



Welcome

Introduction to Data Sharing and Data Exploration on the ClinEpiDB Platform



ASTMH Workshop, Seattle – 30 October 2022

Share, explore, and visualize clinical and epidemiological data



i Join a hands-on workshop on ClinEpiDB resources in Seattle WA (30 October 2022) ... or visit the ClinEpiDB booth during the ASTMH meeting, or click the 'Contact Us' link

Explore the Studies

Study summaries table

SCORE Zanzibar S. haematobium Cluster Randomized Trial

S

Zanzibar, 2012-2017

- Cluster randomized intervention
- 8,147 participants
- Study investigates the possible benefits of mass drug administration (MDA), chemical snail control, and behavior change interventions in Zanzibar over 5 years. Major outcomes are prevalence and intensity in the 5th year

EXPLORE THE DATA



South Asia ICEMR Surveillance

M

1 Site in Goa, India from 2012-2017

- Surveillance study with daily observations for inpatients
- 1,546 participants with 4,995 observations
- The South Asia surveillance study is part of the International Centers of Excellence for Malaria Research (ICEMR) Program

EXPLORE THE DATA



WASH Benefits Bangladesh Cluster Randomized Trial

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Bangladesh, 2012-2015

- Cluster-randomized controlled trial
- Over 10,000 participants from 5,551 household compounds distributed over 720 clusters in Bangladesh
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India ICEMR DAMaN Quasi-experimental Stepped-wedge

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2 Sites in Odisha, India

- Quasi-experimental stepped-wedge study
- The Center for the Study of Complex Malaria in India (CSCM) is part of the International Centers of Excellence for Malaria Research (ICEMR) Program. They examined the effectiveness of malaria camps as part of the Durgama Anchalare Malaria Nirakaran (DAMaN) program in Odisha, India: Phase 1
- See the study page to learn more about the study and its predicted release

COMING SOON!

Grid view

LAKANA Cluster Randomized

Study Details

Mali, 2020-2023

- Cluster randomized
- 830 villages
- The Large-scale As health-promoting A drug administration Azithromycin (LAK/ effect of azithromy more among infant

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News

ClinEpiDB 24 Released

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We are pleased to announce the release of

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Tweets from @ClinEpiDB


ClinEpiDB

@ClinEpiDB · Sep 27

Our ClinEpiDB and @veupathdb colleagues Sarah Kelly and Sam Rund are at the @pamafrika conference in Kigali, Rwanda this week. If you're at the conference, visit our booth to meet them and learn more about our work!



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i

Explore Example Analyses

ClinEpiDB can be used to explore and visualize study data. Use the example analyses below to see some examples.

[VIEW ALL »](#)


Plasmodium prevalence by age group

PRISM2 ICEMR Cohort



LLINEUP demo

LLINEUP Cluster Randomized Trial



Demonstration of new mapping tool

SCORE Seasonal Transmission S. haematobium Cluster Randomized Trial



Schisto prevalence over time, by study arm

SCORE S. mansoni Cluster Randomized Trial



Effect of annual MDA on schisto prevalence

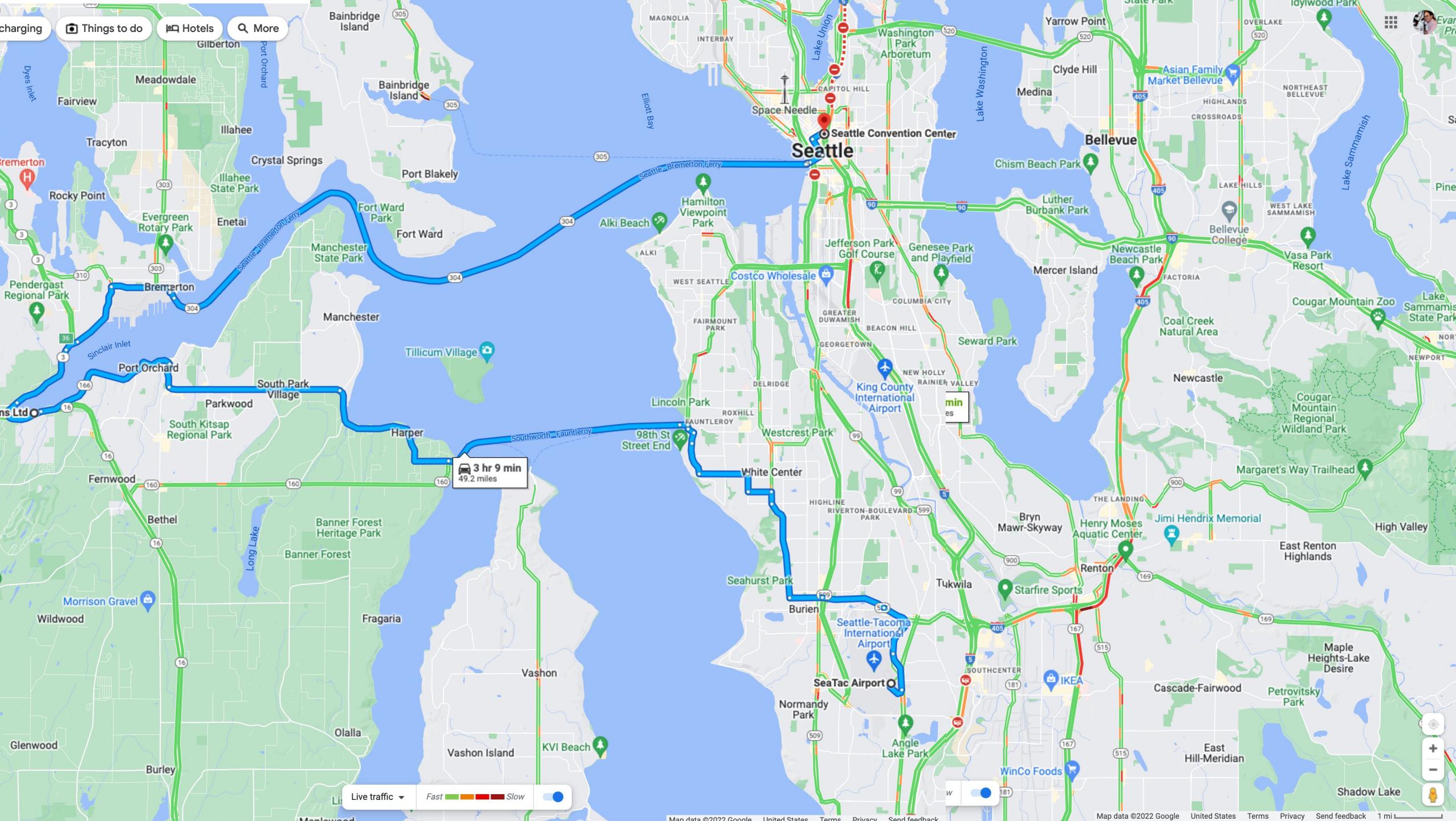
SCORE S. mansoni Cluster Randomized Trial



Uptake & outcomes after

WASH Benefits Random





20+ years of genomic Big Data





My Search Strategies

[Opened \(2\)](#) All (378) Public (51) Help

Plasmodium vaccine antigens?

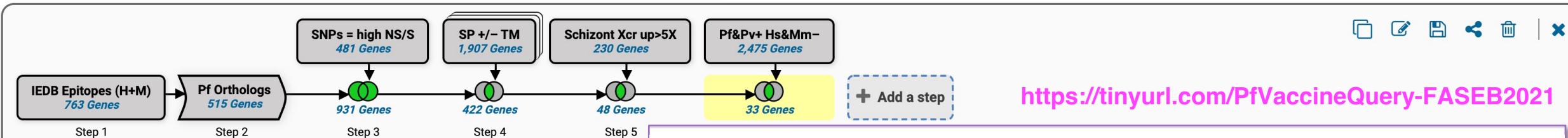
Immunoreactive (manual curation, from Immune Epitope DB)

P. falciparum Orthologs (of any *Plasmodium* antigen)

Under diversifying selection (dN/dS)

Surface expression (SP ± TM)

Expressed at the desired stage (schizonts)

Orthologs in *P. falciparum* & *P. vivax*; not in humans/mice

33 Genes (24 ortholog groups)

active targets (positive controls)
other targets of interest
novel candidates?

[Gene Results](#) [Genome View](#) [Analyze Results](#)
Genes: 33 Transcripts: 34 (hiding 1) Show Only One Transcript Per Gene

Rows per page: 50

Gene ID	Transcript ID	Product Description	?	X	Graph
PF3D7_1133400	PF3D7_1133400.1	apical membrane antigen 1			
PF3D7_1352900	PF3D7_1352900.1	Plasmodium exported protein, unknown function			
PF3D7_0202100	PF3D7_0202100.1	liver stage associated protein 2			
PF3D7_0930300	PF3D7_0930300.1	merozoite surface protein 1			
PF3D7_0508000	PF3D7_0508000.1	6-cysteine protein			
PF3D7_1335100	PF3D7_1335100.1	merozoite surface protein 7			
PF3D7_0207500	PF3D7_0207500.1	serine repeat antigen 6			
PF3D7_0831600	PF3D7_0831600.1	cytoadherence linked asexual protein 8			
PF3D7_0832200	PF3D7_0832200.1	Plasmodium exported protein (PHISTa-like), unknown			

Research article

2344 Mol. Biol. Evol. 27(10):2344–2351. 2010 doi:10.1093/molbev/msq119 Advance Access publication May 9, 2010

Allele Frequency-Based and Polymorphism-Versus-Divergence Indices of Balancing Selection in a New Filtered Set of Polymorphic Genes in *Plasmodium falciparum*

Lynette Isabella Ochola,¹ Kevin K. A. Tetteh,² Lindsay B. Stewart,² Victor Rütho,¹ Kevin Marsh,¹ and David J. Conway^{*2}

¹Kenya Medical Research Institute, Centre for Geographic Medicine Research Coast, Kilifi, Kenya²Department of Infectious and Tropical Diseases, London School of Hygiene and Tropical Medicine, London, United Kingdom

*Corresponding author: E-mail dconway@mrcgm, david.conway@lshtm.ac.uk.

Associate editor: John H. McDonald

Abstract

Signatures of balancing selection operating on specific gene loci in endemic pathogens can identify candidate targets of naturally acquired immunity. In malaria parasites, several leading vaccine candidates convincingly show such signatures when subjected to several tests of neutrality, but the discovery of new targets affected by selection to a similar extent has been slow. A small minority of all genes are under such selection, as indicated by a recent study of 26 *Plasmodium falciparum* merozoite-stage genes that were not previously prioritized as vaccine candidates, of which only one (locus PF10_0348) showed a strong signature. Therefore, to focus discovery efforts on genes that are polymorphic, we scanned all available shotgun genome sequence data from laboratory lines of *P. falciparum* and chose six loci with more than five single nucleotide polymorphisms



DOCS HELP LOGIN

Genomic epidemiology of SARS-CoV-2 with subsampling focused globally since pandemic start

[Nextstrain.org](https://nextstrain.org)

Built with [nextstrain/ncov](#). Maintained by the Nextstrain team. Enabled by data from [GenBank](#).

Showing 2776 of 2776 genomes sampled between Dec 2019 and Oct 2022.

Dataset

ncov
open
global
all-time

Date Range
 2019-12-22 2022-10-21
PLAY RESET

Color By
i
 Clade

Filter Data
i
 Type filter query here...

Tree Options
i
 Layout
RECTANGULAR
RADIAL
UNROOTED
CLOCK
SCATTER

Branch Length
TIME DIVERGENCE

Show confidence intervals

Branch Labels
clade

Show all labels

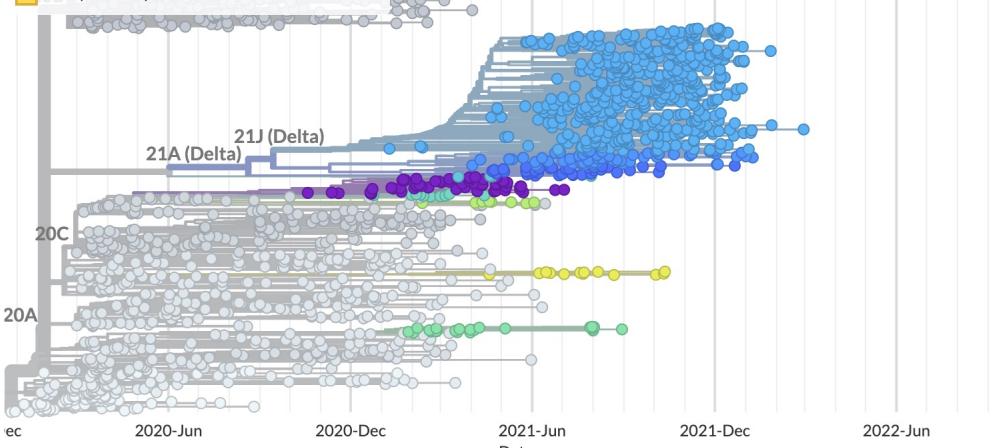
Tip Labels
Sample Name

Second Tree

Phylogeny

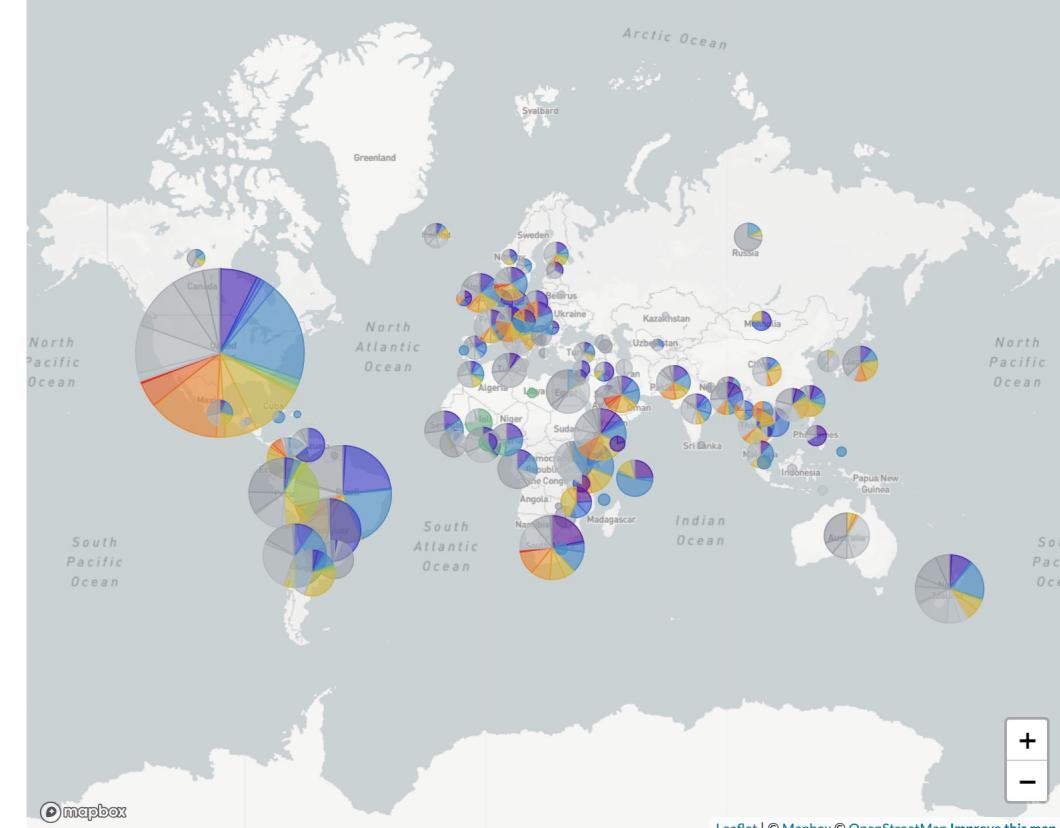
Clade ^

- 20H (Beta, V2)
- 22A (Omicron)
- 20I (Alpha, V1)
- 22B (Omicron)
- 20J (Gamma, V3)
- 22C (Omicron)
- 21A (Delta)
- 22D (Omicron)
- 21I (Delta)
- 22E (Omicron)
- 19A
- 19B
- 20A
- 20E (EU1)
- 21D (Eta)
- 21E (Theta)
- 21F (Iota)
- 21G (Lambda)
- 20J (Delta, V3)
- 21H (Mu)
- 21K (Omicron)
- 21L (Omicron)
- 20F



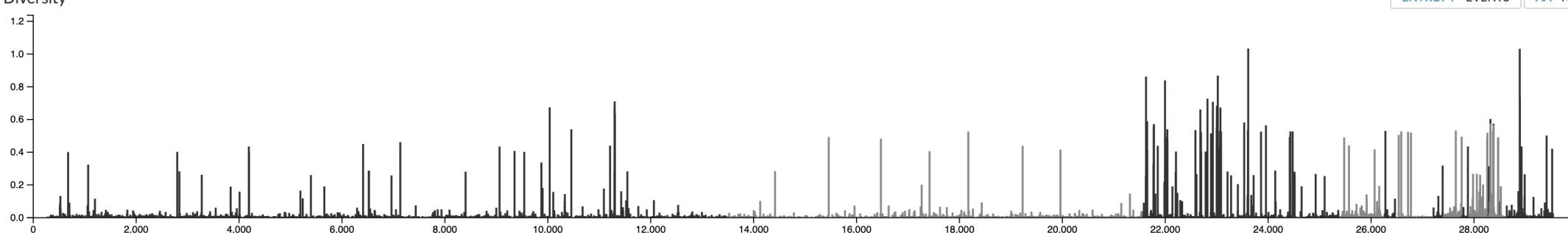
Geography

RESET ZOOM



Diversity

ENTROPY EVENTS AA NT



COV3001: No Relevant Differences at Baseline Between Vaccine and Placebo Groups Globally

Full Analysis Set

Sex, female

Mean Age (SD), years

Age group

18-59

≥ 60

≥ 65

≥ 75

Race

American Indian or Alaska Native

Asian

Black or African American

Native Hawaiian or other Pacific Islander

White

Multiple, unknown, not reported

Ethnicity

Hispanic or Latino

Full Analysis Set

Baseline Comorbidity* Category, ≥ 2%

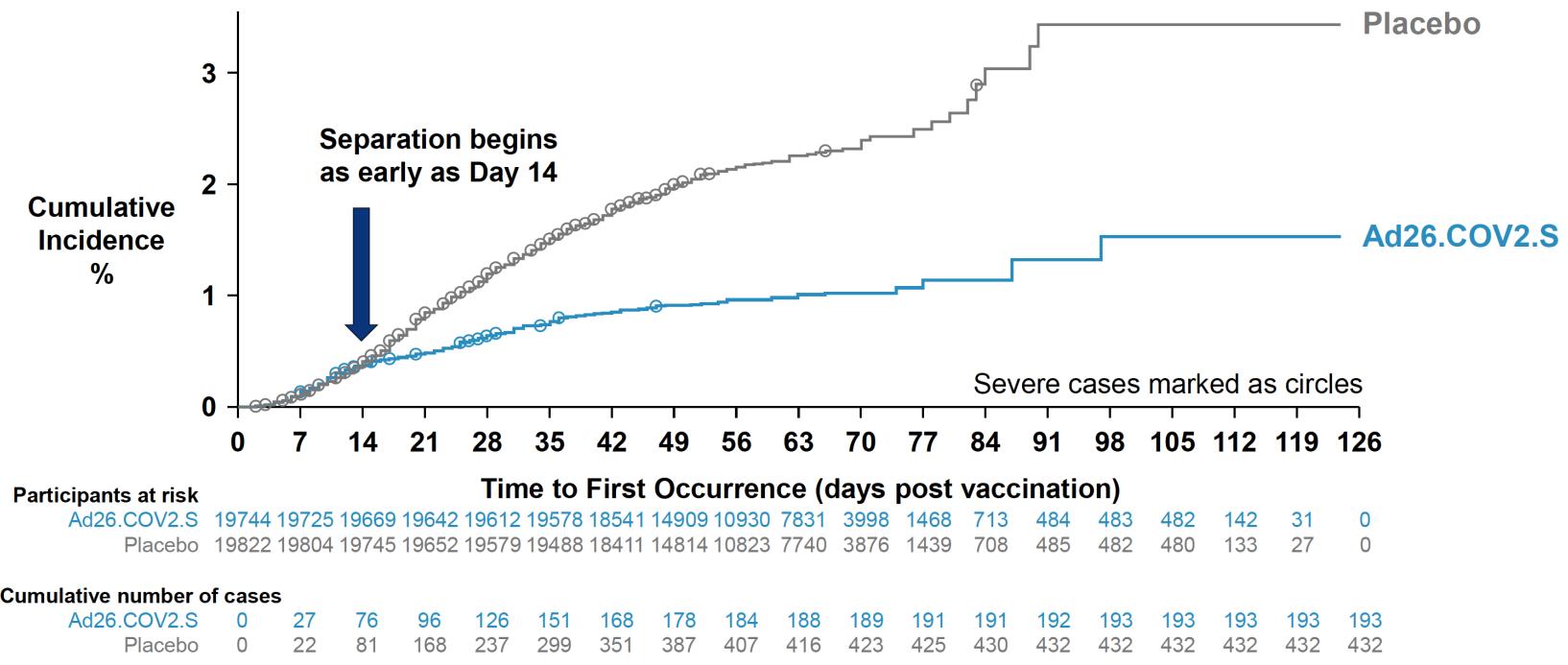
≥ 1 risk factor

Obesity ≥ 30 kg/m²

Hypertension

Kaplan Meier Shows Early Onset of Protection Against Moderate to Severe/Critical COVID-19

CO-36



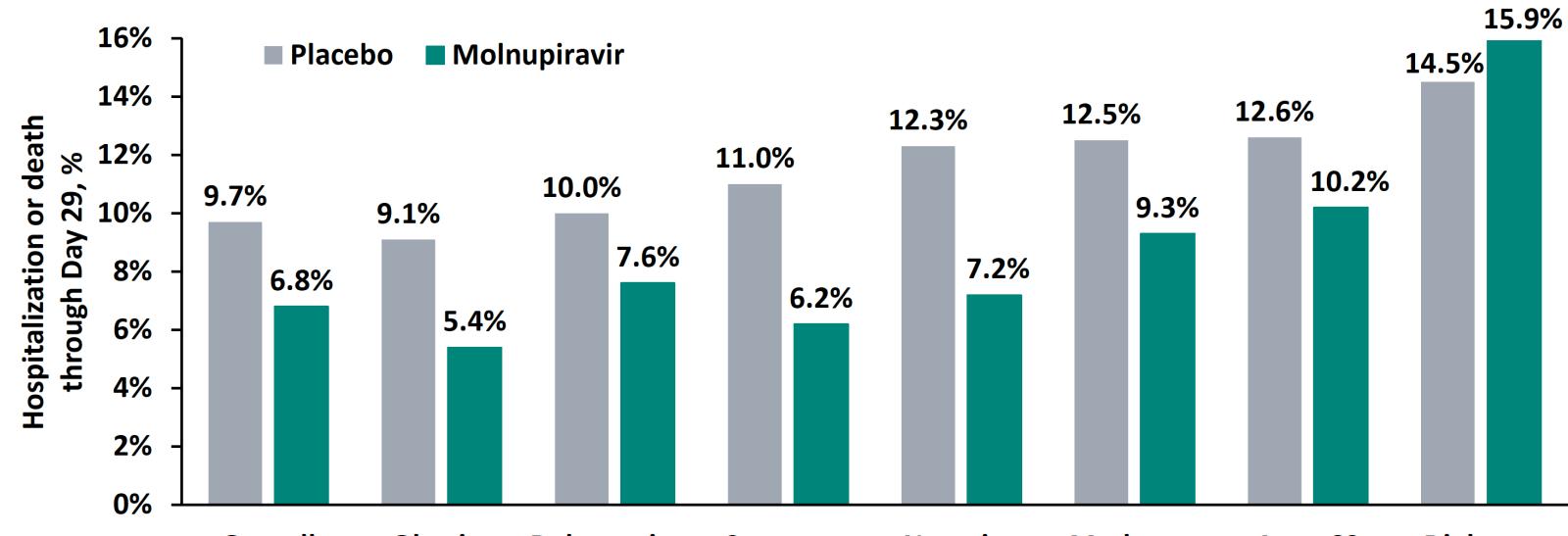
Hypertension	2,225	10.2%	2,296	10.5%
Type 2 Diabetes Mellitus	1,600	7.3%	1,594	7.3%
Serious heart conditions	497	2.3%	511	2.3%

Moderna Covid-19 vaccine
EUA hearing, FDA – Dec 2020

Participants, n (%)

	Interim Analysis Population		All Randomized Population	
	Molnupiravir N=387	Placebo N=388	Molnupiravir N=716	Placebo N=717
Sex				
Male	187 (48)			
Female	200 (52)			
Age, yr				
18-49	274 (71)			
50-64	82 (21)			
65-74	24 (6)			
≥75	7 (2)			
Mean	43.2			
Median	41.0			
Range	18-87			
Time from symptom onset to randomization				
≤3 days				
>3 days				
Median days				
Risk factors for severe illness from COVID-19				
≥1 risk factor				
Age >60 years				
Active cancer				
Chronic kidney disease				
Chronic obstructive pulmonary disease				
Obesity (BMI ≥30)				
Serious heart condition	42 (11)	36 (9)	86 (12)	81 (11)
Diabetes mellitus	48 (12)	57 (15)	107 (15)	121 (17)
Baseline disease severity				
Mild	222 (57)	212 (55)	395 (55)	390 (54)
Moderate	162 (42)	174 (45)	315 (44)	323 (45)

For Most Key Subgroups, A Lower Proportion of Participants in the Molnupiravir Group Were Hospitalized or Died
P002 Phase 3 All Randomized Population



*Merck Covid-19 treatment
EUA hearing, FDA – Nov 2021*

CC-27

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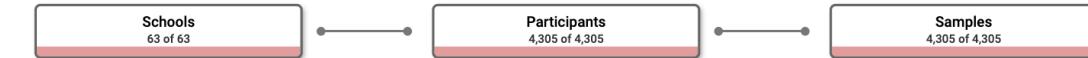


Uptake & outcomes after

WASH Benefits Random



SCORE Five Country CCA Evaluation Cross-sectional

[Unnamed Analysis](#) Edit
▼ Show all filters

+ New Analysis My Analyses
◀ Share Analysis

[View Study Details](#) [Browse and Subset](#) [Visualize](#) [Download](#) [Record Notes](#)

Primary publication: A five-country evaluation of a point-of-care circulating cathodic antigen urine assay for the prevalence of *Schistosoma mansoni*. Colley et al. Am J Trop Med Hyg 2013;88(3):426-432

Primary contact: Dan Colley, University of Georgia, Athens, GA, USA

Release # / date: ClinEpiDB rel. 21, 2022-MAR-03

Summary: The Schistosomiasis Consortium for Operational Research and Evaluation (SCORE) supported the evaluation of a commercial point-of-care circulating cathodic antigen (POC-CCA) test for assessing *Schistosoma mansoni* infection prevalence in areas at risk in 5 countries- Cameroon, Côte d'Ivoire, Ethiopia, Kenya, and Uganda. The study concluded that one urine POC-CCA test can replace Kato-Katz testing for community-level *S. mansoni* prevalence mapping.

1 Data Provenance §

Data accessibility ? Controlled

Study Characteristics

Disease	Sex	Sample Type	Population included	Investigation Type	Study Design	Country	Years	Variables	Households	Participants	Participant Repeated Measures	Samples	Additional Data	WHO indicator subdomain	Project Name
Schistosomiasis	Female, Male	Stool sample, Urine sample	Child	Observational	Cross-sectional	Cameroon, Côte d'Ivoire, Ethiopia, Kenya, and Uganda	2012	10	N/A	4,305	N/A	4,305	N/A	Communicable disease	SCORE

Selected Publications

- A five-country evaluation of a point-of-care circulating cathodic antigen urine assay for the prevalence of *Schistosoma mansoni*. Colley et al. Am J Trop Med Hyg 2013;88(3):426-432

Description

Related studies:

- SCORE Rwanda Mapping Cross-sectional
- SCORE Burundi Mapping Cross-sectional

Background: Schistosomiasis is a parasitic disease caused by infection with blood flukes of the genus *Schistosoma*. An estimated 800 million people are at risk of infection and more than 200 million people are infected globally.

SCORE Five Country CCA Evaluation Cross-sectional

expand all | collapse all

Search section names...

▼ 1 Data Provenance ✓

- Data accessibility
- Study Characteristics
- Selected Publications
- Description
- Data Versions

Principal Investigator and Collaborators

Data Access Statistics

Data Access Records

▼ 2 Link outs ✓

External Resources

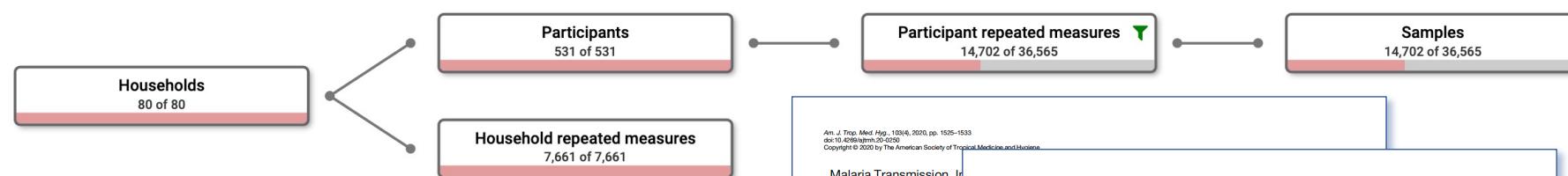
expand all | collapse all

PRISM2 ICEMR Cohort

+ New Analysis My Analyses

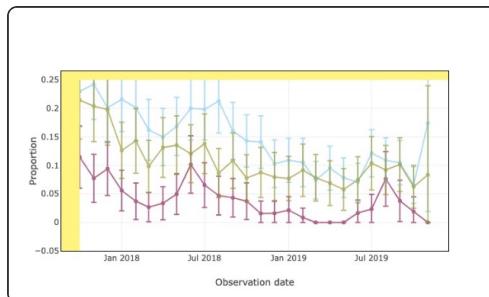
Plasmodium prevalence by age group 💡

Show all filters

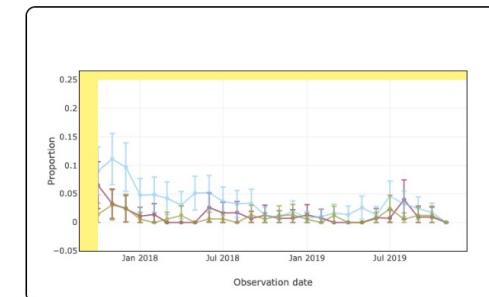


[View Study Details](#) [Browse and Subset](#) [Visualize](#) [Download](#) [Record Notes](#)

+ New visualization



Prevalence of microscopic or submicroscopic parasitemia



Prevalence of microscopic parasitemia

Malaria Transmission, Ir

Joaniter I. Nankabirwa,^{1,2*} Phillip J. Rosenthal,⁴ Isabel Ro³, David S. Roos,¹

¹Infectious Diseases Research Collaboration, Kampala, Uganda; ²Faculty of Infectious Diseases and Microbiology, University of Nijmegen Medical Centre, Nijmegen, The Netherlands; ³Department of Medicine, University of Pennsylvania, Philadelphia, PA, United States; ⁴Tropical Medicine, London, United Kingdom

Abstract Tororo, a district control interventions, including indoor residual spraying (IRS) of insecticide-treated nets (LLINs), artemisinin-based combination therapy (ACT), and mass drug administration (MDA), has been associated with marked reduction in the burden of malaria. However, programs have shown that the incidence of malaria in 2018, alone, there were cases of malaria, of which 93% were asymptomatic. After 5 years of follow-up, 15,789 females and 15,789 males were included. The daily biting rate was 0.33 bites per person per night. Only 38 episodes of malaria, 38 episodes of malaria, or malaria or malariasis were reported. The incidence of malaria was 0.054 episodes/perso

INTRODUCTION
The scale-up of proven malaria control interventions, including indoor residual spraying lasting 4 weeks, artemisinin-based combination therapy (ACT), and mass drug administration (MDA), has been associated with marked reduction in the burden of malaria. However, programs have shown that the incidence of malaria in 2018, alone, there were cases of malaria, of which 93% were asymptomatic. After 5 years of follow-up, 15,789 females and 15,789 males were included. The daily biting rate was 0.33 bites per person per night. Only 38 episodes of malaria, 38 episodes of malaria, or malaria or malariasis were reported. The incidence of malaria was 0.054 episodes/perso

RESULTS

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DISCUSSION

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ACKNOWLEDGMENTS

The scale-up of proven malaria

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CONCLUSIONS

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CONCLUSIONS

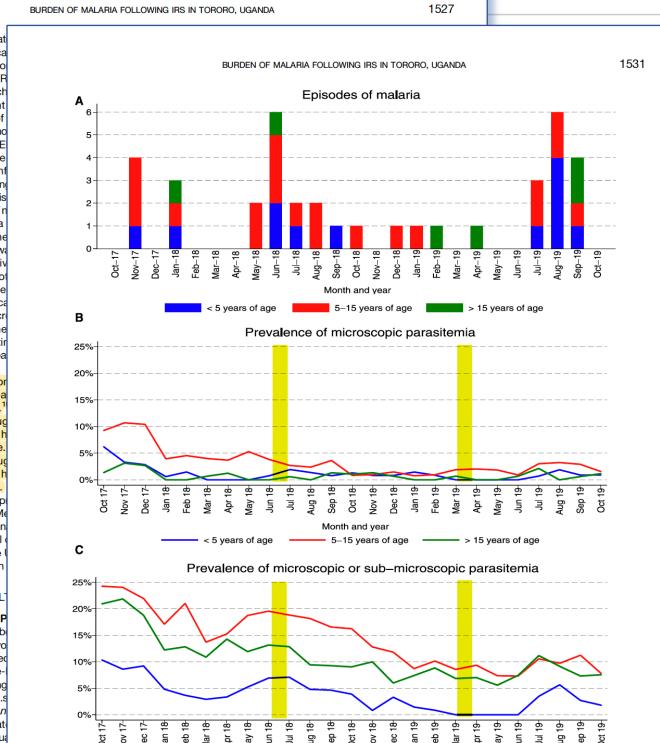
The scale-up of proven malaria

therefore, this metric was estimated. The incidence of malaria was 0.054 episodes/perso

DATA ACCESSIBILITY

Data access to the dataset is available through a novel open-access database resource, ClinEpiDB.¹ Data from October 2011 through to November 2019 can be found at [https://clinedb.org/dataset/DS_000509829e](#). Data from October 2017 through to November 2019 can be found at [https://clinedb.org/dataset/DS_51140fece2e](#).

Ethics statement. Ethical approval was obtained from Makerere University School of Medicine Ethics Committee, the Uganda National Council for Science and Technology, the London School of Economics and Political Science Ethics Committee, and the Francisco Committee on Human



Goals for Today



Facilitators



Danica Helb



Sarah Kelly



Nupur Kittur



David Roos



Weilu Song



Sheena Tomko

Agenda



8:00- 8:40	Welcome; Introduction to ClinEpiDB and FAIR data
8:40- 9:40	Navigating ClinEpiDB
9:40- 10:00	Uploading your own data
10:00- 10:20	Break
10:20- 11:40	Exploratory data analysis
11:40- 12:00	Downloading data
12:00- 12:20	Exploring your uploaded data
12:20- 1:00	Wrap-up

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- ❖ Our goal is to expedite discovery research and evidence-based public health decisions, by facilitating the exploration of high-quality, high-value field & epidemiological datasets ... by the study team & collaborators, national control programs & other stakeholders, reviewers & editors, epidemiology students & researchers, and the broader community if/as appropriate.
- ❖ Straightforward, FAIR data access & release policy: all control rests with the providers ... nothing is ever released unless providers agree that it is properly represented and appropriate to share. Others may mandate sharing, but we never will; 20+ year history of community trust.
- ❖ ClinEpiDB ensures that all datatypes, including metadata, are appropriately structured ... in a robust ontological framework, harmonized with global standards to facilitate cross-study analysis. Support for various study designs (X-sectional, case-control, longitudinal, trials, etc).
- ❖ Long experience navigating compliance with diverse data access, sharing & ethics policies around the world: CDISC, REDCap, HIPAA, GDPR, NIH-DMS, Nagoya, FAIR, etc.
- ❖ User-friendly platform enables study exploration & rapid data analysis directly within the browser, and data downloads for further analysis off-line ... even without experience in scripting, command-line analysis, etc. URLs for direct sharing / publication of your analyses.
- ❖ DIY platform for rapid, private analysis of your own data, using the ClinEpiDB platform.
- ❖ Contact Us: on-line resources, email support, workshops, Virtual Lab Meeting with your group.

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