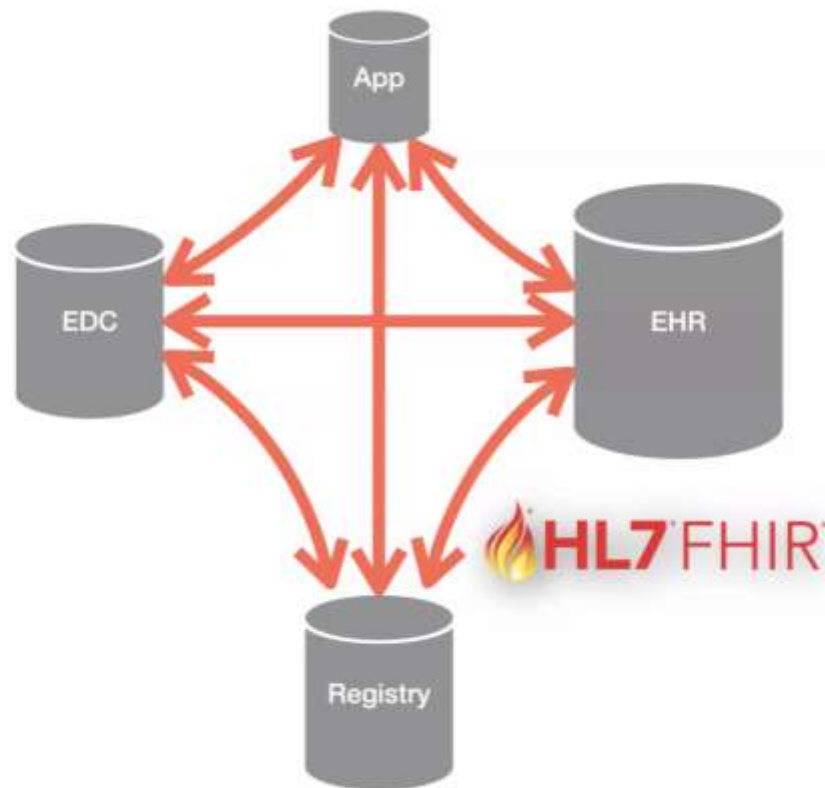
AI is changing our ability to go
both deep and broad

Trustworthy AI
Provenance

Reusable
Reproducible

shutterstock

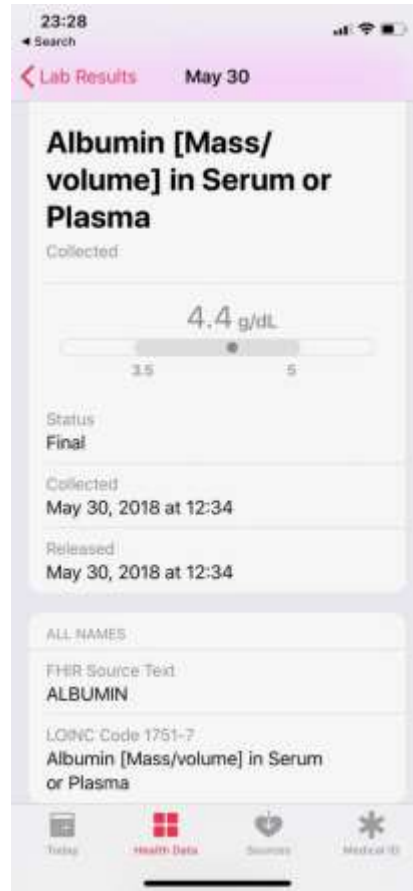
FHIR enables vertical and horizontal integration



Access to data has changed-Epic

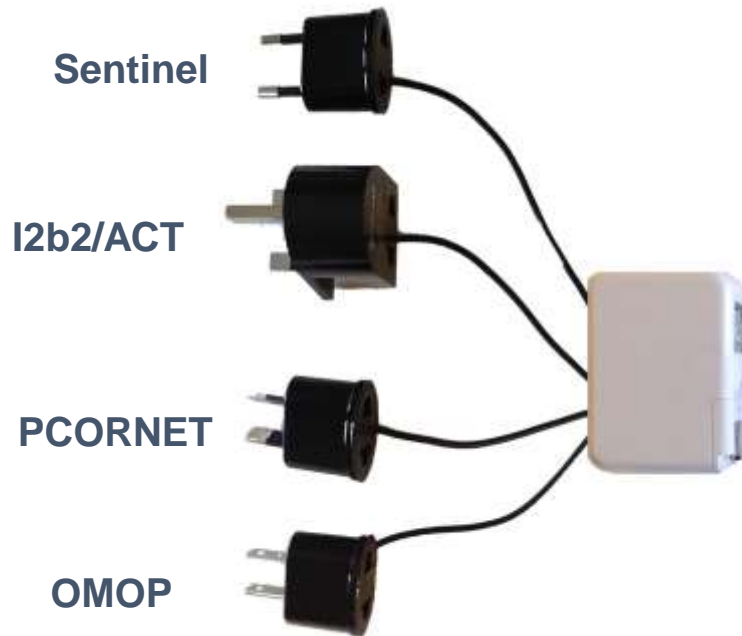
Details	Past Results	Graph of Past Results
Comments from the Doctor's Office		
Liver and kidney function are normal. Electrolytes are normal		
Component Results		
Component	Your Value	Standard Range
Sodium	140 mmol/L	135 - 145 mmol/L
Potassium	4.3 mmol/L	3.5 - 5.0 mmol/L
Chloride	104 mmol/L	98 - 107 mmol/L
CO2	23.0 mmol/L	22.0 - 30.0 mmol/L
BUN	16 mg/dL	7 - 21 mg/dL
Creatinine	0.85 mg/dL	0.70 - 1.30 mg/dL
BUN/Creatinine Ratio	19	
EGFR MDRD Non Af Amer	≥ 60 mL/min/1.73m ²	≥ 60 mL/min/1.73m ²
EGFR MDRD Af Amer	≥ 60 mL/min/1.73m ²	≥ 60 mL/min/1.73m ²
Anion Gap	13 mmol/L	9 - 15 mmol/L
Glucose	126 mg/dL	65 - 99 mg/dL
Calcium	8.9 mg/dL	8.5 - 10.2 mg/dL
Albumin	4.4 g/dL	3.5 - 5.0 g/dL
Total Protein	7.2 g/dL	6.6 - 8.0 g/dL
Total Bilirubin	0.5 mg/dL	0.0 - 1.2 mg/dL
AST	36 U/L	19 - 55 U/L
ALT	36 U/L	19 - 72 U/L
Alkaline Phosphatase	45 U/L	38 - 126 U/L

From Apple Health App



Note the FHIR JSON source in the last panel. Cool!

Project Highlight: Harmonizing clinical data models



- Different countries use different “outlets”.
- There is a need for travel adapters.

The Solution:

- Use a converter between various adapters.
- Allow researchers to ask a question once and receive results from many different sources



Chris Chute

Johns Hopkins
University



NATIONAL CENTER
FOR DATA TO HEALTH

Project Highlight: LOINC2HPO

Develop a tool for converting LOINC laboratory codes and values into more phenotypically meaningful language (Human Phenotype Ontology) to allow for translational interoperability and new analytics

Steps

- ◆ Develop a software tool to map LOINC codes to HPO terms
- ◆ Develop software to convert EHR observations into HPO terms for use in clinical research

LOINC

Outcome

2657-5 "Nitrite [Mass/volume] in Urine"	Numeric
20407-3 "Nitrite [Mass/volume] in Urine by Test strip"	Numeric
32710-6 "Nitrite [Presence] in Urine"	Positive/Negative
5802-4 "Nitrite [Presence] in Urine by Test strip"	Positive/Negative
5802-6 "Nitrite [Presence] in Urine by Test strip"	Positive/Negative

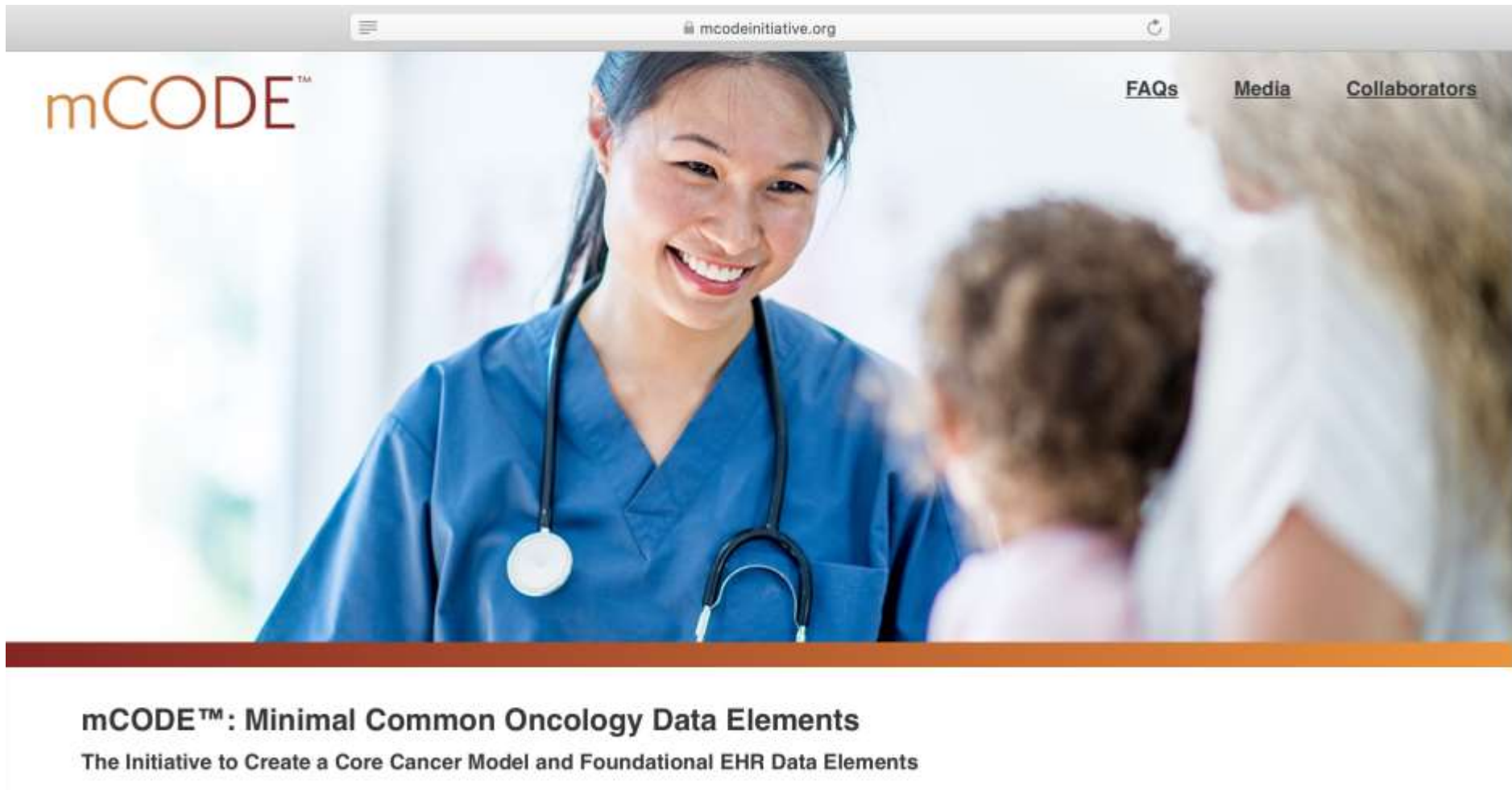
HPO: Nitrituria



Peter Robinson

Jackson
Laboratories

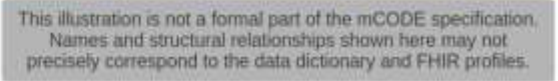
mCODE



mCODE™: Minimal Common Oncology Data Elements

The Initiative to Create a Core Cancer Model and Foundational EHR Data Elements

1000




mCODE on FHIR

Not Secure — hl7.org/fhir/us/mcode/

HL7
International

HL7 FHIR Implementation Guide: minimal Common Oncology Data Elements (mCODE) Release 1 - US Realm | STU1
1.0.0 - STU1



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This page is part of the HL7 FHIR Implementation Guide: minimal Common Oncology Data Elements (mCODE) Release 1 - US Realm | STU1 (v1.0.0: STU 1) based on FHIR R4. This is the current published version. For a full list of available versions, see the [Directory of published versions](#)

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M-CODE Pilot

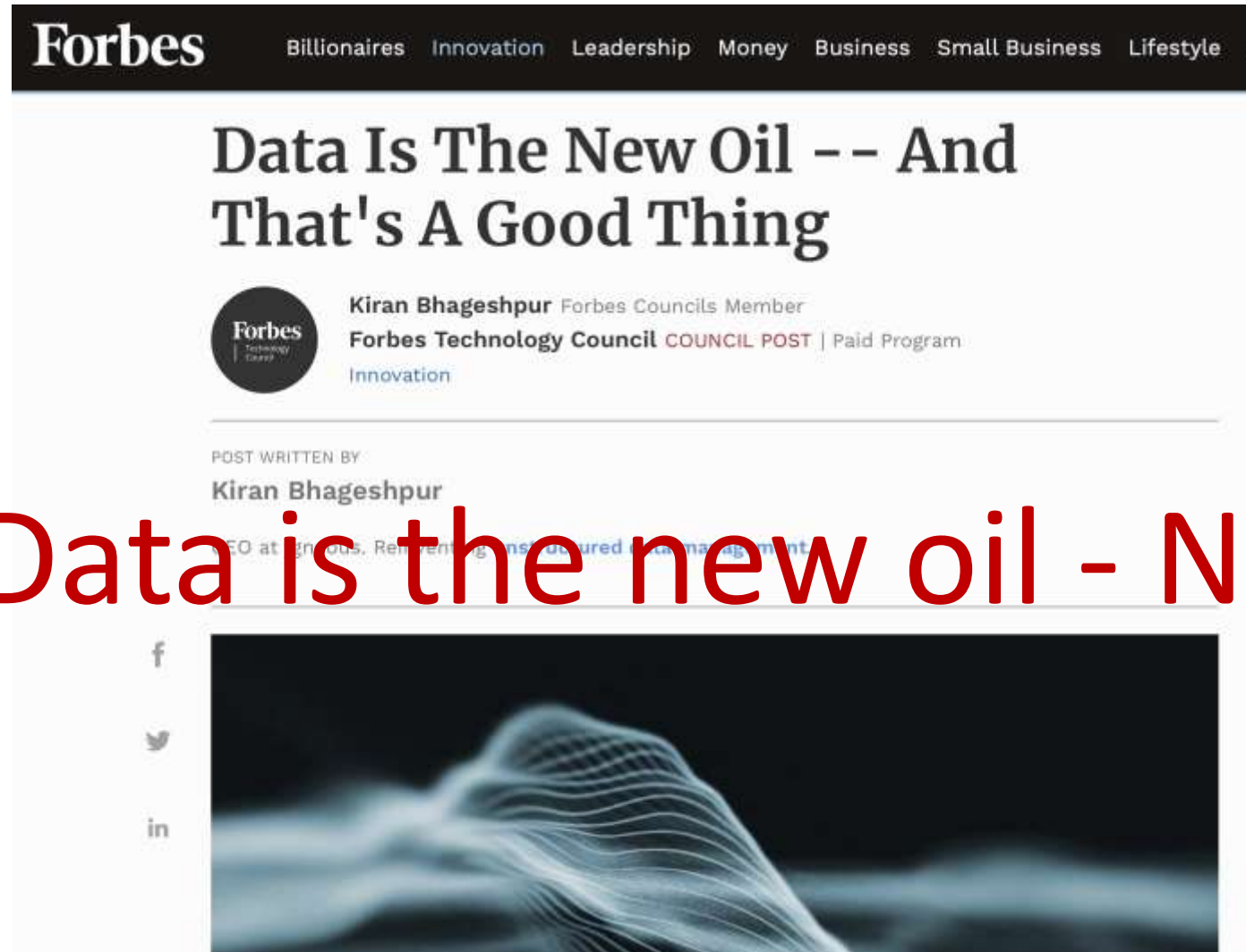
Demonstrating the M-CODE's ability to advance cancer care

- **Get M-CODE data collected by adapting existing workflows at Intermountain**
- **Create a FHIR API for M-CODE data on top of Cerner EHR**
- **Construct a real-time, shared decision making SMART-on-FHIR application**
 - Extract the M-CODE patient data from Cerner via API
 - Query against the de-identified dataset at CancerLinQ
 - Bring back similar cohort of patients, stratified by treatment and outcome
 - Present for shared decision making in real time at the point of care

MITRE
ASCO


Intermountain
Healthcare
CancerLinQ

Data Science Hype



Data Science Hype



Using data
increases its value

A word cloud featuring the phrase "Thank You" in various languages. The words are arranged in a roughly rectangular shape, with "THANK YOU" being the largest and most central. Other prominent words include "GRACIAS", "ARIGATO", "SHUKURIA", "BOLZIN", and "MERCI". Smaller words include "DANKSCHEEN", "TASHAKKUR ATU", "SUKSAMA", "EKMET", "YAQHANYELAY", "TINGKI", "BIYAN", "SHUKRIA", "JUSPAXAR", "GOZAIMASHITA", "EFCHARISTO", "KOMAPSUMBIDA", "MAAKE", "GRAZIE", "MEHRBANI", "PALDIJS", "BOLZIN", and "MERCI".

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