



Drug Repurposing Roadmap that Optimizes Patient Impact through Collaboration

Nov 15, 2022



An Introduction

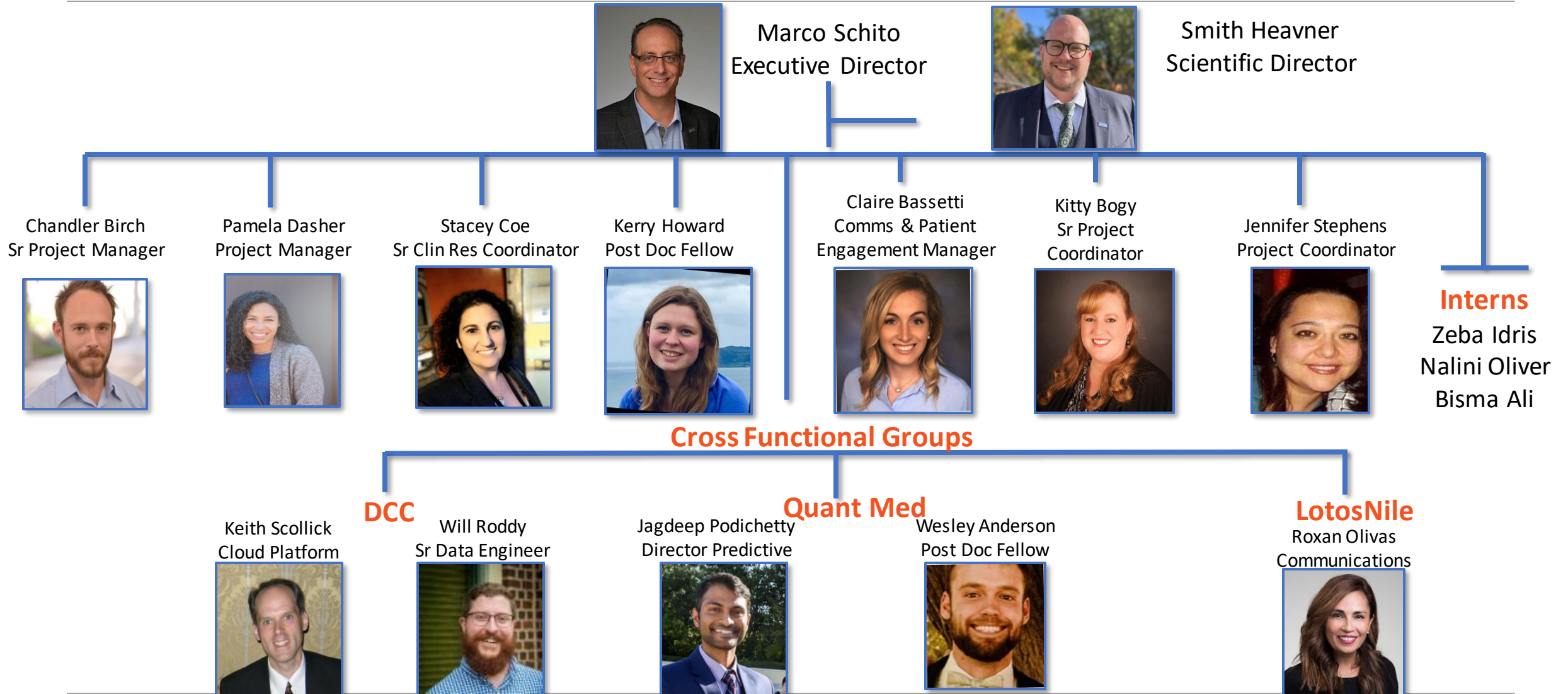
- “Smitty” Heavner
 - Pronouns: He/They
- Registered Nurse
 - 10 years, specialized in ED
- PhD in Evaluation Science
- Scientific Director
 - CURE Drug Repurposing Collaboratory
- Adjunct Faculty
 - Clemson University – Public Health Sciences
 - University of South Carolina School of Medicine Greenville



Scan for contact

- CDRC is a public-private partnership with FDA and NIH National Center for Advancing Translational Science
- Critical Path Institute is supported by the Food and Drug Administration (FDA) of the U.S. Department of Health and Human Services (HHS) and is 54.2% funded by the FDA/HHS, totaling \$13,239,950, and 45.8% funded by non-government source(s), totaling \$11,196,634.
- The views expressed are those of the presenter and do not necessarily represent the official views of, nor an endorsement by, FDA/HHS NIH or the U.S. Government.

- CDRC Overview
- Drug Repurposing
- Real-World Data
- The Edge Tool
 - Use Case: COVID-19
- Real-World Evidence
- Future Directions



CDRC Team Collaborators



David Fajgenbaum
CDRC Co-director

FDA OMP

FDA OCE

NIH NCATS

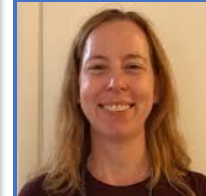
Leonard Sacks
(Team lead)



Heather Stone
(Policy Analyst)



Julie Schneider
(Team lead)



Ewy Mathe
(Informaticist)



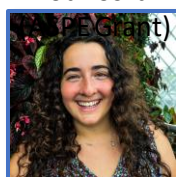
Milli Duggal
(Special Pop)



Shira Strongin
(Rare Dis)



Maya
Younoszai



Reema Charles
(Infectious Dis)



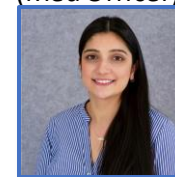
Tahsin Farid
(Clinical Fellow)



Leslie Doros
(Med Officer)



Sonia Singh
(Med Officer)



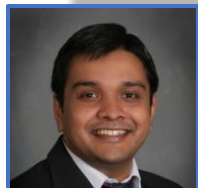
Tim Sheils
(App Developer)



Hyun Cho
(App Designer)



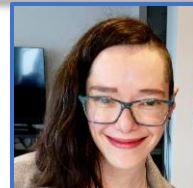
Consultants



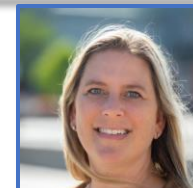
Raghav Tirupathi
(ID doc)



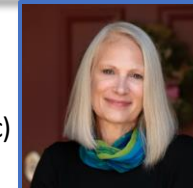
Nitin Gupta
(ID doc)



Ruth Kurtycz
(Statistician)

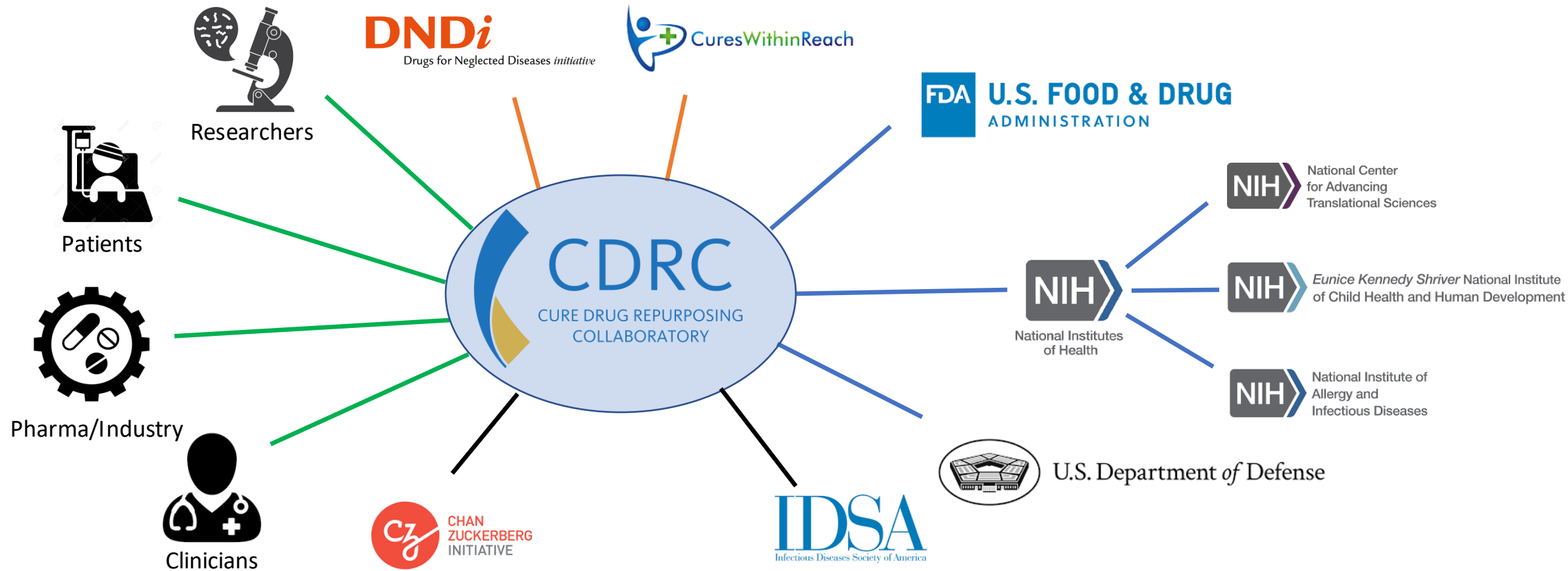


Lisa Schill
(Patient Advoc)



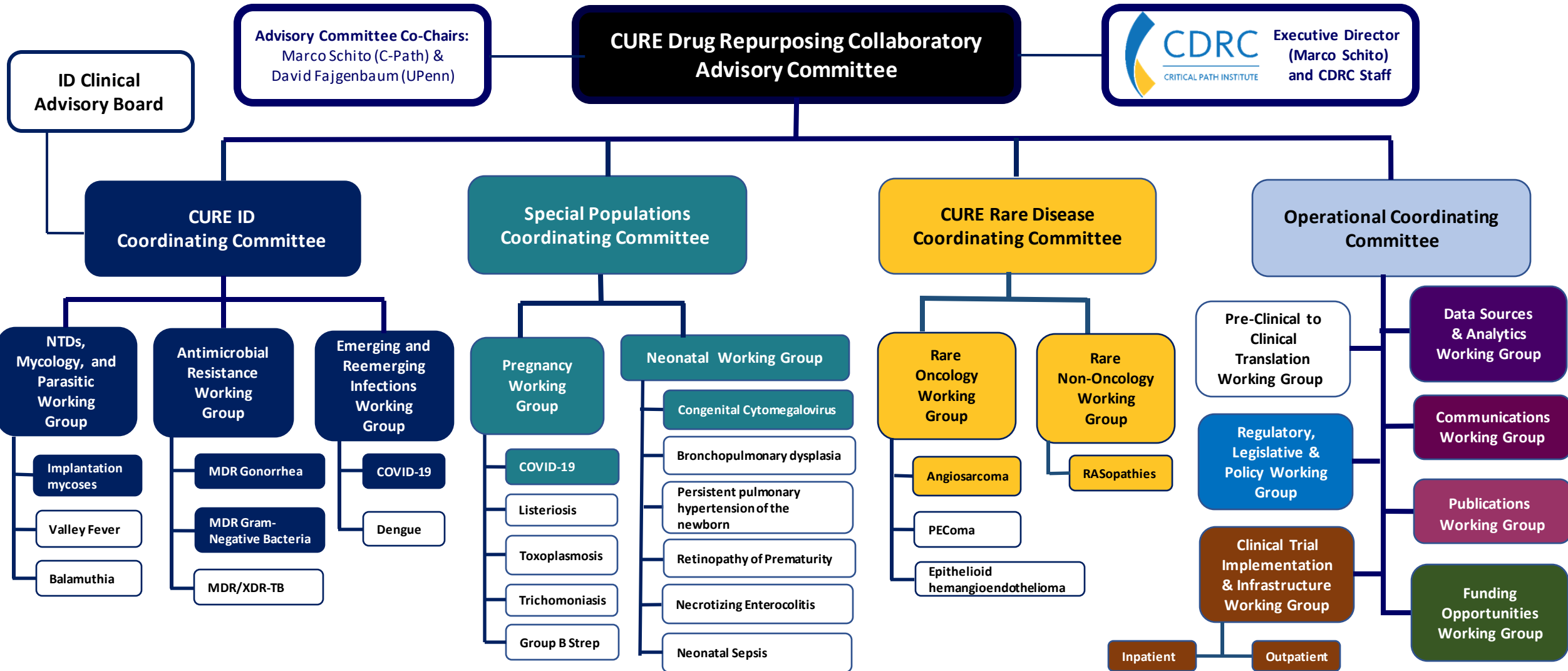
Denise Reinke
(Patient Advoc)

CDRC: Advisory committee members



Goal: Facilitate a drug's demonstrated utility in clinical practice, harnessing a combination of traditional trials and real-world evidence

CDRC Structure



- Significant portion of conditions have no FDA approved treatments
- Traditional drug development and labeling is slow and expensive.
- Repurposing may be needed in diseases which are:
 - rapidly emerging
 - extremely rare
 - impacting vulnerable groups
 - treated by standardized guidelines

Examples of Diseases where Drug Repurposing may be important

Antimicrobial-Resistant Organisms



- MDR Gram Negative bacteria
- DR Gonorrhea and Mycoplasma treatment failures
- Resistant fungal infections

Emerging Infectious Threats



- COVID-19
- Lassa Fever
- Nipah Virus
- Powassan Virus

Unusual Infections



- Balamuthia mandrillaris
- Acinetobacter baumannii
- Mycobacterium abscessus
- Fusarium

Infections in Challenging Sites

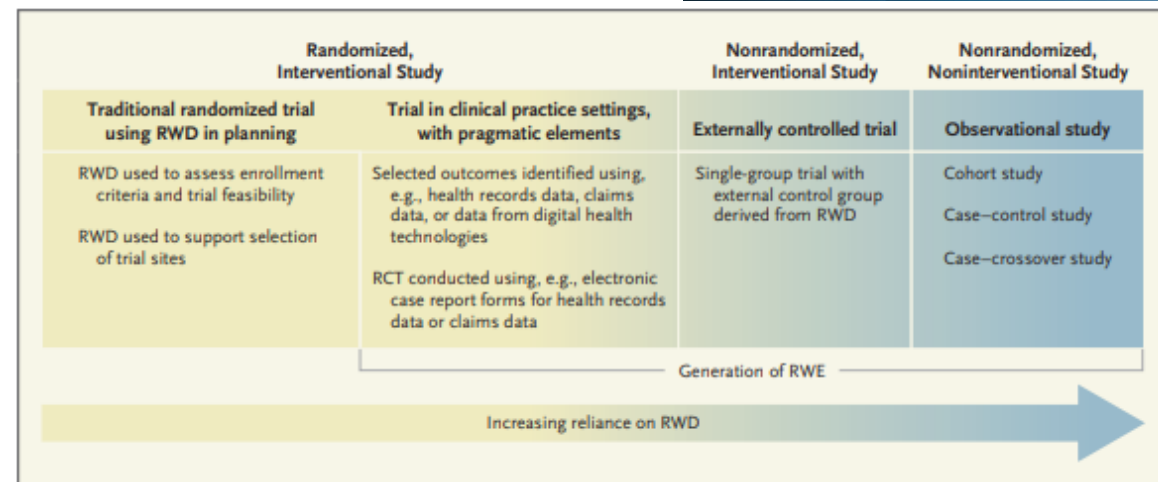
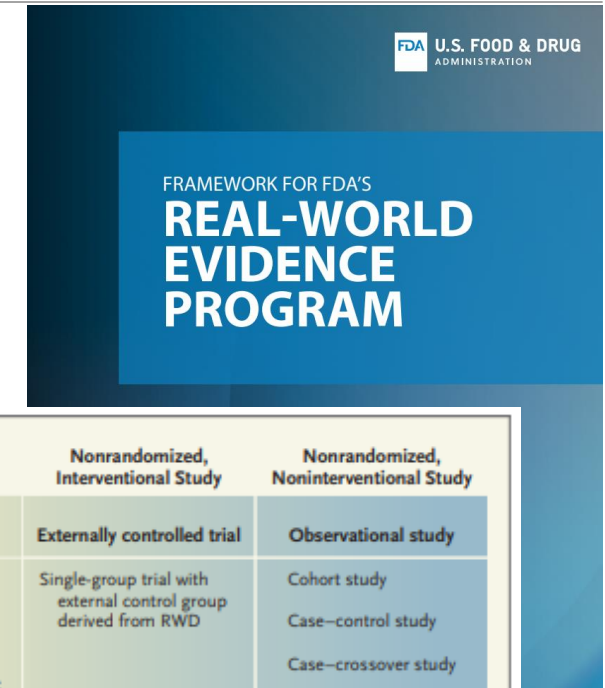


- Osteomyelitis
- Infective endocarditis
- Meningitis
- Endophthalmitis

The best use case for CURE ID is for diseases where clinical trials are not or cannot be conducted.

In some instances (e.g., start of outbreak), it may be helpful to capture data that could later be used to inform the design and conduct of RCTs.

- Explore clinical practice
- Develop and refine hypotheses
- Provide external controls
- Observational research



Reliance on RWD in Representative Types of Study Design.

RCT denotes randomized, controlled trial; RWD real-world data; and RWE real-world evidence.

Concato J, Corrigan-Curay J. Real-World Evidence — Where Are We Now? *N Engl J Med.* 2022;386(18):1680-1682. doi:10.1056/NEJMp2200089

CURE ID data sources

- Case reports from literature
- Clinician submitted infectious disease case reports
 1. What disease did your patient have?
 2. How did you make the diagnosis?
 3. **What made your patient's infection difficult to treat?**
 4. What drug(s) did you use to address this difficult to treat infection?
 5. What was the patient's outcome?
 6. Did the patient experience any adverse events?

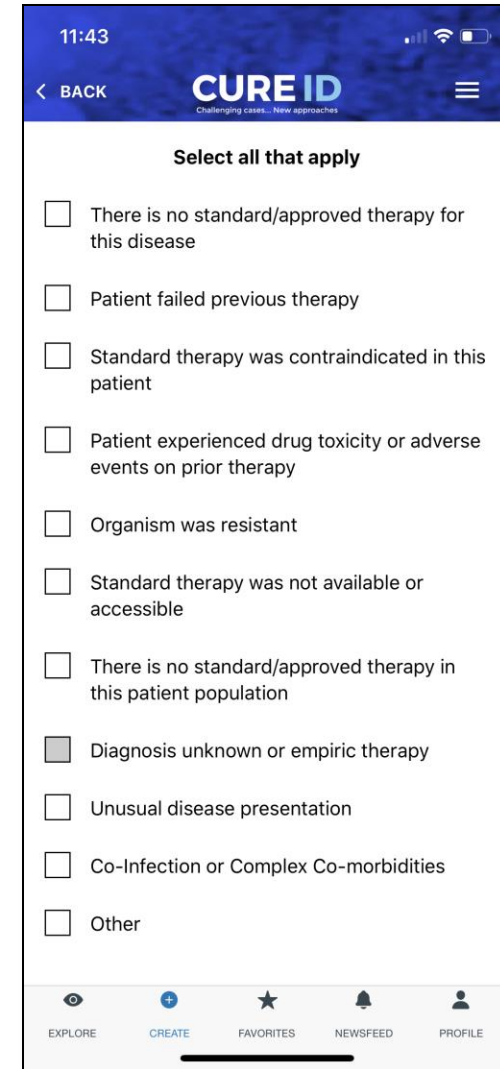
Download the CURE ID
App Today!




 <https://cure.ncats.io>

 @id_cure

 curesupport@nih.gov



11:43

< BACK CURE ID 

Challenging cases... New approaches

Select all that apply

- There is no standard/approved therapy for this disease
- Patient failed previous therapy
- Standard therapy was contraindicated in this patient
- Patient experienced drug toxicity or adverse events on prior therapy
- Organism was resistant
- Standard therapy was not available or accessible
- There is no standard/approved therapy in this patient population
- Diagnosis unknown or empiric therapy
- Unusual disease presentation
- Co-Infection or Complex Co-morbidities
- Other

EXPLORE CREATE FAVORITES NEWSFEED PROFILE

A Platform to Capture Novel Uses of Existing Drugs

- Web-based tool
 - Computer, smartphone or mobile device
- Capture and share real-world experiences treating patients through a simple online case report form
- HIPAA compliant, contains no PII
- Newsfeed
- Link to [www.clinicaltrials.gov](https://cure.ncats.io/explore)

CONTRIBUTE

Contribute your knowledge and expertise to this global health open-source community

Enter or update a case
Participate as a curator
Get involved in the initiative

EXPLORE

Explore experiences of clinicians globally and stay up to date on the latest ID news

Search by disease
View clinical trials
Look up published cases
Review user-submitted cases

DISCUSS

Discuss and share your most challenging clinical cases and treatment questions

Ask your questions and get replies
View discussion posts and comment
Consult with colleagues

<https://cure.ncats.io/explore>

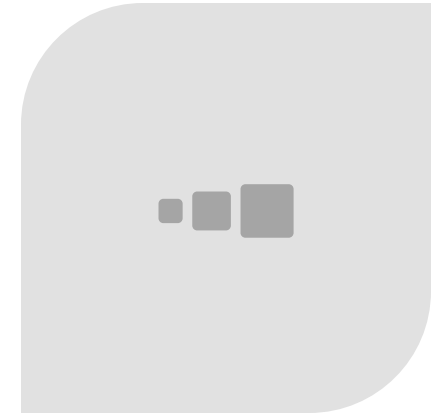
- Unstructured data
- Defining outcomes
- Privacy concerns
- Probabilistic linkage
- Data harmonization



EXTRACT



TRANSFORM



LOAD

ETL

- Centralized harmonization
- Sites use common data model at baseline
- Only for US data
- Limited to COVID-19

National COVID Cohort Collaborative (N3C)

The N3C is a partnership among the NCATS-supported [Clinical and Translational Science Awards \(CTSA\) Program](#) hubs, the [National Center for Data to Health \(CD2H\)](#), and NIGMS-supported [Institutional Development Award Networks for Clinical and Translational Research \(IDeA-CTR\)](#), with overall stewardship by NCATS. Collaborators will contribute and use COVID-19 clinical data to answer critical research questions to address the pandemic.



Scientists Use N3C Data to Identify Common Features of Long COVID

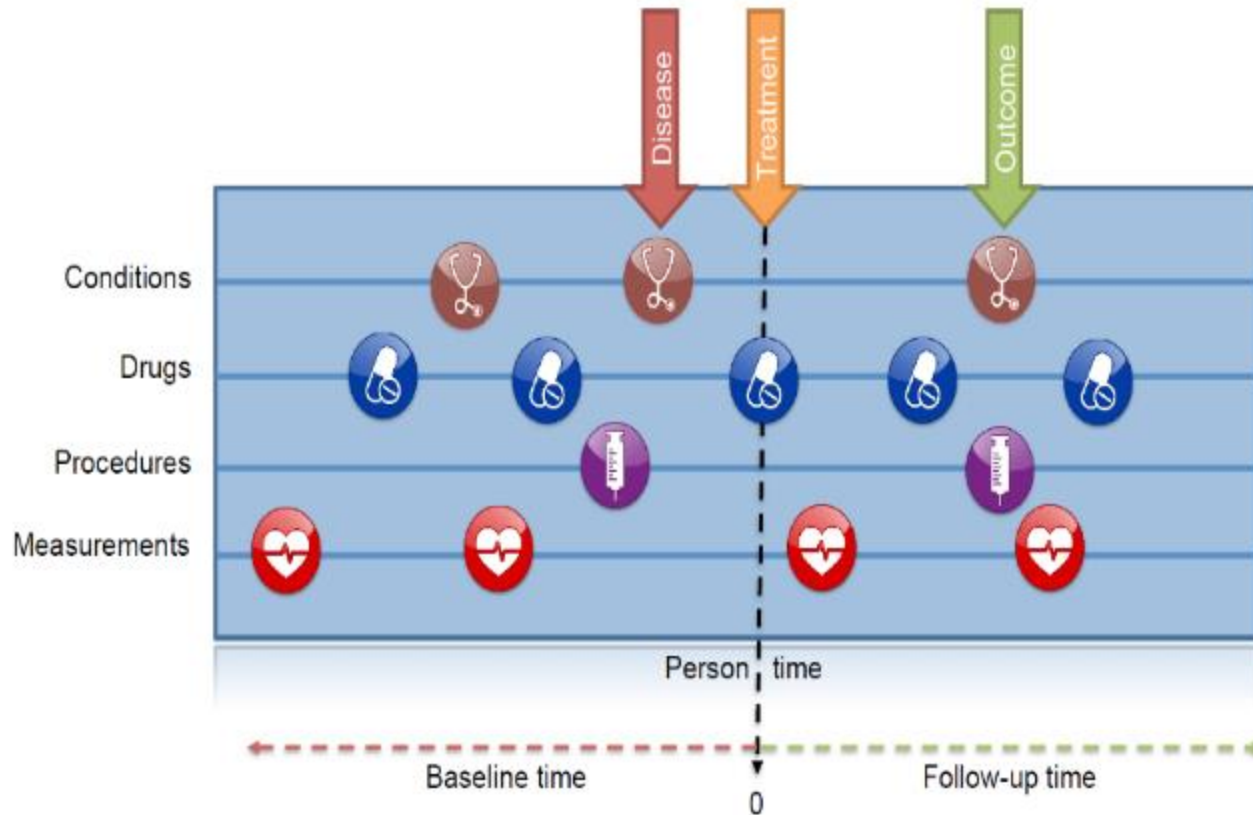
NIH-supported researchers used electronic health record data from the National COVID Cohort Collaborative (N3C) Data Enclave to identify people with long COVID and those likely to have it. [▶](#)

ncats.nih.gov/n3c

Observational Medical Outcomes Partnership (OMOP)



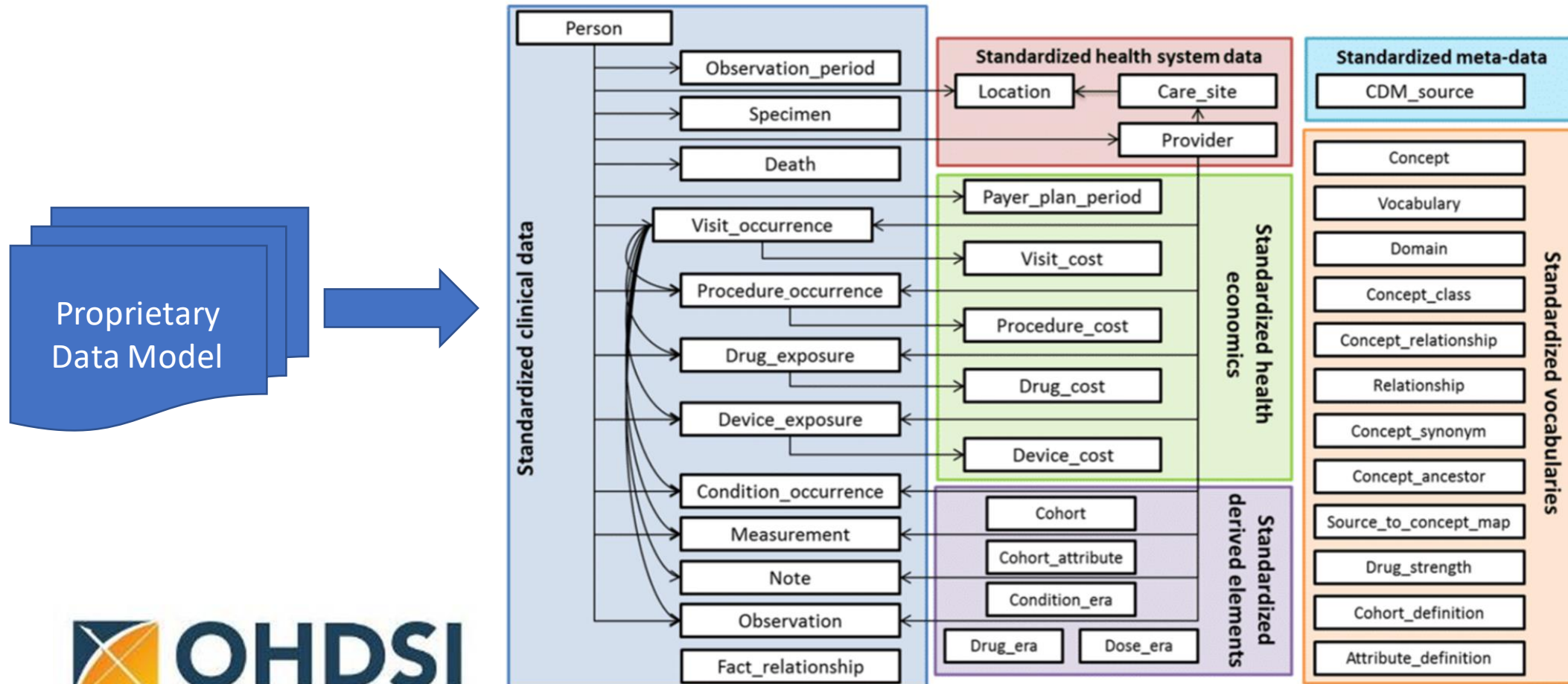
153 Controlled
Vocabularies
9 Million concepts



- Color by First(vocabulary_id)
- APC
 - ATC
 - Cohort
 - CPT4
 - DRG
 - ETC
 - Gemscript
 - Genseqno
 - GPI
 - HCPCS
 - ICD10
 - ICD10CM
 - ICD9CM
 - ICD9Proc
 - Indication
 - LOINC
 - MDC
 - MedDRA
 - MESH
 - Multilex
 - Multum
 - NDC
 - NDFRT
 - OPCS4
 - OXNIS
 - PCORNet
 - Read
 - RxNorm
 - SMQ



The Edge Tool



OMOP CDM V5.3.1

- Web-based decision support for concept mapping
- Base configuration settings for major EMR Vendors.
- Configuration management documentation tool
- Inspection Report of DevOps on ETL processes
- Data Quality Dashboard framework of 3,000+ data quality tests
- Collaborative cohort subset definition
- Perform de-identification and submission
- **All open-source resources**

The Edge Tool on Azure



docker

ETL

- Perseus
- EMR base config
- Usagi
- White Rabbit
- Rabbit in the Hat



docker

DevOps

- Data Quality Dashboard
- Documentation Engine
- Submission extraction
- Change control



docker

Analysis

- Atlas
- WebAPI
- Hades
- R-Studio
- Methods Library



Azure SQL Server
OMOP Data Model
Vocabulary Management
Authentication and Authorization

- Reassignment of Person IDs: Person IDs are regenerated sequentially from a sorted copy of the Person table. These new Person IDs are carried throughout the CDM to all tables that reference it.
- Date Shifting:
 - Each person is assigned a random date shift value between -186 and +186 days. All dates for that person are then shifted by that amount.
 - Birthdays: After date shifting a person's birthday, the day is then set to the first of the new birth month. If the person would be > 89 years old then they are assigned a random birth year that would make them 90-99 years old.
- Date Truncation:
 - A user-defined Start and End date are used to exclude any date shifted data that falls outside of the target date range (E.G. Procedures, conditions occurrences, etc. Does not include Birthdates).
- Removal of other identifiers:
 - Other potentially identifying datapoints are removed from the dataset such as `location_id`, `provider_id`, and `care_site_id`

Preserving temporal relations in clinical data while maintaining privacy

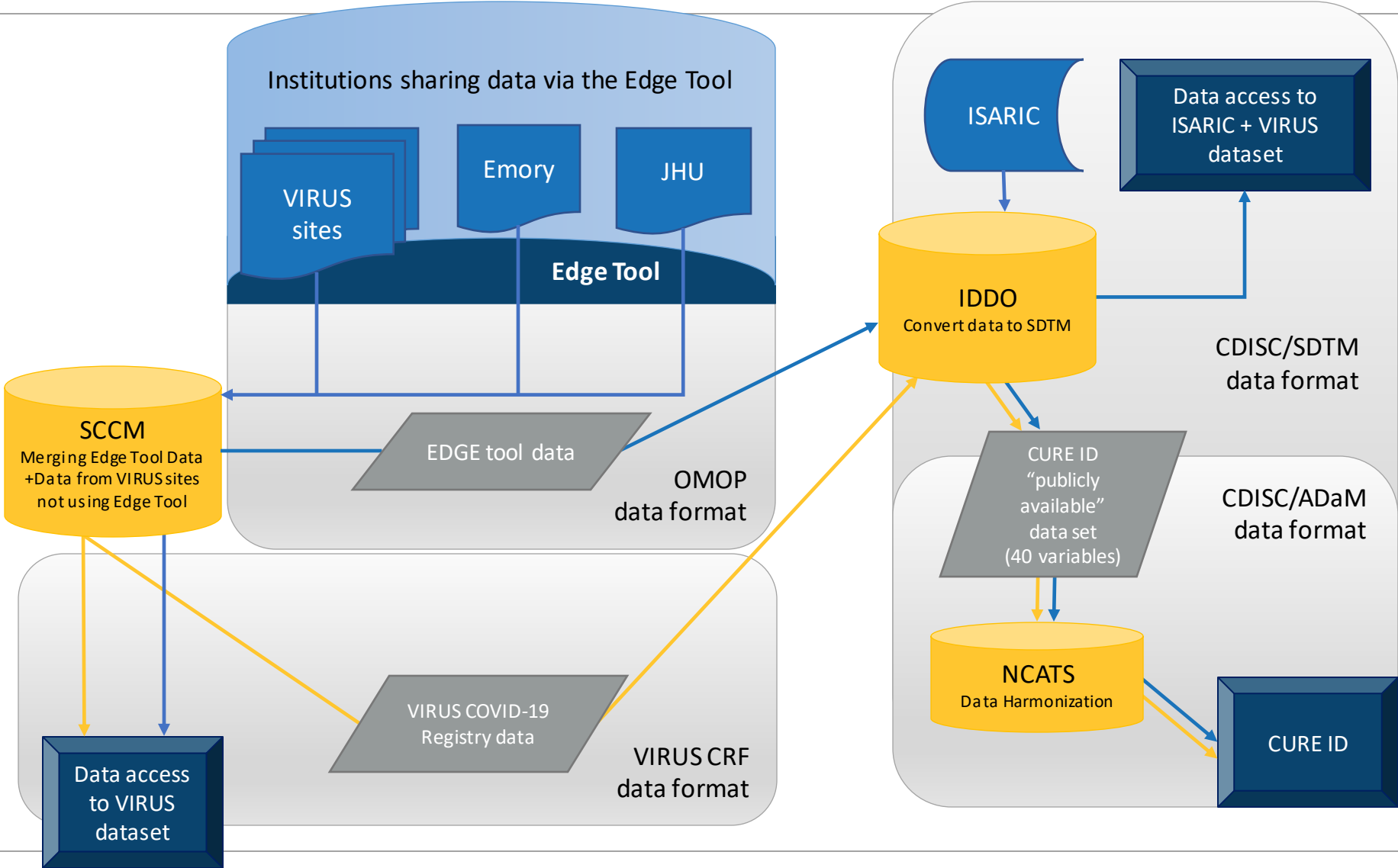
George Hripcsak,¹ Parsa Mirhaji,² Alexander FH Low,³ and Bradley A Malin^{4,5}

ABSTRACT

RECEIVED 30 September 2015
REVISED 4 January 2016
ACCEPTED 6 January 2016
PUBLISHED ONLINE FIRST 24 March 2016

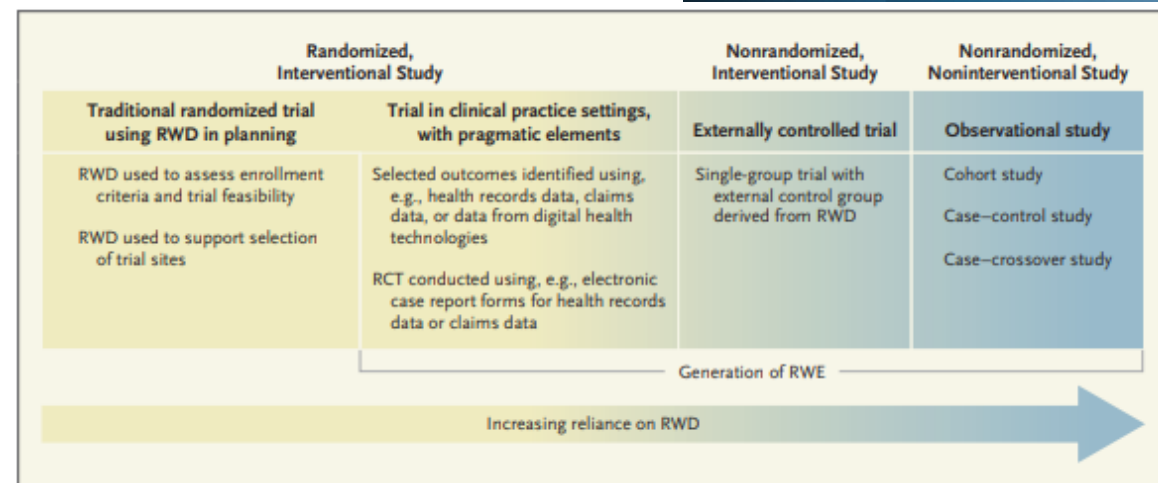
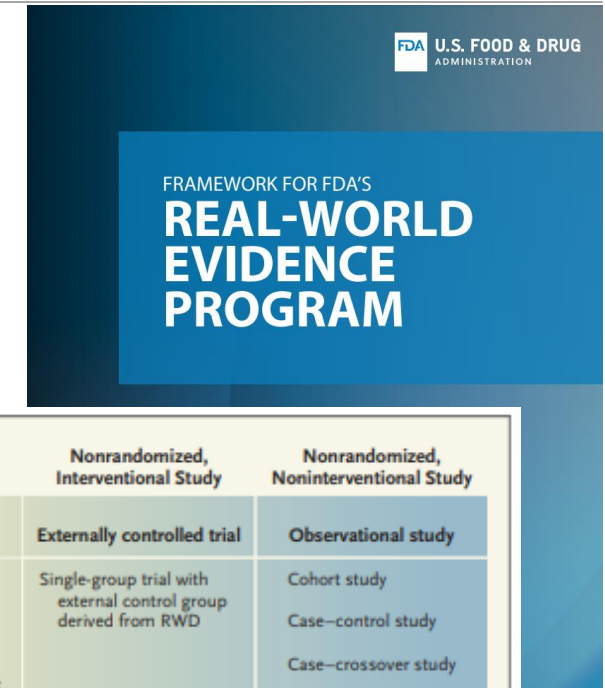
- Drug Repurposing
- Broad Impact
- Identifiable Cases
- Discreet Data
- Acute Disease
- Definitive Outcomes

Data Flow



Real-World Evidence: COVID-19

- Replicate findings of clinical trials
- Evaluate key agents: dexamethasone, baricitinib, tocilizumab
- Demonstrate utility of Edge Tool



Reliance on RWD in Representative Types of Study Design.

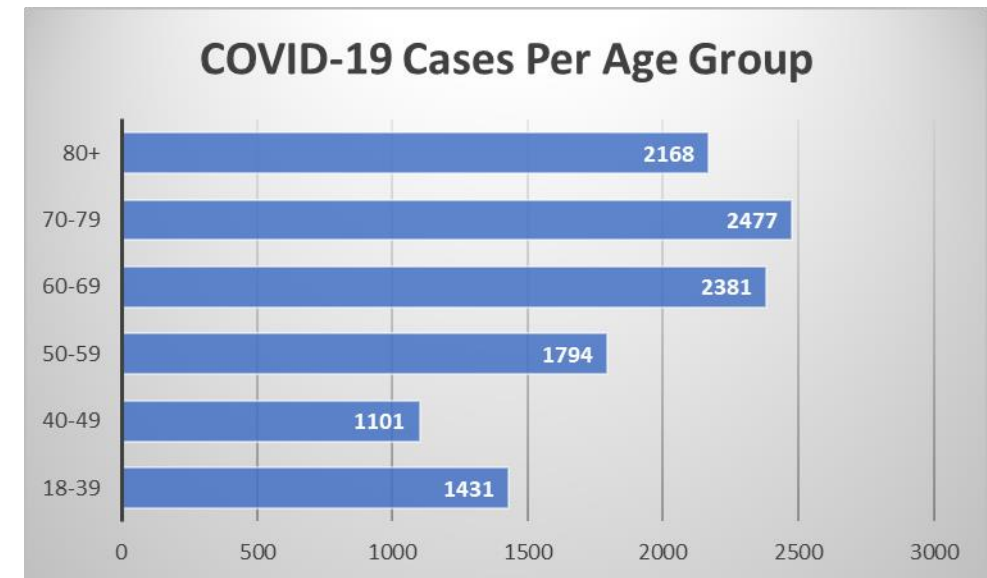
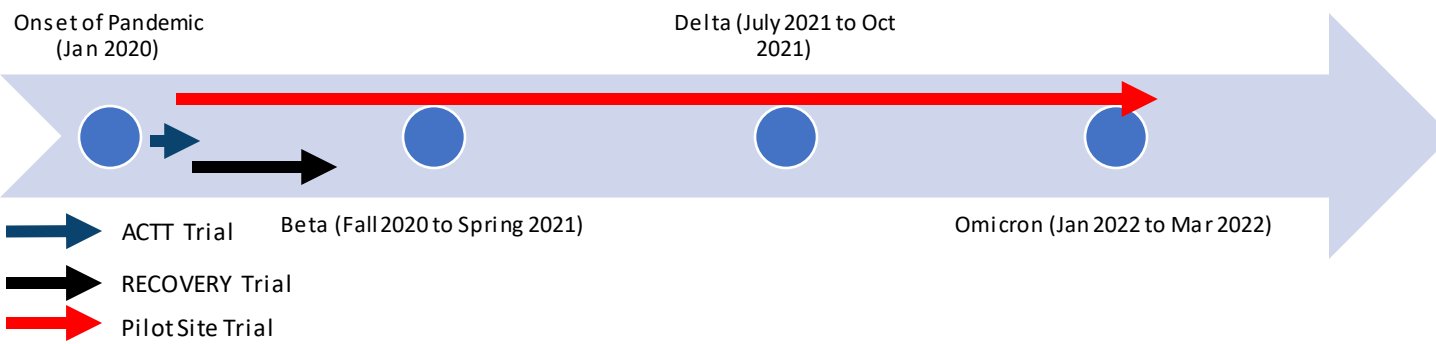
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- Methodology: Data cleaning

- Observational Medical Outcomes Partnership Common Data Model (OMOP CDM)
- Originally, N = 12,129 patients
 - Inclusion criteria: 18+, no missing demographic data (ethnicity, race)
 - N = 11,297 patients

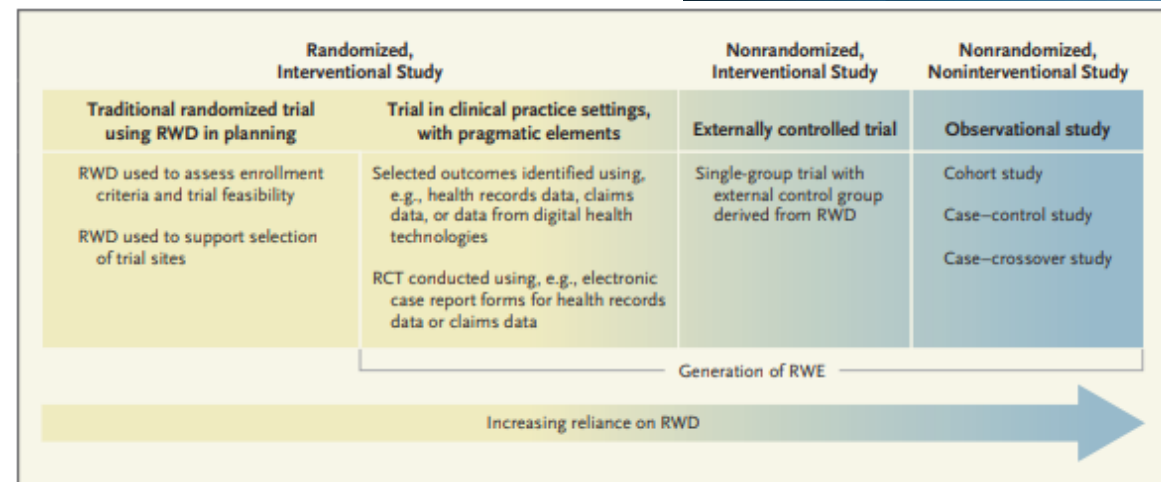
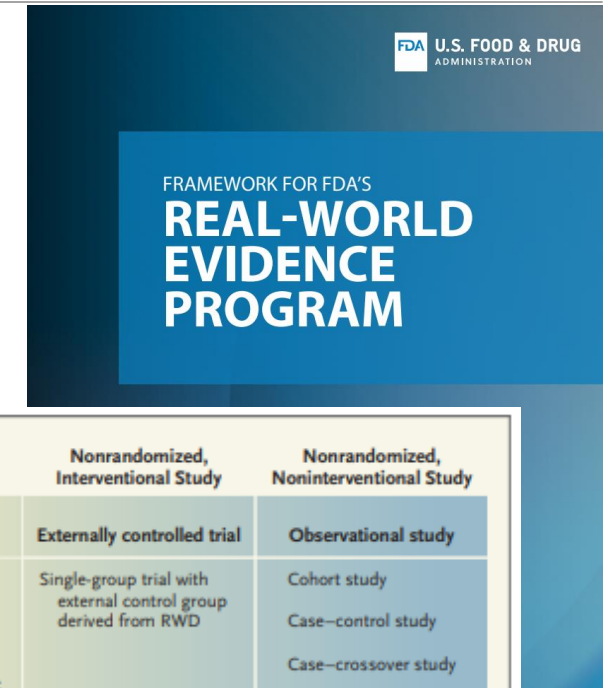
COVID-19 Pandemic Timeline



- Unmeasured covariates
- Small sample size, control matching with replacement
- Single site
- Timing limitations
 - Shift-and-truncate
 - Data collection after dexamethasone was shown to be effective
- Covariates outside of data collected in trial not accounted for
- Context of treatment (timing and dosage) not accounted for

Future Directions: Beyond COVID

- Sepsis
 - Isolating organisms
 - Case definition
- Meningitis
 - Isolating organisms
 - Rarer cases of more interest
- Osteomyelitis
 - Isolating organisms
 - Linking encounters
 - Lost to follow up

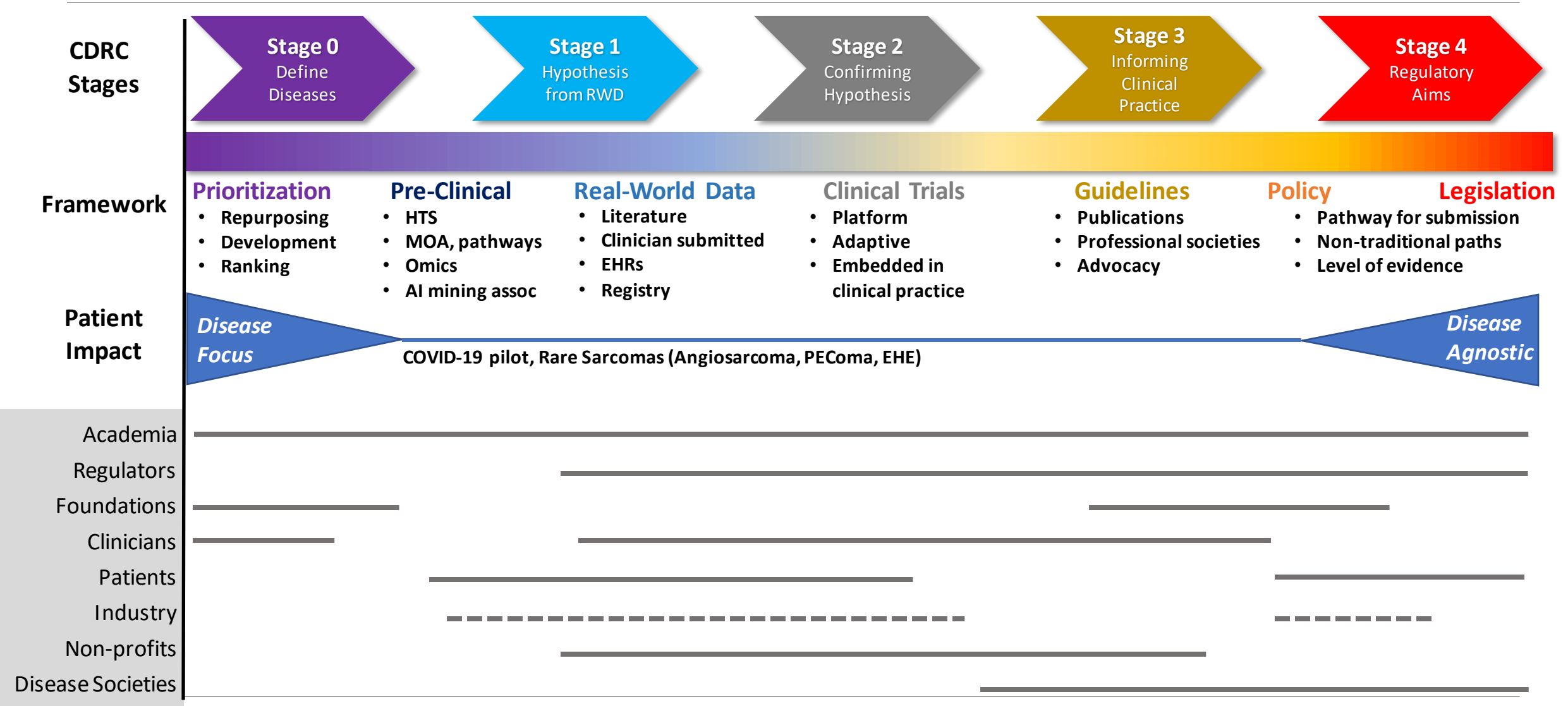


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Developing partnerships and infrastructure to provide sustainable resources to impact patient treatments globally





Thank You



<- scan for contact information



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Edge Tool Screen Grabs

Concept Mapping Decision Support

PAT2

Create Group ⓘ

Field	Type
day_of_birth	Text
deathdate	Date
died	Int
frd	Date
gender	Int
month_of_birth	Smallint
observation_period_end_date	Date
observation_period_start_date	Date

PERSON

Clone ⓘ Add Condition

Field	Type	Comments
person_id	Integer	
gender_concept_id	Integer	
year_of_birth	Integer	
month_of_birth*	Integer	
day_of_birth*	Integer	
birth_datetime*	Datetime	

Filters

- Gender (X)
- Gender (X)
- Domain
- Concept
- Class

Filter

- 10th level (0)
- 11-digit NDC (0)
- 11th level (0)

Clear Apply

Local Athena Show by 10 Total 19

ID	Code	Name	Class	Concept	Validity	Domain	Vocab
8507	M	MALE	Gender	Standard	Valid	Gender	Gender
8521	O	OTHER	Gender	Non-standard	Invalid	Gender	Gender
8532	F	FEMALE	Gender	Standard	Valid	Gender	Gender
8551	U	UNKNOWN	Gender	Non-standard	Invalid	Gender	Gender
8570	A	AMBIGUOUS	Gender	Non-standard	Invalid	Gender	Gender
4214687	394743007	Gender unknown	Clinical Finding	Non-standard	Valid	Gender	SNOMED
4215271	394744001	Gender unspecified	Clinical Finding	Non-standard	Valid	Gender	SNOMED
4231242	407379008	Surgically transgendered transsexual, female-to-male	Clinical Finding	Non-standard	Valid	Gender	SNOMED
4234363	407375002	Surgically transgendered transsexual	Clinical Finding	Non-standard	Valid	Gender	SNOMED
4251434	407378000	Surgically transgendered transsexual, male-to-female	Clinical Finding	Non-standard	Valid	Gender	SNOMED

Vocabulary

Delete Links Preview Generate Fake Report Convert to CDM

Documentation Engine



The JHM Epic to OMOP
ETL Guideline

Search this book...

Introduction

PREPARING YOUR SYSTEM

Epic to OMOP ETL Project

OMOP_FILL_PREP

OMOP_ETL_care_site

OMOP_ETL_derived_epic_patient

OMOP_ETL_derived_ip_encounters

OMOP_ETL_derived_op_encounters

OMOP_ETL_edw_geocode_patient

OMOP_ETL_epic_provider

OMOP_INS_SrcIDMaps_CareSite

OMOP_INS_SrcIDMaps_Location

OMOP_INS_SrcIDMaps_Person

OMOP_INS_SrcIDMaps_Provider

OMOP_INS_SrcIDMaps_Visit

OMOP_INS_SrcToConcept_JHMAdmitSource

OMOP_INS_SrcToConcept_JHMDischDisp

OMOP_INS_SrcToConcept_JHMEthnicity

OMOP_INS_SrcToConcept_JHMGender

OMOP_INS_SrcToConcept_JHMOpVisitType

OMOP_INS_SrcToConcept_JHMPatClass

OMOP_INS_SrcToConcept_JHMRace

OMOP_FILL_MAIN

OMOP_ETL_condition_occurrence_era



Epic to OMOP ETL Project

Goals

- Publish a guide that can be computable (ipynb) as well as easily searchable in html and pdf formats.
- Have the guide be compiled by the scripts so as new scripts are added they are automatically added to the guide
- Encode the scripts with markdown to enable navigation and readability
- Have sufficient meta data in the scripts to help users of the guide index the data for common questions.
- Whenever possible documentation should not be separated from the code.

Assumptions

- Epic data model is proprietary, distribution should be through Epic customer portal (galaxy)
- Epic uses SQL Server so we will base our scripts on MS T-SQL
- There is setup necessary to configure an OMOP CDM database with tables, vocabulary, and constraints.
- There are 60+ SQL stored procedures to transform Epic Clarity data into the OMOP CDM 5.3.1
- There is a sequence of operations to orchestrate the transformation
- The SQL scripts use an Ansi UTF text file with basic documentation capabilities (/* Comments */) for inline comments
- There are resources online available that are key to doing a transformation. Ie CDM github conventions and Book OHDSI
- Sites will need to change ETL scripts for site specific localizations where data is coming from flowsheets and smartdata forms.
- ETL scripts should be human readable

Users of the guide

- Database administrators implementing this ETL in their organization.
- Researchers wanting to see the clear provenance of data transformations from the clinical information system.

Questions the guide should facilitate

- Show the epic tables involved in the ETL process
- Show the source Epic clarity tables that feed into an OMOP Domain (condition, measurements, etc)
- Show the domains that are fed from a particular epic table
- Show the order of operations of the scripts



Contents

Goals

Assumptions

Users of the guide

Questions the guide should facilitate

Steps taken in compiling this guide

```
--for logging
DECLARE @RC INT = 0 , @procName VARCHAR(50) = 'OMOP_Fill_Prep', @tablename VARCHAR(50) = 'ETL_Pre
DECLARE @elapsed_seconds INT = 0 , @comment VARCHAR(255), @start_datetime Datetime = getdate(),
        @end_datetime Datetime, @block_number INT;

-- Flush the tables
--EXEC stage.OMOP_DEL_Flush;

-- Load SrcIDMaps
EXEC stage.OMOP_INS_SrcIDMaps_Provider; --from Clarity_SER
EXEC stage.OMOP_INS_SrcIDMaps_Person; -- from derived_inpatient_encounters, derived_outpat
EXEC stage.OMOP_INS_SrcIDMaps_CareSite; -- from Clarity_DEP, Clarity_POS
EXEC stage.OMOP_INS_SrcIDMaps_Location; --from edw_geocode_patient
EXEC stage.OMOP_INS_SrcIDMaps_Visit; --from from derived_inpatient_encounters, derived_ou

--refresh Source_to_Concept_map
--new proc loading from Clarity ZC tables and refreshing STCH
EXEC stage.OMOP_INS_SrcToConcept_JHMRace;
EXEC stage.OMOP_INS_SrcToConcept_JHMEthnicity;
EXEC stage.OMOP_INS_SrcToConcept_JHMGender;

EXEC stage.OMOP_INS_SrcToConcept_JHMPatClass;
EXEC stage.OMOP_INS_SrcToConcept_JHMOpVisitTypes;
EXEC stage.OMOP_INS_SrcToConcept_JHMAdmSource;
EXEC stage.OMOP_INS_SrcToConcept_JHMDischDisp;
--EXEC stage.OMOP_INS_SrcToConcept_JHMVisit; replaced by JHMPatClass and JHMOpVisitTypes
--EXEC stage.OMOP_INS_SrcToConcept_JHMAdmDisch; replaced by JHMAdmSource and JHMDischD

-- Fill core block
EXEC stage.OMOP_ETL_edw_geocode_patient; --creates
EXEC stage.OMOP_ETL_care_site; --
EXEC stage.OMOP_ETL_epic_provider; --

-- person, visit
--EXEC STAGE.OMOP_ETL_derived_inpatient_encounters__expired;
EXEC stage.OMOP_ETL_derived_epic_patient; --
EXEC stage.OMOP_ETL_derived_ip_encounters @block_total = 10; --creates visit_occurrence
EXEC stage.OMOP_ETL_derived_op_encounters @block_total = 10; --creates visit_occurrence

set @end_datetime = getdate();
set @elapsed_seconds = DATEDIFF(second,@start_datetime,@end_datetime);
```

Data Quality Dashboard

Examples of DQ Checks from Kahn et al (2016)

DATA QUALITY ASSESSMENT

JOHNS HOPKINS MEDICINE ENTERPRISE

DataQualityDashboard Version: 1.0.0

Results generated at 2021-08-28 09:20:06 in 7 hours

Atemporal
Plausibility

- 48% of labs outside of normal range

Temporal
Plausibility

- Unexpected change in number of records from month to month

Completeness

- 62% of *route_concept_id* is missing

Value Conformance

- ICD9 codes in *condition_concept_id*

Relational
Conformance

- *visit_date* and *visit_datetime* inconsistency in

	Verification				Validation				Total			
	Pass	Fail	Total	% Pass	Pass	Fail	Total	% Pass	Pass	Fail	Total	% Pass
Plausibility	1938	75	2013	96%	283	4	287	99%	2221	79	2300	97%
Conformance	643	3	646	100%	100	0	100	100%	743	3	746	100%
Completeness	356	7	363	98%	15	0	15	100%	371	7	378	98%
Total	2937	85	3022	97%	398	4	402	99%	3335	89	3424	97%

Data Quality Dashboard

Examples of DQ Checks from Kahn et al (2016)

Atemporal Plausibility

- 48% of labs outside of normal range

Temporal Plausibility

- Unexpected change in number of records from month to month

Completeness

- 62% of *route_concept_id* is missing

Value Conformance

- ICD9 codes in *condition_concept_id*

Relational Conformance

- *visit_date* and *visit_datetime* inconsistency in

DATA QUALITY ASSESSMENT

JOHNS HOPKINS MEDICINE ENTERPRISE

DataQualityDashboard Version: 1.0.0

Results generated at 2021-08-28 09:20:06 in 7 hours

	Verification		Validation				Total			
	Pass	Fail	STATUS	CONTEXT	CATEGORY	SUBCATEGORY	LEVEL	DESCRIPTION	% RECORDS	
Plausibility	1938	75	FAIL	Verification	Completeness					
Conformance	643	3	+	FAIL	Verification	Completeness	None	FIELD	The number and percent of records with a value of 0 in the standard concept field UNIT_CONCEPT_ID in the SPECIMEN table. (Threshold=5%).	0%
Completeness	356	7		FAIL	Verification	Completeness	None	FIELD	The number and percent of records with a value of 0 in the standard concept field UNIT_CONCEPT_ID in the DOSE_ERA table. (Threshold=0%).	0%
Total	2937	85	+							

Showing 6 to 7 of 7 entries (filtered from 3,424 total entries)

Previous

1

2

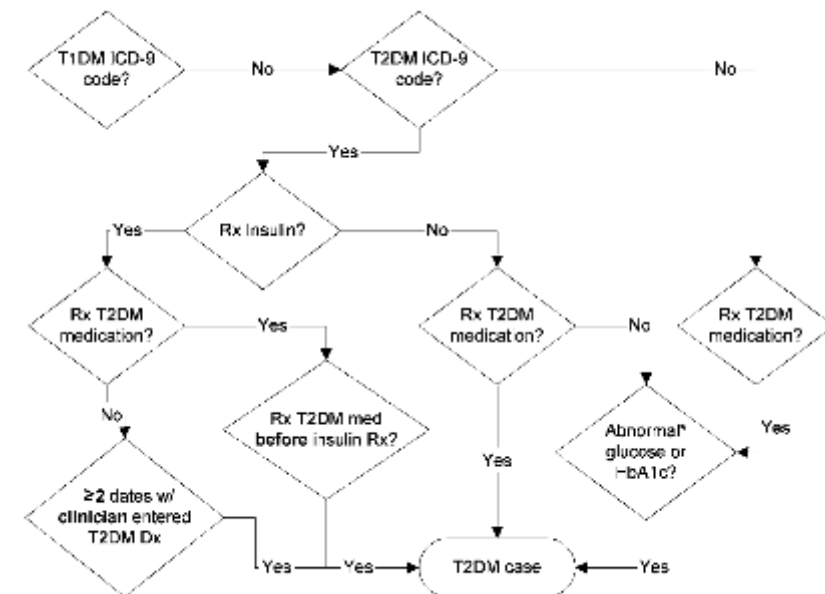
Next

Events having any of the following criteria:

a condition occurrence of **Type 2 Diabetes Mellitus Diagn...**a drug exposure of **Type 2 Diabetes Mellitus Prescri...**with continuous observation of at least **0** days before and **0** days after event index dateLimit initial events to: **all events** per person.**Restrict initial events to:**having **all** of the following criteria:with **at most** **0** using **all** occurrences of:a condition occurrence of **Type 1 Diabetes Mellitus Diagn...**where **event starts** between **All** days **Before** and **All** days **After** **index start date** [add additional constraint](#) restrict to the same visit occurrence allow events from outside observation periodAnd having **any** of the following criteria:having **all** of the following criteria:with **at most** **0** using **all** occurrences of:a condition occurrence of **Type 2 Diabetes Mellitus Diagn...**where **event starts** between **All** days **Before** and **All** days **After** **index start date** [add additional constraint](#) restrict to the same visit occurrence allow events from outside observation periodand with **at least** **1** using **all** occurrences of:a drug exposure of **Type 2 Diabetes Mellitus Prescri...**where **event starts** between **All** days **Before** and **All** days **After** **index start date** [add additional const](#) restrict to the same visit occurrence allow events from outside observation period

Use of diverse electronic medical record systems to identify genetic risk for type 2 diabetes within a genome-wide association study

Abel N Kho,¹ M Geoffrey Hayes,¹ Laura Rasmussen-Torvik,¹ Jennifer A Pacheco,¹ William K Thompson,¹ Loren L Armstrong,¹ Joshua C Denny,² Peggy L Peissig,³ Aaron W Miller,³ Wei-Qi Wei,¹ Suzette J Bielinski,⁴ Christopher G Chute,¹ Cynthia L Leibson,¹ Gail P Jarvik,⁵ David R Crosslin,⁵ Christopher S Carlson,⁶ Katherine M Newton,⁷ Wendy A Wolf,⁸ Rex L Chisholm,¹ William L Lowe¹



PheKB >1,000 lines of code