Poll 1

“

Have you ever used (or developed) an open source model?

Multiple choice

- **Yes (in precision medicine)**
- **Yes (*not* in precision medicine)**
- **No**

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ISPOR

Improving healthcare decisions

Open source in precision medicine: the perfect fit?

Chris Sampson, Office of Health Economics

On behalf of the Open Source Models Special Interest Group

#ISPORAnnual #OSMSIG @ChrisSampson87

Brought to you by the ISPOR Open Source Models Special Interest Group

- A new SIG, established in 2020
- Current leadership: Chair Me | Past (and founding) Chair Renée Arnold | Chair-Elect Raymond Henderson
- ~150 members across
  - 46% US 9% UK 7% India
  - 29% academia
- 4 journal clubs, 1 webinar
  - Watch them online!
- 1 publication


ISPOR Report

Opportunities and Barriers to the Development and Use of Open Source Health Economic Models: A Survey

Xavier G.L.V. Pouwels, PhD, Christopher J. Sampson, PhD, Renée J.G. Arnold, PharmD, RPh, On behalf of the Open Source Models Special Interest Group

Join us!

www.ispor.org/member-groups/special-interest-groups/open-source-models

Our objectives

To identify **opportunities and challenges** for open source modelling in precision medicine.

To explore **technical aspects of modelling** in precision medicine and their link to open source practices

To consider **strategic questions** for the development of open source models

To **discuss** your views!

OHE

> Open source is source code that is made freely available for possible modification and redistribution
>
> (says Wikipedia)

- ✓ Transparent reporting
- ✓ Sharing underlying code
- ✓ Removing restrictions on use

- ! Inclusive approach
  - ! ‘Free’ as in freedom *or* ‘free’ as in free beer
- ! As much about intention as realisation
  - ! 100% open source is often impossible

Why open source?

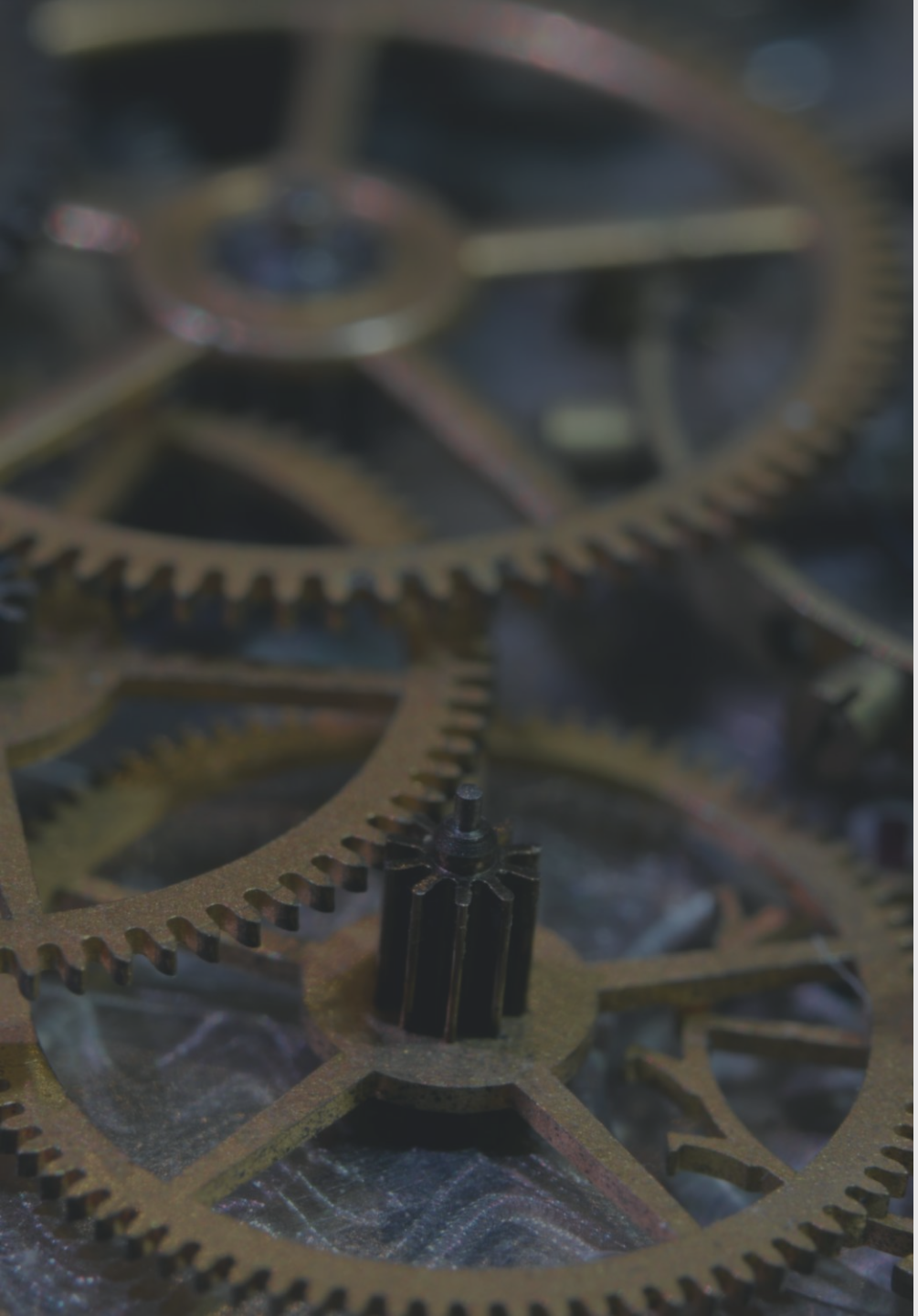
Good science

Efficiency savings

Improved methods

Better decisions

Learning



Why precision medicine?

Improve cost-effectiveness

Recognise patient trajectories

Therapeutic adjacency

Decision complexity

Software flexibility

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Improving healthcare decisions

Today's speakers

Susan Snyder

Co-Chair, Precision Medicine and Advanced Therapies SIG

Georgia State University

Deborah Marshall

University of Calgary

Koen Degeling

Lumen Value & Access

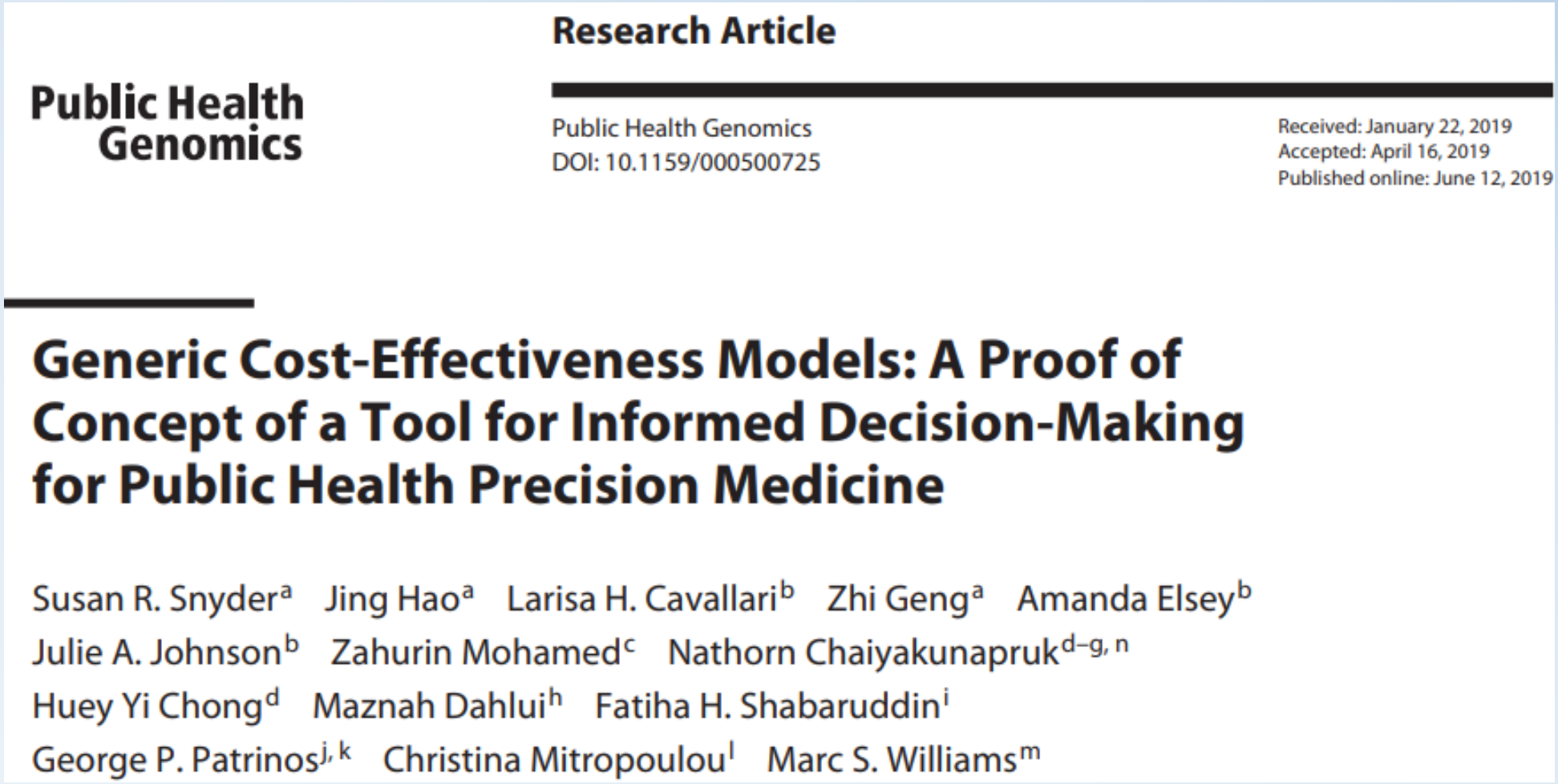
Generic Modeling for Precision Medicine:

A Pharmacogenomic Decisionmaking Tool

Presented at ISPOR 2022 in Washington, DC

Susan R. Snyder, PhD, MBA
Associate Professor
School of Public Health | Georgia State University
Co-Chair ISPOR Precision Medicine and Advanced Therapies SIG, Next Generation Testing Project

Case Example: Pharmacogenomic Open-Source Model and Decision Tool



Research Article

Public Health Genomics

Public Health Genomics
DOI: 10.1159/000500725

Received: January 22, 2019
Accepted: April 16, 2019
Published online: June 12, 2019

Generic Cost-Effectiveness Models: A Proof of Concept of a Tool for Informed Decision-Making for Public Health Precision Medicine

Susan R. Snyder[a] Jing Hao[a] Larisa H. Cavallari[b] Zhi Geng[a] Amanda Elsey[b]
Julie A. Johnson[b] Zahurin Mohamed[c] Nathorn Chaiyakunapruk[d–g, n]
Huey Yi Chong[d] Maznah Dahlui[h] Fatiha H. Shabaruddin[i]
George P. Patrinos[j, k] Christina Mitropoulou[l] Marc S. Williams[m]

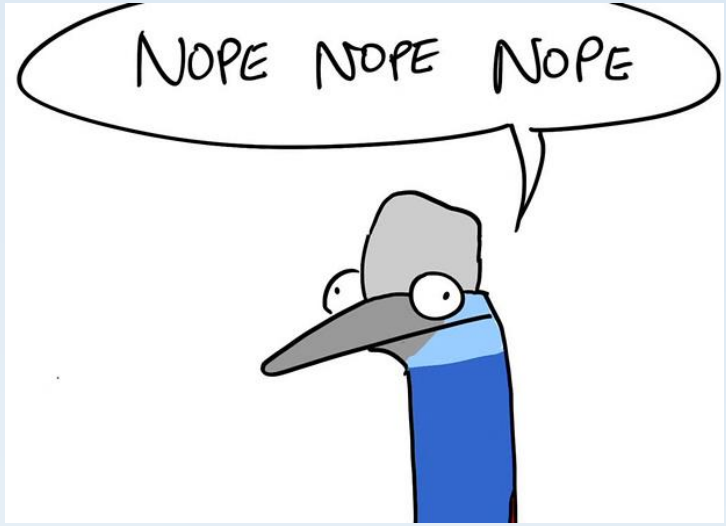
Study funded by the US National Human Genome Research Institute (research grant number U01 HG007269).

Why Open-Source Generic Model?

- Value-based decisionmaking
- Emerging evidence base
- Disparate modeling approaches
- Transparency
- Efficiency

Challenges?

- Generalizability
- Validity
- Usability
- Relevance

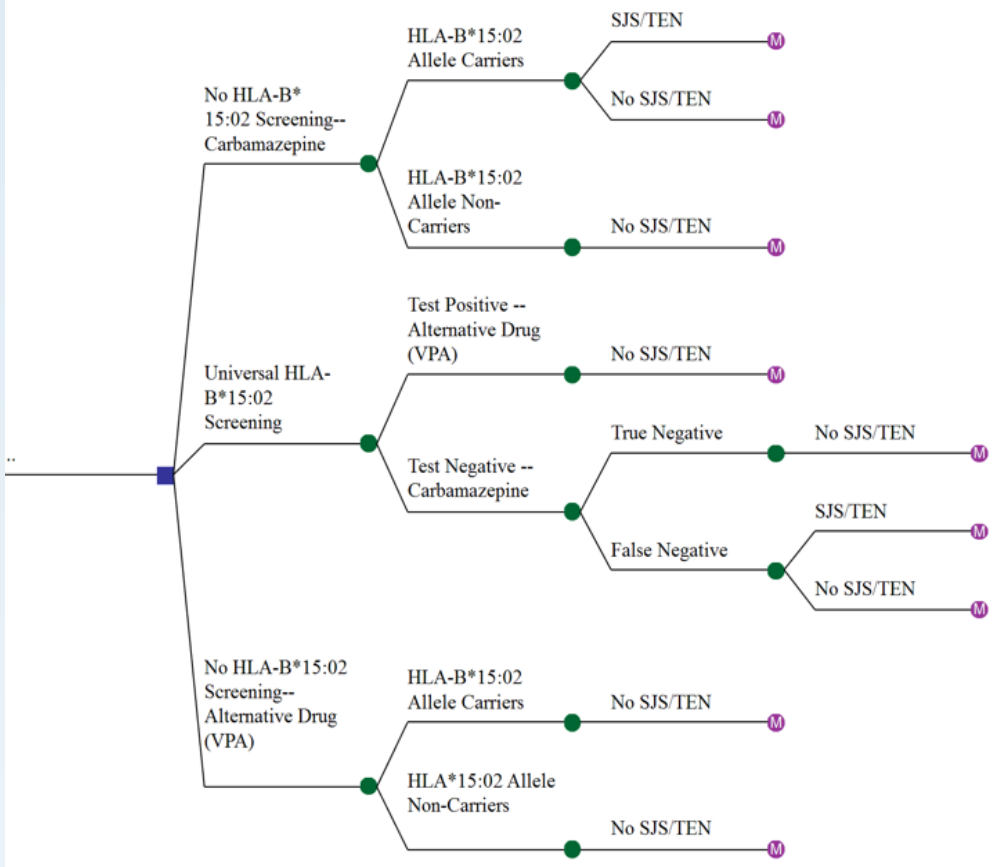


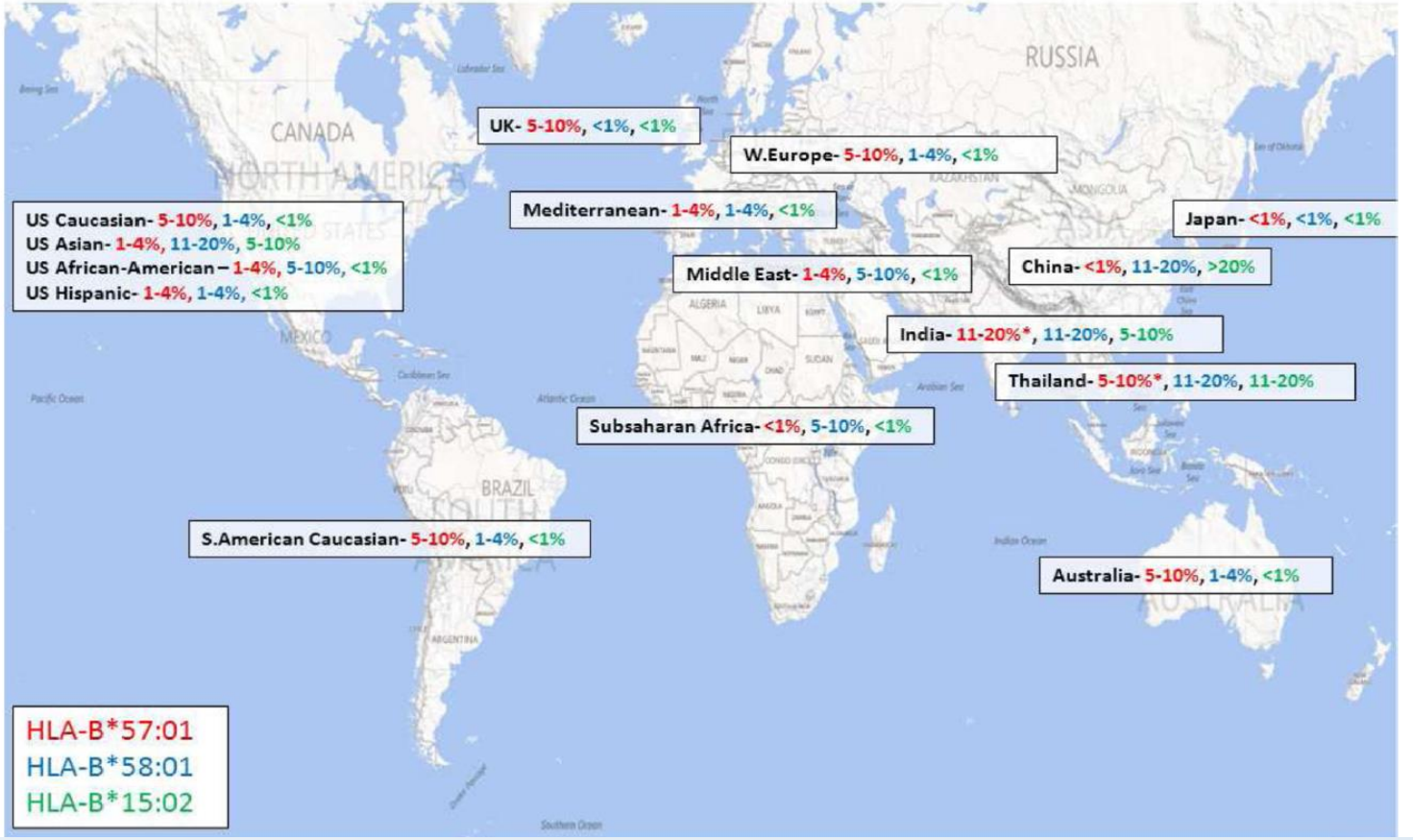
Generic Pharmacogenomic Screening Economic Model: Adult-Onset Epilepsy

Georgia State University

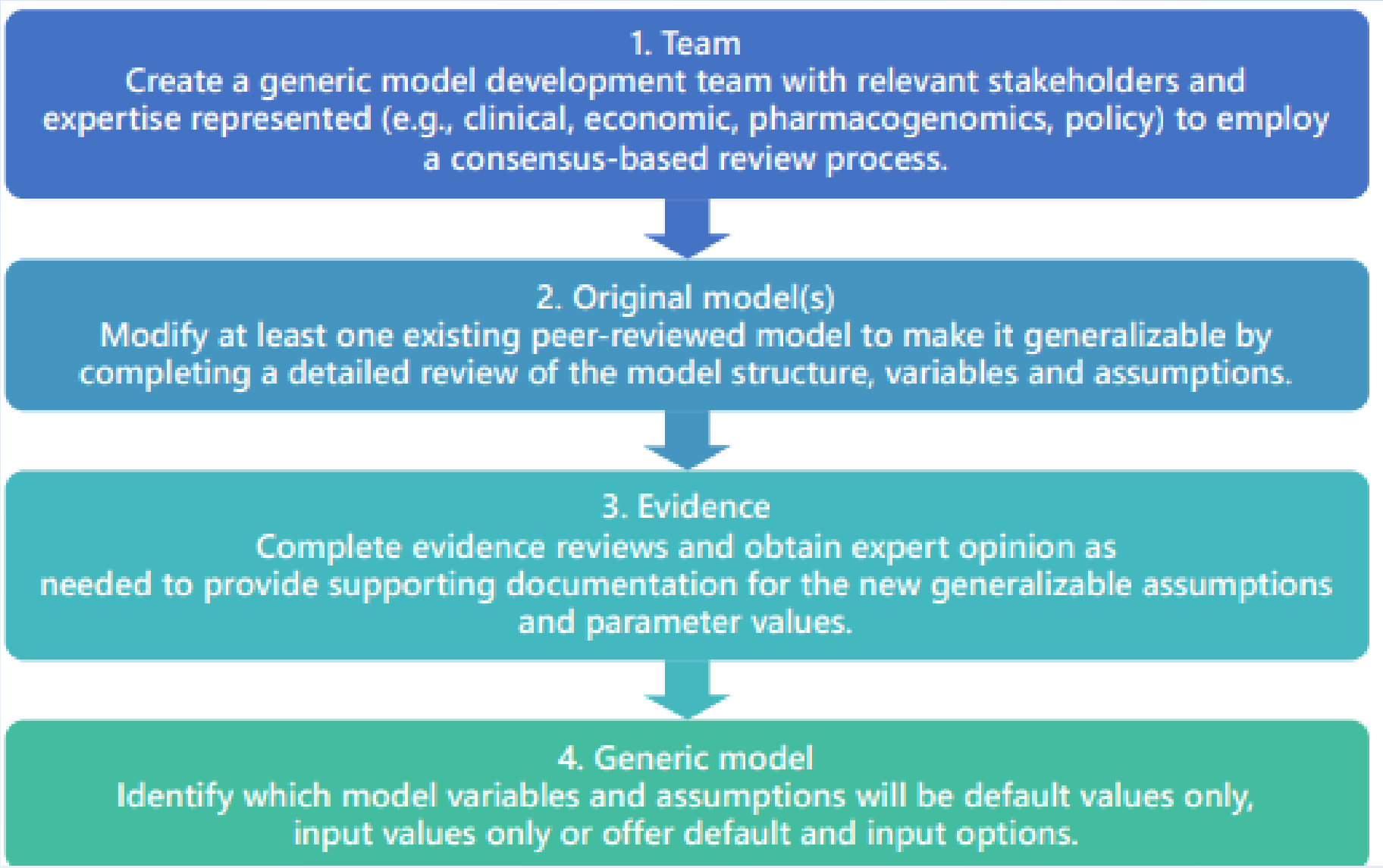
Economic evaluation of HLA-B*15:02 screening for carbamazepine-induced severe adverse drug reactions in Thailand

Figure 1. Decision tree model showing 3 strategies for epilepsy treatment





Generic Economic Evaluation Decision Analysis Model and Tool Development Process



Generic Model Inputs

Variables and assumptions retained requiring an input value assigned to three categories

1) ***Input value only***

User-specified value (e.g., all medical cost variables, population allele prevalence for pharmacogenomics test) (Table1)

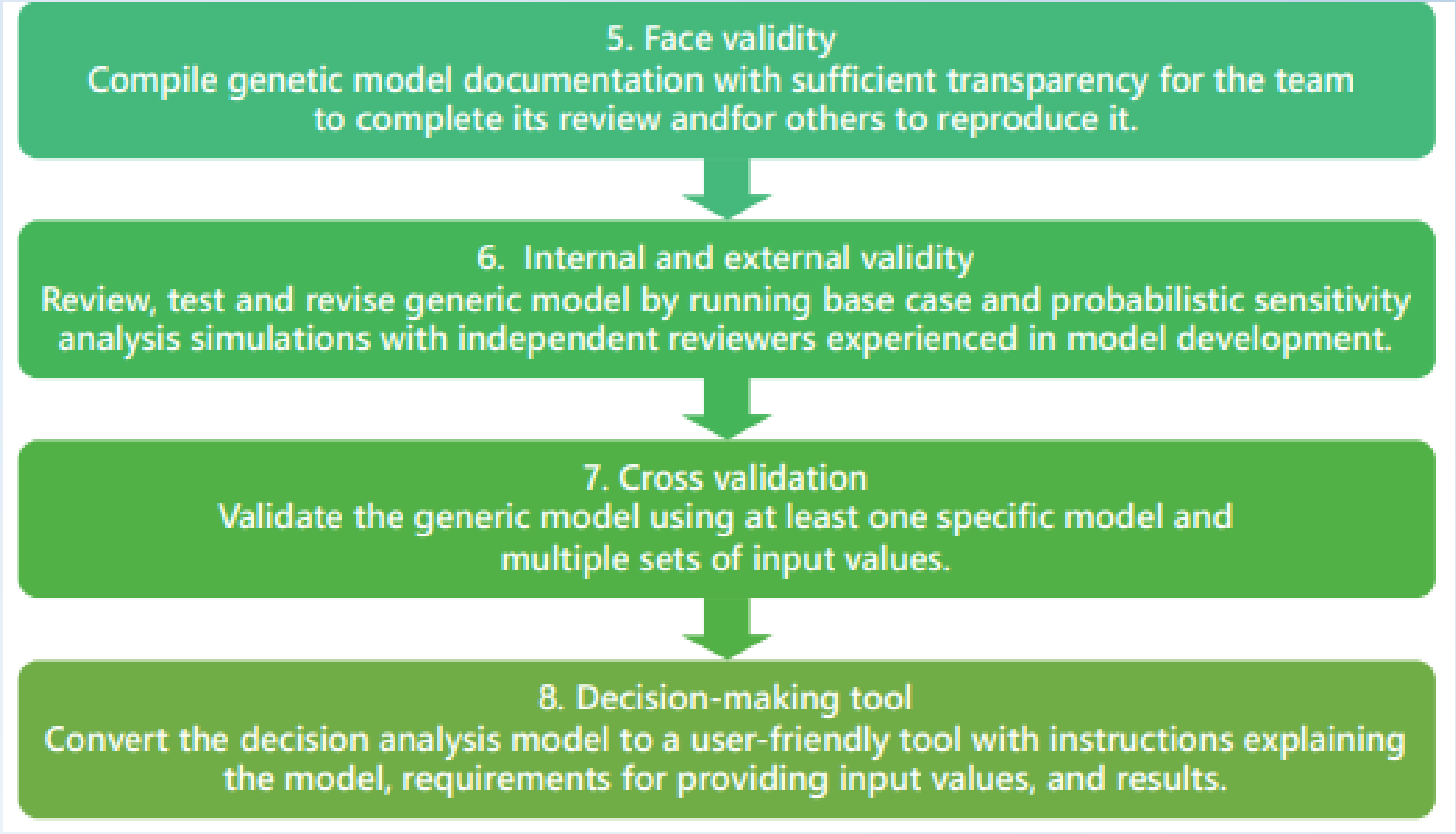
2) ***Default value only***

- Supported by very strong evidence (e.g., test sensitivity and specificity)
- Likely unavailable due to very limited evidence (e.g., health state utility of a very rare disease), or otherwise required by the model to meet certain logic requirements (e.g., health state utility value is constrained by its relationship to other state values).

3) ***Default value with an input option***

Allowed user to select either approach to address the need for information for an input value which is not readily available by providing a default based on available evidence

Generic Economic Evaluation Decision Analysis Model and Tool Development Process



Generic Model Cross-Validation: Country-Specific Input Values & Models

	Thailand Model			Generic Model with Thailand Inputs		
Result (THB)	Baseline	Option 1	Option 2	Baseline	Option 1	Option 2
	Current practice	HLA-B*1502 screening	No HLA-B*1502 screening	Current practice	HLA-B*1502 screening	No HLA-B*1502 screening
Cost	17,915	26,006	61,104	16425	24,752	61,212
QALYs	25.18	25.21	25.22	13.81	13.83	13.83
Incremental cost	-	8,091	43,190	-	8,327	44,787
Incremental QALYs	-	0.032	0.038	-	0.017	0.017
ICER	-	250,896	1,140,944	-	493,483	2,651,431
Threshold ICER	160, 000					

	Singapore Model			Generic Model with Singapore Inputs		
Result (US Dollars)	Baseline	Option 1	Option 2	Baseline	Option 1	Option 2
	Current practice	HLA-B*1502 screening	No HLA-B*1502 screening	Current practice	HLA-B*1502 screening	No HLA-B*1502 screening
Cost	4,110	4,680	6,780	1,203	1,668	3,016
QALYs	18.846	18.865	18.865	17.88	17.92	17.92
Incremental cost	-	570	2,100	-	465	1,813
Incremental QALYs	-	0.019	-	-	0.048	0.048
ICER	-	29,750	-	-	9,717	37,834
Threshold ICER	50,000					

Generic Model & Decision Tool: Input Table

- Overview
- Model Diagrams
- Input Tables
- Results
- ICER
- CE Plane
- CEAC

Required Input Variables		Input Value
Prevalence		
Prevalence of HLA-B*1502 allele (carrier status) in study population, please note that this is not allele frequency, it is twice the allele frequency	Mean	0.1487
	Min	0.11
	Max	0.1874
Cost		
Selected Currency		US dollars
Base year		2010
Cost of HLA-B*1502 screening test (includes all costs related to screening test)		270
Cost of SJS/TEN treatment (1 year): Annual direct medical cost of CBZ-induced SJS/TEN		10,250
Cost of follow up with SJS/TEN sequelae: Annual direct medical cost of sequelae (base-case value assume ~ dry eye syndrome)	Min	42.5
	Max	170
Cost of disease treatment		
Annual direct medical cost of epilepsy treatment with CBZ		170
Annual direct medical cost of epilepsy treatment with VPA		470
Ceiling ratio and threshold value		
Maximum acceptable ceiling value for use in the maximum acceptable ceiling ratio (in selected currency/QALY gained)		200,000
Cost-effectiveness threshold value (in selected currency/QALY gained)		50,000

Optional Input Variables		Input value
Probabilities		
Probability of CBZ-induced SJS/TEN in HLA-B*1502 +ve patient		0.0596
Utility		
Utility score of patient with epilepsy	Mode	0.907
	Min	0.7
	Max	0.999
Utility score of patient with SJS/TEN sequelae	Mode	0.68
	Min	0.57
	Max	0.79
Treatment Duration		
Treatment duration of epilepsy		7
Discount rate		
Discount rate for costs		0.03
Discount rate for outcomes		0.03

Generic Model Decisionmaking Tool: Cost-Effectiveness Results

Deterministic/Base-Case (US Dollar)	Baseline	Option 1	Option 2
	Current practice	HLA-B*1502 screening	No HLA-B*1502 screening
Cost	1,203	1,668	3,016
QALYs gained	17.88	17.92	17.92
Incremental cost		465	1,813
Incremental QALYs		0.048	0.048
ICER		9,717	37,834
Threshold ICER	50,000		
	Number Needed to Screen and Cases Prevented		
Cases prevented by screening 1 epilepsy patient	0.0089		
Number needed to screen to prevent 1 SJS/TEN	113		

Figure 2. Cost-effectiveness Acceptability Curve of Singapore Model

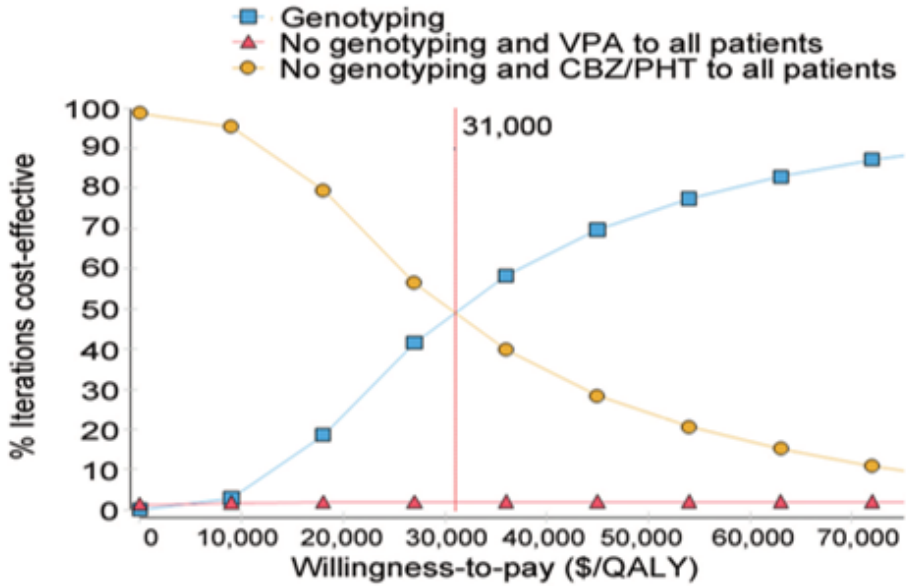
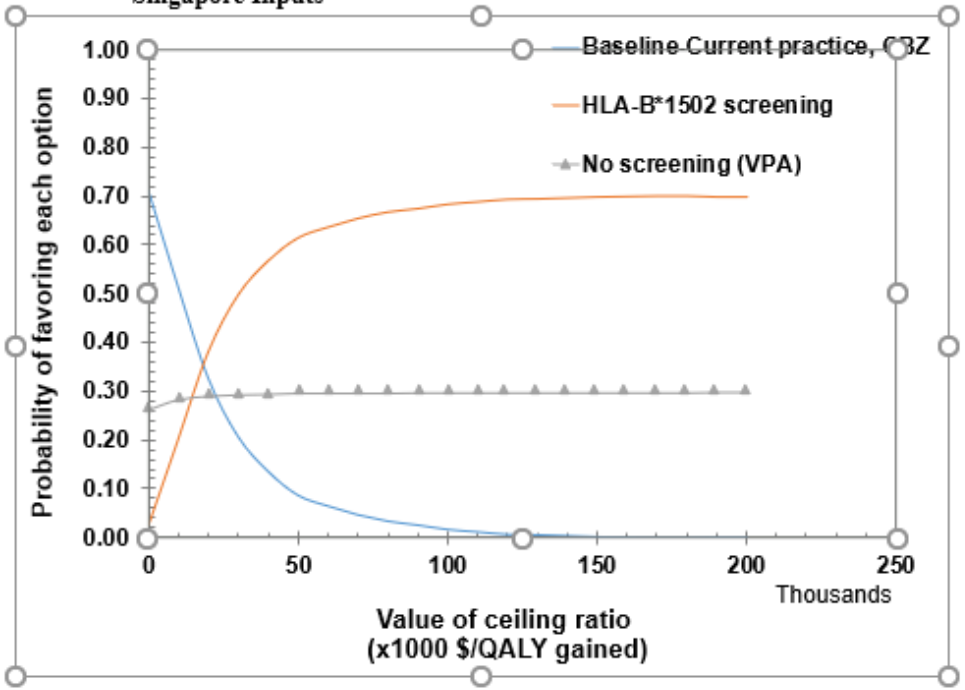


Figure 3. Cost-effectiveness Acceptability Curve of Generic Model with Singapore Inputs



Generic Model Applications

Pharmacogenomics J. 2021 Aug;21(4):476-483. doi: 10.1038/s41397-021-00225-9. Epub 2021 Apr 6.

Cost-effectiveness analysis of genotyping for HLA-B*15:02 in Indonesian patients with epilepsy using a generic model

Rika Yuliwulandari [1 2], Jae Gook Shin [3 4], Erna Kristin [5], Fransiscus D Suyatna [6], Iwan Dwi Prahasto [5], Kinasih Prayuni [7], Surakameth Mahasirimongkol [8], Larisa H Cavallari [9], Christina Mitropoulou [10], George P Patrinos [11 12], Jing Hao [13], Marc S Williams [14], Susan R Snyder [15]

GENERAL DERMATOLOGY

BJD
British Journal of Dermatology

Is universal *HLA-B*15:02* screening a cost-effective option in an ethnically diverse population? A case study of Malaysia

H.Y. Chong,[1] Z. Mohamed,[2] L.L. Tan,[3] D.B.C. Wu,[1] F.H. Shabaruddin,[4] M. Dahlui,[5] Y.D. Apalasamy,[2] S.R. Snyder,[6] M.S. Williams,[7] J. Hao,[6] L.H. Cavallari[8] and N. Chaiyakunapruk[1,9,10,11]

Thank you

Susan R. Snyder

ssnyder2@gsu.edu

Case Example
UCAN CAN-DU: Precision Health in Childhood Arthritis

Presented by: Deborah A Marshall, PhD

Professor and Arthur J.E. Child Chair Rheumatology Outcomes Research
Cumming School of Medicine, University of Calgary

ISPOR Conference, Washington, May 2022

SHARE Initiative for Collaborative Research

Recommendation

Recommendations for collaborative paediatric research including biobanking in Europe: a Single Hub and Access point for paediatric Rheumatology in Europe (SHARE) initiative

Total of 21 recommendations:

- general principles (1–3)
- ethics (4–7)
- paediatric principles (8-9)
- consent to paediatric research (10–14)
- paediatric databank and biobank (15-16)
- sharing of data and samples (17–19)
- commercialisation and third parties (20-21)

Kuemmerle-Deschner JB, Hansmann S, Wulffraat NM, Vastert SJ, Hens K, Anton J, Avcin T, Martini A, Kone-Paut I, Uziel Y, Ravelli A, Wouters C, Shaw D, Ozen S, Eikelberg A, Prakken BJ, Ruperto N, Horneff G, Constantin T, Beresford MW, Sikken M, Foster HE, Haug I, Schuller S, Jagle C, Benseler SM. Recommendations for collaborative paediatric research including biobanking in Europe: a Single Hub and Access point for paediatric Rheumatology in Europe (SHARE) initiative. Ann Rheum Dis. 2018;77(3):319-27

WEF White paper

White Paper

Global Data Access for Solving Rare Disease

A Health Economics Value Framework

- Highlights that access to global data critical

Framework identifying the **benefits of data sharing** in federated data system, potential for return on investment across four major areas:

- **Diagnostic benefit**: The identification of pathogenic or likely pathogenic variants in known disease genes
- **Clinical benefit**: Changes in the medical or surgical management of patients as a result of the diagnosis being made
- **Clinical trial benefit**: Changes related to the improvement of clinical trial operations
- **Personal benefit**: The presence of non-clinical outcomes that are important from a personal point of view to patients.

- Belsey J, Chaihorsky L, Chediak L, Currie GR, Goranitis I, Marshall DA. Global Data Access for Solving Rare Disease: A Health Economics Value Framework. World Economic Forum, February, 2020. (http://www3.weforum.org/docs/WEF_Global_Data_Access_for_Solving_Rare_Disease_Report_2020.pdf)

Need for Open Source Health Economics Modeling in Precision Medicine

….key next step is to integrate information on both clinical utility and implementation to assess the overall impact…

Global Economics and Evaluation of Clinical Genomics Sequencing Working Group (GEECS) - health economists and policy researchers on genomics into clinical care

https://pharm.ucsf.edu/transpers/grants-programs/pghe-working-group

VIEWPOINT

Expanding Use of Clinical Genome Sequencing and the Need for More Data on Implementation

Kathryn A. Phillips, PhD
Center for Translational and Policy Research on Personalized Medicine (TRANSPERS), Department of Clinical Pharmacy, University of California, San Francisco; and Philip R. Lee Institute for Health Policy Studies, University of California, San Francisco.

Michael P. Douglas, MS
Center for Translational and Policy Research on Personalized Medicine (TRANSPERS), Department of Clinical Pharmacy, University of California, San Francisco.

Deborah A. Marshall, PhD
Cumming School of Medicine, Department of Community Health Sciences, University of Calgary, Calgary, Alberta, Canada; and O'Brien Institute for Public Health, University of Calgary, Calgary, Alberta, Canada.

Author Audio Interview

Supplemental content

Corresponding Author: Kathryn A. Phillips, PhD, Center for Translational and Policy Research on Personalized Medicine (TRANSPERS), Department of Clinical Pharmacy, University of California, San Francisco, 490 Illinois St, Third Floor, PO Box 0613, San Francisco, CA 94143-2510 (kathryn.phillips@ucsf.edu).

During the past 5 years, next-generation sequencing (NGS) has transitioned from research to clinical use.[1] At least 14 countries have created initiatives to sequence large populations (eg, All of Us, Genomics England), and it is projected that more than 60 million people worldwide will have their genome sequenced by 2025.[1] However, there has not been an assessment of global NGS implementation (defined here as the use of testing in routine clinical care as measured by clinical applications, utilization, and coverage/funding/reimbursement). Implementation is a key pillar in the translational continuum of discovery, utility, implementation, and population health impact.[2] Understanding how NGS is being used and paid for is critical for determining its clinical and economic benefits and addressing current and future challenges to appropriate implementation.

What Is NGS and How Is It Used in Clinical Care?

NGS is a broad term that encompasses several modern sequencing technologies that measure variations in genes that are present at birth or emerge later in life (eg, cancers or viruses). Many NGS tests are available for clinical care and are being used for clinical applications, including risk assessment, diagnosis, prognosis, and therapy selection. The eTable in the Supplement provides examples of tests currently in use in countries that have widespread NGS implementation, as well as several emerging and future tests. Emerging tests (eg, liquid biopsy tests for cancer screening) could influence clinical outcomes and health care budgets. Thus, the identification of emerging and future tests can guide the collection of data needed by clinicians and policy makers to inform appropriate implementation.

This Viewpoint examines use, payment/coverage, and gaps in data availability on implementation of NGS worldwide using 3 common tests[3] as examples of NGS: (1) noninvasive prenatal testing (NIPT), (2) whole-exome sequencing (WES)/whole-genome sequencing (WGS) for suspected genetic disorders, and (3) tumor sequencing (TS).

Use of NGS Around the World

NIPT is widely used and is currently available in at least 90 countries. In the commercially insured population in the US, almost a half-million NIPT tests were reimbursed in 2019, along with 5600 WES tests and 70 300 TS tests.[4] There is increasing, but variable, use of NIPT, WES/WGS, and TS in Canada, Europe, the Middle East, and Asia, and to a more limited extent in Central/South America and Africa. Even some middle-income countries are implementing NGS in clinical care.

Payment and Coverage

Whether tests are covered or funded varies by the type of health care system (private or public). The UK is recognized as a leader in nationally funded coverage for NGS testing, although several other European and Asian countries also have national coverage for some NGS tests.

The US provides an example of how coverage varies depending on the clinical scenario and payer type.[5] Almost all (97%) insured individuals have NIPT coverage, although about half (48%) of this coverage is for women in high-risk categories (eg, advanced maternal age, family history of abnormal pregnancy) only. Most Medicaid enrollees (90%) also have NIPT coverage, but a greater percentage (62%) of this coverage is for women in high-risk categories only. More than half of insured individuals (63%) have WES and/or WGS coverage, although the percentage of Medicaid enrollees with coverage is lower (39%). Most insured individuals (80%) have coverage for TS, although this declines to 56% of Medicaid enrollees having coverage. In contrast, all Medicare enrollees have select TS coverage based on a 2018 National Coverage Determination.

NIPT and small TS panels (<50 genes) have the lowest reimbursement rates (up to approximately $1000), whereas WES/WGS and comprehensive TS have the highest (up to approximately $5000). Patients in the US who self-pay can obtain NIPT for $99 and exome sequencing (trio) for $2500.[5] Despite the high costs of some NGS tests, expenditures for NGS in the US represent a small percentage of health care expenditures (approximately 0.13% of Medicare expenditures).[6]

Gaps in Data Availability on Implementation

There is no central source of information on implementation across countries and clinical applications. Much of the available data are from the US only; in many other countries, little or no data are publicly available. A consistent gap is data on usage, with sparse data available on how many tests are performed even in countries with high implementation, such as the US. Peer-reviewed publications only provide data on select tests and specific health care systems and are based on historical vs current data. As a result of these gaps, data on implementation must be compiled across diverse sources. For example, some data can be found in the gray literature (eg, white papers, health system reports, market analyses, regulatory filings, company websites, news reports, national/international consortia websites) and some data can be obtained from administrative/clinical resources (eg, electronic health records, claims data, fee schedules, industry databases, registries). Much of the needed data are proprietary, costly to obtain, or both, such as lab data and market

- Phillips KA, Douglas MP, Marshall DA. Expanding Use of Clinical Genome Sequencing and the Need for More Data on Implementation. JAMA 2020;324(20):2029-2030. doi:10.1001/jama.2020.19933

UCAN CAN-DU and beyond: Towards a global genomics partnership for childhood arthritis (JIA)

Overall Aim: To create a transformative roadmap for global, secure sharing of genomic, phenotypic and health economic data across borders that considers genomic, clinical and economic data mandates and is guided by diverse legal, ethical and regulatory requirements across borders.

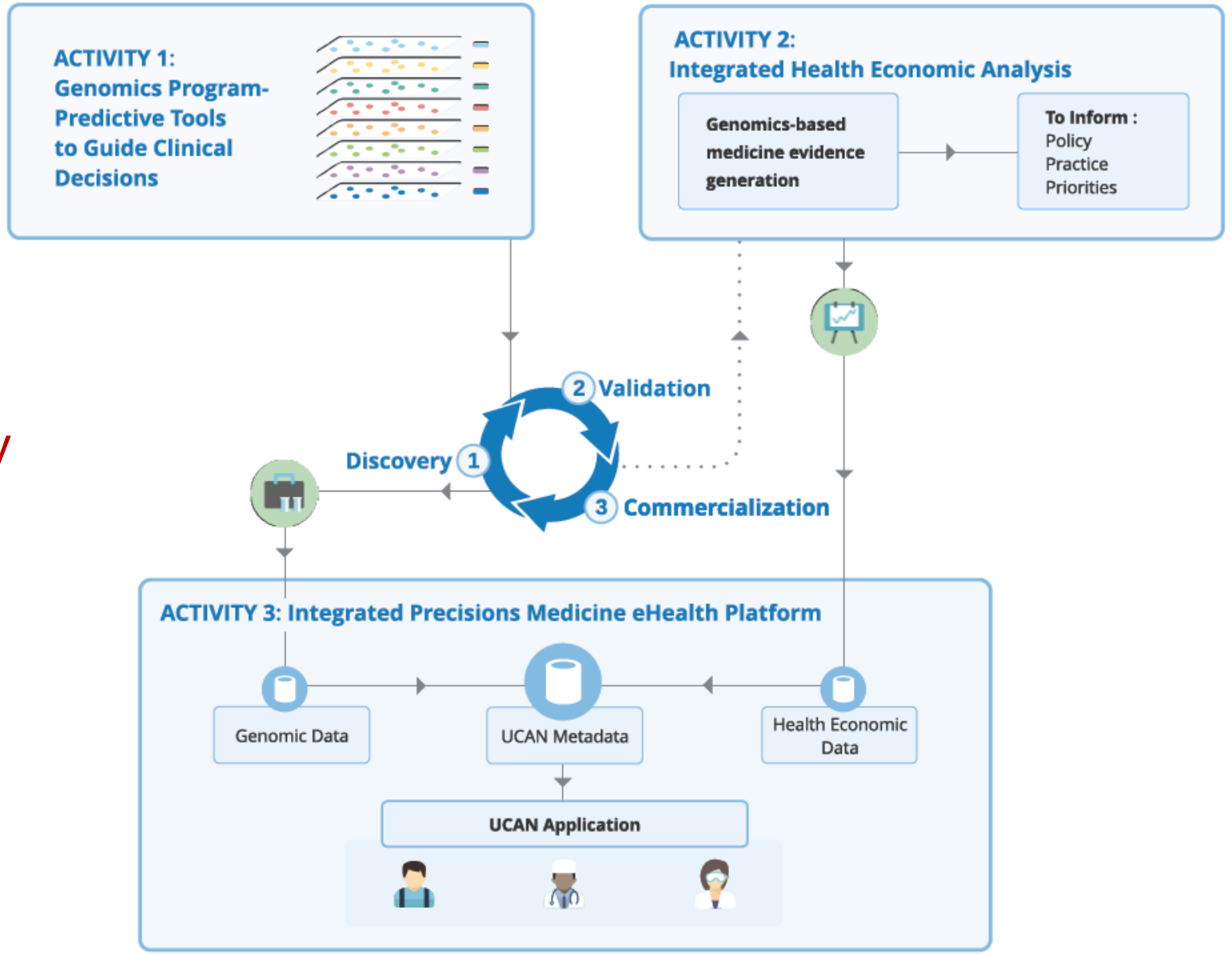
Aim 1. To develop a deep understanding of the current provincial, national and international childhood arthritis datasets, related data sources such as administrative datasets and their specific ethical, legal and technical frameworks.

Aim 2. To establish a UCAN stakeholder team enriched by ethics and legal experts to define the organizational principles of a federated, transparently interconnected database system.

Aim 3. To take steps towards transforming the Dutch-Canadian UCAN data framework into aglobal federated database systems that integrate the Global Alliance for Genomics in Health data access and sharing standards and FAIR principles.

Project Overview – Integrated Thematic Activities

Evidence-based tools to Guide Therapy



Integrated Health Economics

(GE³LS) Genomics Ethical, Environmental, Economic Legal and Social Aspects

Standardized Measurement Framework; Key Performance Indicators

Predictive Tools (Activity 1)

Patient Preferences (Risk vs Benefit)

Simulation Models of Clinical and Health Policy Decisions

Individualized Treatment Pathways

Cost Effectiveness (Value for Money)

Affordability

Dynamic model of risks, benefits and costs associated with genomics-based care for JIA

Complexity of Treatment Patterns in Childhood Arthritis

- Assessment of treatment sequences for different drug classes in current routine practice
- 112 unique treatment sequences in cohort of 325 patients over 5 years

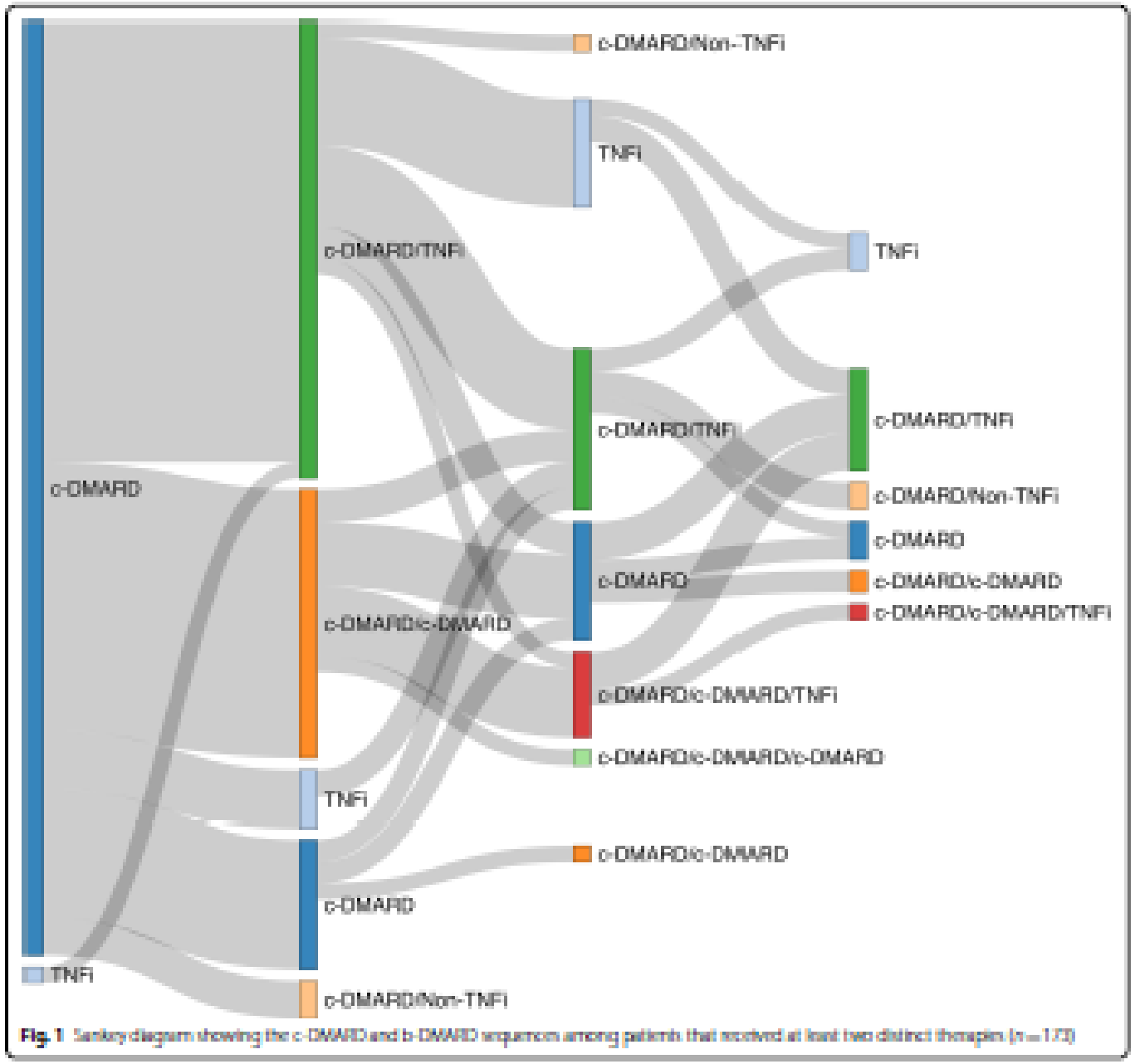
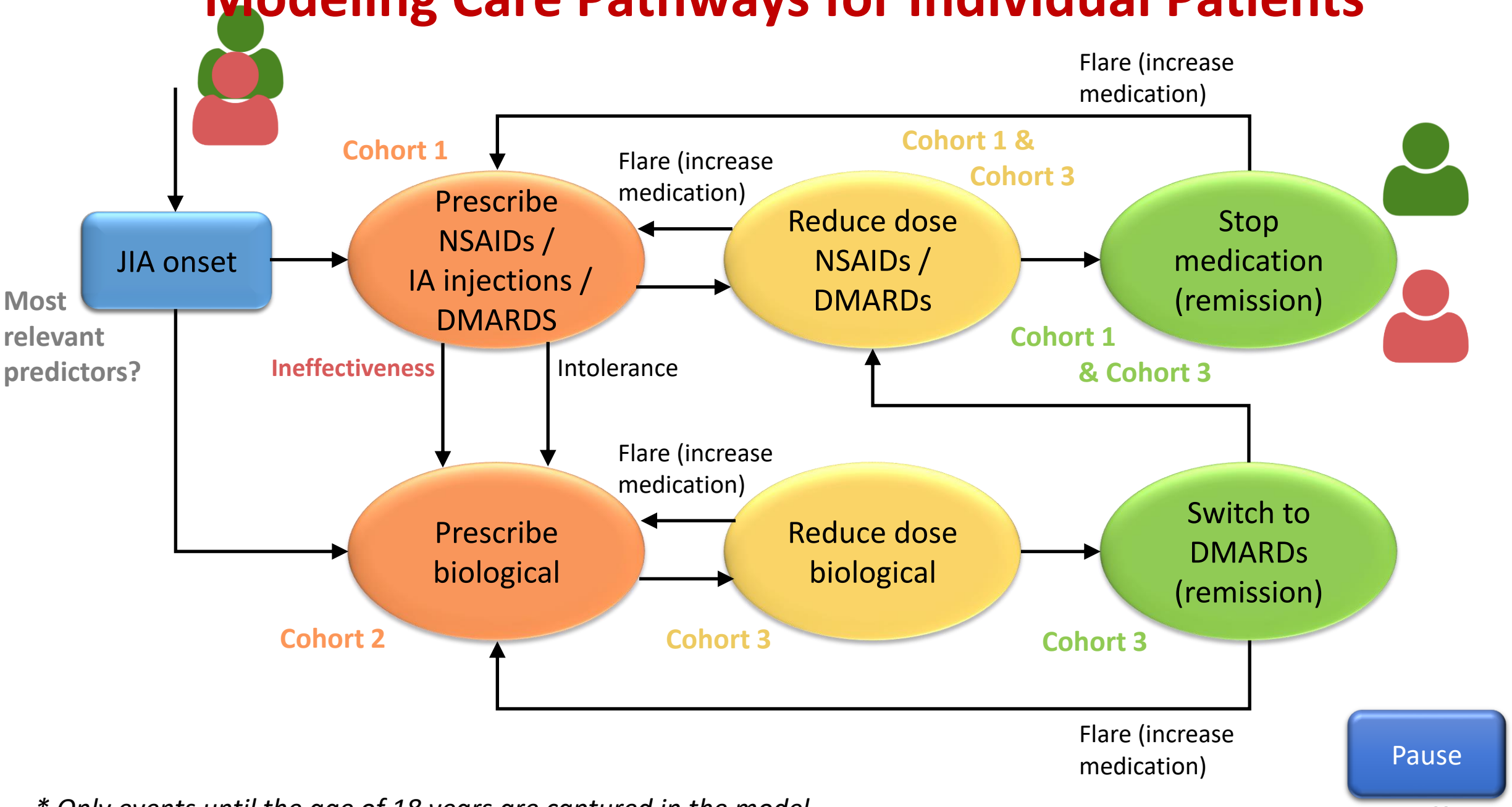


Fig. 1 Sankey diagram showing the c-DMARD and b-DMARD sequences among patients that received at least two distinct therapies (n = 173)

- Grazziotin, L.R., Currie, G., Twilt, M. et al. Real-world data reveals the complexity of disease modifying anti-rheumatic drug treatment patterns in juvenile idiopathic arthritis: an observational study. Pediatr Rheumatol 2022; 20, 25.

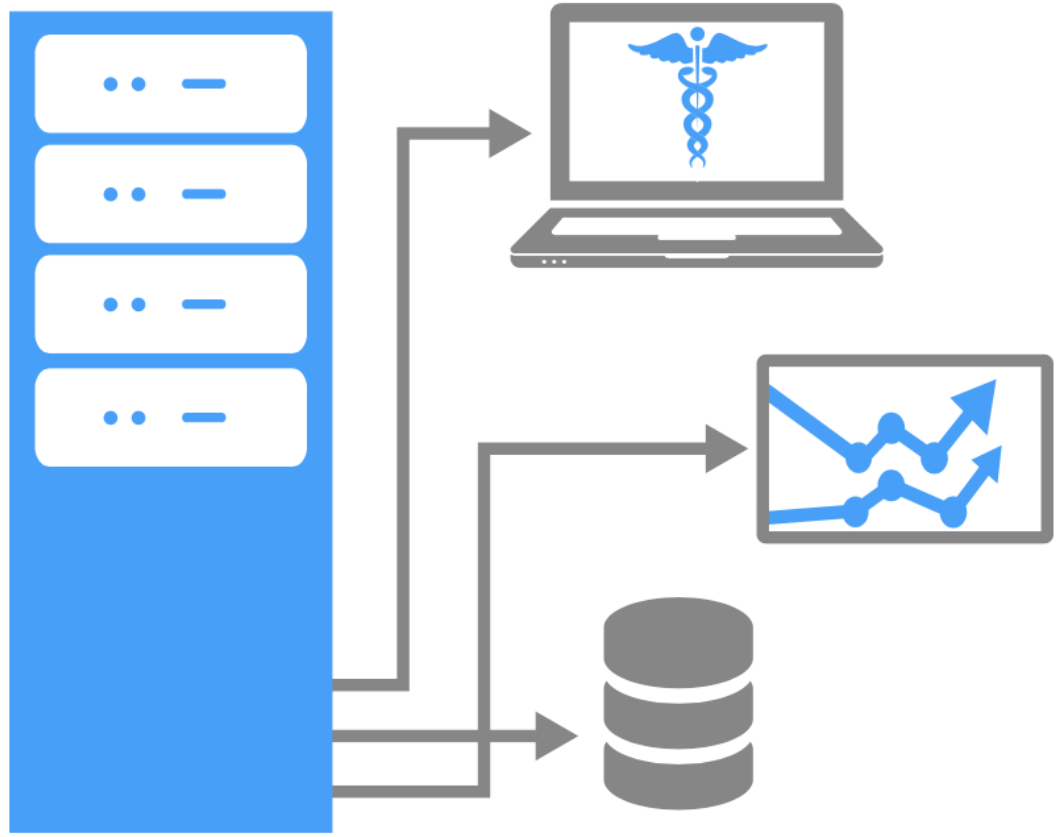
Modeling Care Pathways for Individual Patients



** Only events until the age of 18 years are captured in the model*

High Performance Computing for Health

- Compute cloud framework as node in the Compute Canada supercomputing infrastructure
- Capable of processing large genomics or other types of data sets (”Big Data”)
- Enterprise level governance, management and technical support
- Best practices to maintain patient data confidentiality
- Houses all UCAN CANDU research participant data, eHealth application webservers and webapps for demographic, clinical, patient reported outcomes measures, bioassay data and genomic data



HPC4Health
www.hpc4health.com

- UCAN data management compliant with GDPR effected by Data and Material Transfer Agreements and a Data Processing
- Data is harmonized and stored using codified standardized vocabularies and allows integration with various third-party systems
- Data protection officer (DPO) ensures adherence to FAIR principles.
- FAIR: Findable, Accessible, Interoperable, Reusable (syntaxes, codes, protocols made available to researchers)

- Data management following GDRP and FAIR principles enables sharing of data in real-time and integration of real-time data in analytic models throughout the study course.

Why Open-Source in Precision Medicine ?

- Efficiency required particularly in rare disease research where sample sizes are small
- In precision health, complexity and heterogeneity of clinical pathways and treatment trajectories with clinical, biologic, genomic, preference, and health care resource use data
- To reap the benefits of considerable infrastructure requirements and data collection efforts to enable open-source modeling !

Thank you!
Discussion

damarsha@ucalgary.ca

Tel 403 210 6377

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A Healthcare Consultancy Group Company

Will the Next Generation of Models Make Open-Source Modeling Take Off?

Koen Degeling, PhD
Research Scientist
Health Economic Modeling & Advanced Analytics

Presented at ISPOR 2022 in Washington, DC

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The Next Generation of Models Will Continue to Become Increasingly More “Advanced”

Precision Medicine

Patient-level modeling techniques are required to appropriately represent the complex dynamics of today’s and tomorrow’s clinical pathways

Changing Evidence

Data analysis and evidence synthesis methods are becoming increasingly sophisticated, and models need to match the evidence

Life Cycle Approach

Shift from static one-off modeling efforts to dynamic evidence synthesis frameworks that evolve throughout the product life cycle

Next Generation of Modelers

Increased training and comfort with code-based software empower today’s graduates to be comfortable applying more advanced methods

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The Next Generation of Models Provide Both the Need and the Opportunity for Open-Source Modeling

There is an increased

NEED

- We are still further developing the methodologies
- We are still learning how to use available methodologies
- There is an increased need for transparency

There are ever more

OPPORTUNITIES

- Modular approach to modeling for efficiency and credibility
- Code-based models are better suited for sharing
- Thought leadership integrated in organizations' profiling

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Putting Words Into Action

PharmacoEconomics
https://doi.org/10.1007/s40273-020-00951-1

ORIGINAL RESEARCH ARTICLE

Simulating Progression-Free and Overall Survival for First-Line Doublet Chemotherapy With or Without Bevacizumab in Metastatic Colorectal Cancer Patients Based on Real-World Registry Data

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Collaborators:

THE UNIVERSITY OF MELBOURNE

UNIVERSITY OF TWENTE.

Walter+Eliza Hall Institute of Medical Research
DISCOVERIES FOR HUMANITY

BIOGRID AUSTRALIA
Health through information

VICTORIAN COMPREHENSIVE CANCER CENTRE

Funding:

ZonMw

Manuscript & Supplements

R code & Shiny app

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Putting Words Into Action: *Simulating PFS and OS Based on Real-World Data*

Objective
Simulate conditional outcomes for specific patient profiles based on registry data

Challenges

- Missing data on covariates
- Variable selection for parametric survival models
- Missing data <> variable selection
- Validation of multivariable parametric survival models
- Validation of overall (multivariable) simulation model

Solutions

- Discrete event simulation
- Multiple imputation
- *Forward and backward selection*
- *Pooled statistics for variable selection in each step*
- *Bootstrap approach to correct for optimism in internal validation*
- Kaplan-Meier curves and summary statistics for subgroups

Italics indicate codes for which no existing functions/codes were available

Outcomes

- Successful implementation of all steps in R
- Good model performance
- Results suggest treatment targeting could be improved
- Published in *PharmacoEconomics*

OS = overall survival; PFS = progression-free survival.

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Putting Words Into Action: *Simulating PFS and OS Based on Real-World Data (cont'd)*

Challenges of Going Open-Source

- Complexity of code and analyses: thorough explanation required and discussion of concerns about appropriate use
- Data could not be shared to support transparency

What We Were Able to Do

- Extensive supplementary materials to explain analyses
- Code available in a markdown with explanation ***and results***
- Shiny app for exploration of dummy data and model runs

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Will the Next Generation of Models Make Open-Source Modeling Take Off?

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~~Will t~~The Next Generation of Models ***Will*** Make Open-Source Modeling Take Off~~?~~!

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Lumen
Value & Access

ISPOR Open-Source Models Journal Club

June 1, 2022

11:00 AM – 12:00 PM ET

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Poll 2

“

Where could open source models be most valuable?

Results will be presented as a word cloud

(single-word answers only)

Poll 3

“

When will open source become the norm in precision medicine?

Multiple choice

- **This year**
- **Next 5 years**
- **Next 10 years**
- **Next 20 years**
- **Not in my lifetime**