Combating Antimicrobial Resistance in Africa Using Data Science (CAMRA)

https://camra.acegid.org/

UNIVERSITY OF Nebraska
Medical Center

UNIVERSITY OF Nebraska
Lincoln

CASE WESTERN RESERVE UNIVERSITY
EST 1826
think beyond the possible

DS-I Africa
Data Science for Health Discovery and Innovation in Africa

EAGLE RESEARCH CENTER
EFFICIENCY. PROFESSIONALISM. INTEGRITY

UAB
THE UNIVERSITY OF ALABAMA AT BIRMINGHAM

NIH

JCVI J.CRAIG VENTER INSTITUTE

Connecticut Children's

ACEGID
African Centre of Excellence for Genomics of Infectious Disease
Redeemer's University, Nigeria

UCONN
SCHOOL OF MEDICINE

iFAIN
INTERNATIONAL FOUNDATION AGAINST INFECTIOUS DISEASE IN NIGERIA

CAMRA

Overview

CAMRA is a DS-I Africa research hub focused on **analyzing clinical and molecular data** related to **antimicrobial resistance** (AMR) in pediatric bacterial infections in **Nigeria and Rwanda** with the aim of translating genomics of AMR to **sensitive, rapid diagnostics**, and **effective therapeutics**.

Project Performance Sites

CAMRA Project Map

African Partner Institutions
Nigeria
- Redeemer's University/ACEGID
- International Foundation Against Infectious Disease in Nigeria (IFAIN)

Rwanda
- University of Rwanda
- Eagle Research Center (ERC)

US Partner Institutions
- Case Western Reserve University
- J. Craig Venter Institute
- Connecticut Children's University of Connecticut School of Medicine
- University of Lincoln Nebraska and Medical Center
- University of Alabama at Birmingham

NIGERIA 3

RWANDA 3

Project 1: **Clinical and Molecular Epidemiology of Antimicrobial Resistance in Invasive Bacteria from Nigerian Children.**

1. Analyze the phenotypic & genotypic profiles of archived Enterobacteriales from Nigeria and Rwanda. (Retrospective)

2. Characterize the distribution and determinants of AMR among Enterobacteriales and their attributable diseases in Nigeria and Rwanda. (Prospective)

3. Determine human, animal, and environmental reservoirs of MDRO.

Project 2: Translating Genomics of AMR into Diagnostics and Therapeutics

1. Development of inflammatory biomarkers for bloodstream bacterial infection screening

2. Development of a screening tool for prevalent AMR enzymes

3. Explore novel antimicrobial combinations for treatment of MDROs

CAMRA Leadership

Administrative Core

Christian Happi MPI – Research Hub Director

Professor of Molecular Biology and Genomics in the Department of Biological Sciences (Redeemer's University)
Director African Center of Excellence for Genomics of Infectious Diseases (ACEGID)

Projects 1 & 2

Stephen Obaro MPI

Professor, Pediatric Infectious Diseases (The University of Alabama at Birmingham, School of Medicine)

Data Management & Analysis Core (DMAC)

Derrick Fouts MPI

Professor of Human Genomic Medicine and Infectious Diseases - J. Craig Venter Institute (JCVI), USA

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DMAC CORE

Derrick E. Fouts PhD, Consortium Principal Investigator.

Dr. Fouts has a Ph.D. in Microbiology and is a Professor in the Department of Human Genomic Medicine at the JCVI. He is responsible for the technical oversight of the DMAC and all activities at JCVI. He interacts with the overall PI to optimize genomic analysis strategies and to help train and increase informatics analysis capacity in Africa.

Indresh Singh MS, Co-Investigator.

Mr. Singh has a MS in Computer Science and Engineering and is the Director of Informatics at JCVI. He leads the development and deployment of website, data management & analysis pipelines on CAMRA Cloud Infrastructure. Mr. Singh also train and advise ACEGID informatics staff on data depositions to public repositories.

Daniella Matute, MS, Bioinformatics Engineer.

Ms. Matute is a Bioinformatics Engineer at JCVI. She is responsible for developing, maintaining, integrating, and deploying bioinformatic tools, assist in data management and software supporting the project's mission.

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DMAC's Infrastructure
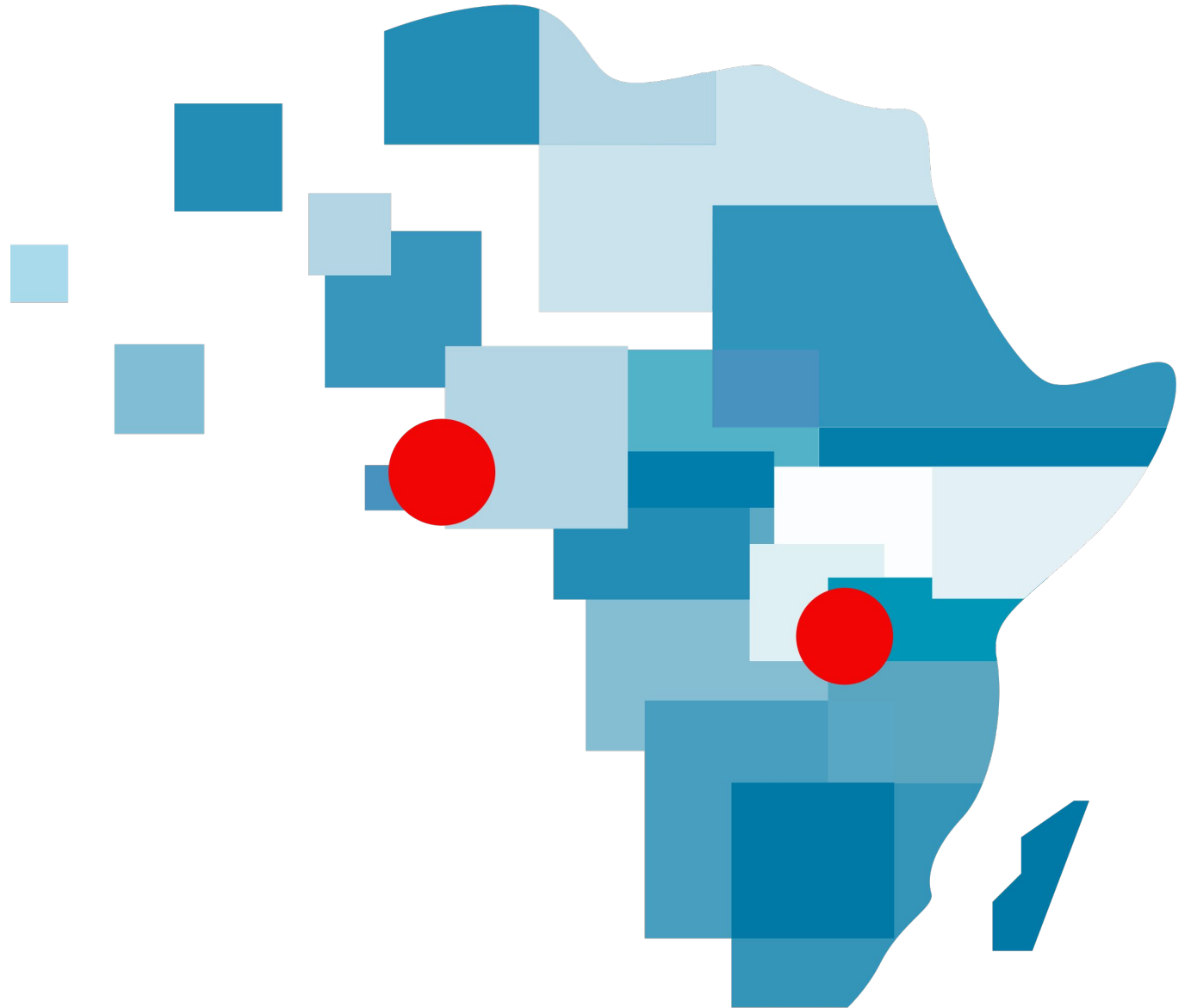
DMAC Tasks

1. Provide **data management, data analysis and data integration** for all projects.

2. Build **cloud based open-source bioinformatics tools** for analysis, training, and outreach (Terra).

3. Provide **resource sharing and dissemination** for all projects to the Africa Open Data Science Platform (DS-I Africa) and public repositories (NCBI).

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DMAC RESPONSIBILITIES

- Conduct Sequencing read QC, Assembly & Assembly QC, annotation on bacterial Isolates.

- Identify AMR genes and bacterial strains from whole genome sequence data for **Project 1.**

- Use novel bioinformatics tools to assist in determining the source(s) of Multidrug-resistant organisms (MDROs) causing human infections and spread of AMR for **Project 1.**

- Support the discovery of potentially novel biomarkers for development into diagnostics for **Project 2**

- Support the pilot projects and training of young African scientists.

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Types at Data at CAMRA

- **Clinical Specimens & Data**
  - Eligible participants <5 years of age with severe infection syndromes
  - Clinical Specimens' Meta-data
  - Time series data

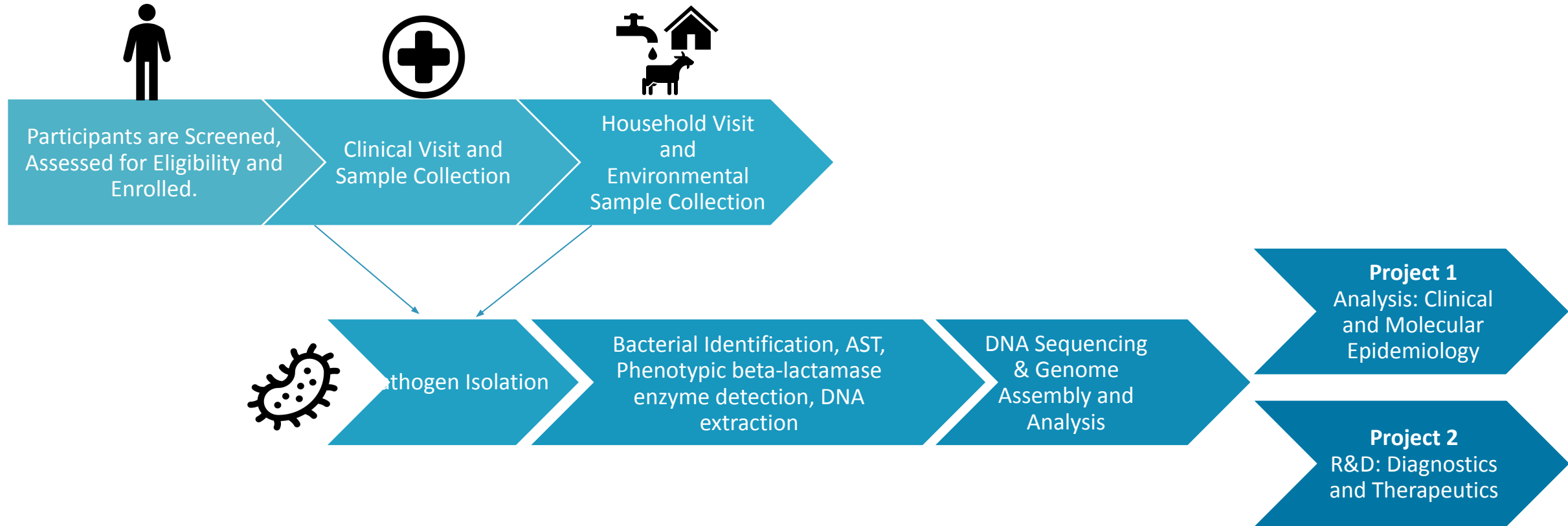- **Environmental Specimens & Data**
  - From participant's environment (e.g., Water source)
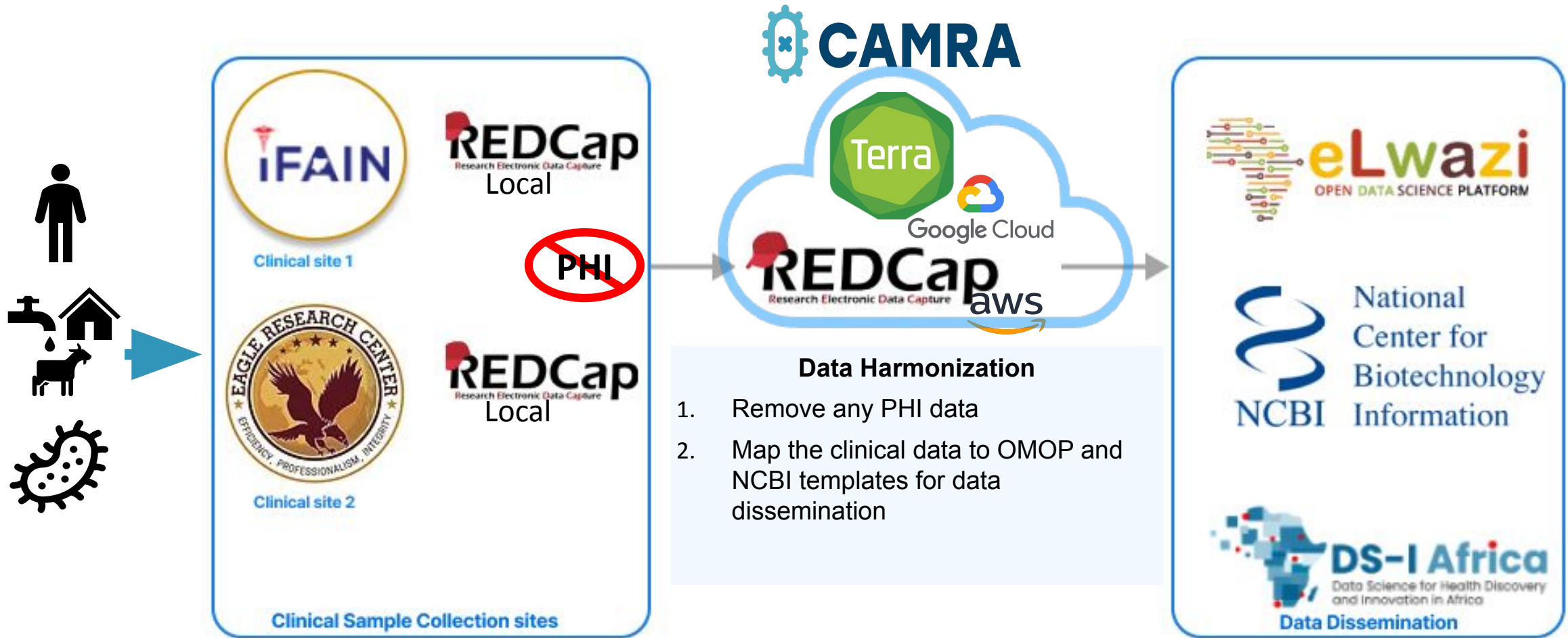 - Environmental Specimens' Meta-data

- **Bacterial Isolates**
  - From retrospective & prospective Clinical and Environmental Specimens
  - Bacterial Isolates' Meta-data and Analysis Data

Specimen and Data **Workflow**

Bacterial Isolate Processing Workflow

Prospective isolates
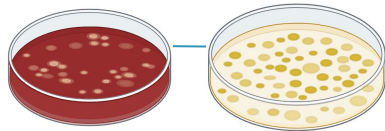
- Blood
- Spinal fluid
- Urine

Retrospective isolates

Household/ Environmental Sampling
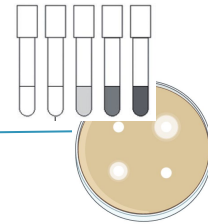
- Rectal swab
- Water
- Surfaces
- Animals

Selective & non selective culturing

Vitek2 Compact

Bacterial identification & AST

Phenotypic detection:
Microbroth dilution (ESBL & AmpC) & mCIM (carbapenemase typing)

selection

Illumina

Short reads

Nanopore

long reads

Terra

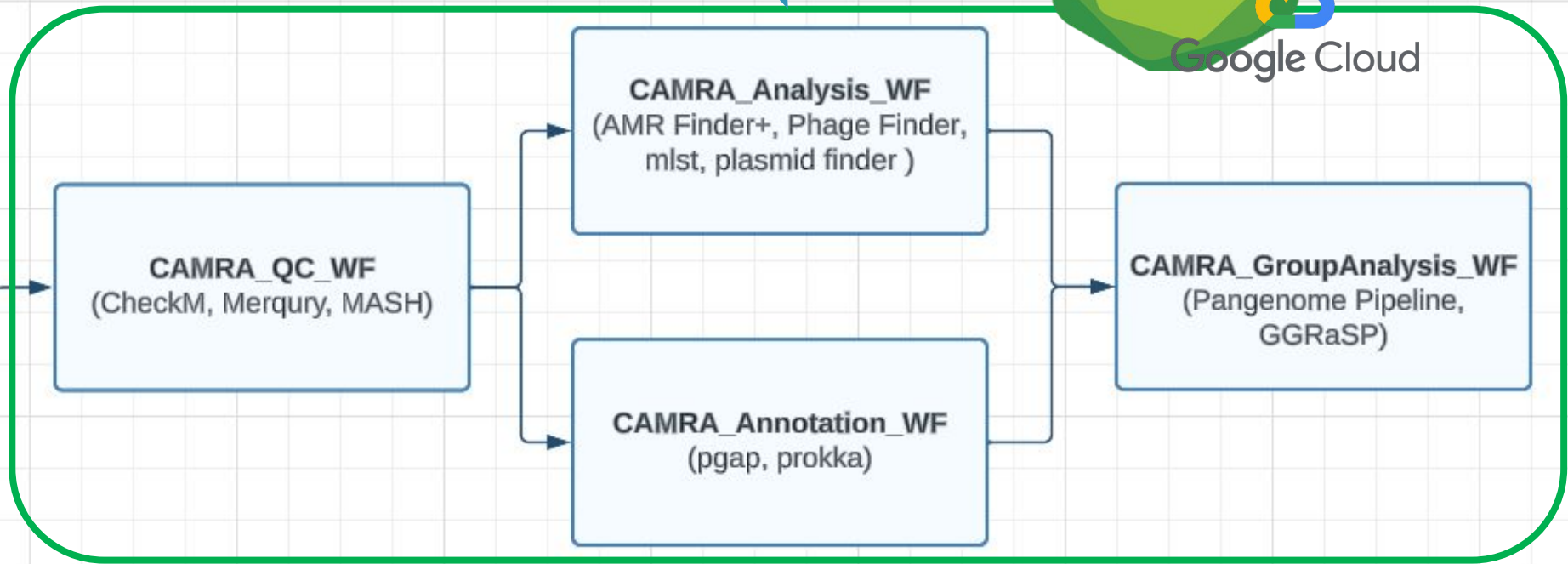Google Cloud

IFAIN/ERC

ACEGID

Bioinformatic Workflow

Cloud-Bioinformatics: Developing & Sharing Tools

Containerized applications

docker

- GGRASP
- PanOCT
- CheckM
- LOCUST
- Pan-genome Pipeline
- Pgap
- Merqury
- Plasmid Finder

Data processing workflows

{wdl}

- CAMRA_QC_WF
- CAMRA_Analysis_WF
- CAMRA_Annotation_WF
- CAMRA_GroupAnalysis_WF

Cloud Computing Environment

Terra

Google Cloud

Data Library	Workspaces	Workflows	Interactive Analysis
Access public and access-controlled datasets	Bring together data and tools into secure, shareable units	Run workflows at scale; bring your own or explore community favorites	Analyze data with built-in applications like Jupyter Notebooks, RStudio, Galaxy

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Mapping, Harmonization & FAIR Principles
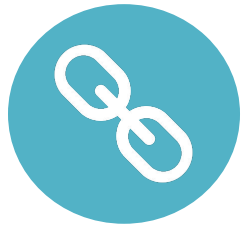
Harmonization & Mapping

- H&M Between RedCaps in CAMRA
- Mapping of Clinical Data to OMOP
  - Tool used: USAGI by OMOP
- Mapping to NCBI templates for Biosamples and SRA repositories

FAIR Principles

- Clinical and Isolate data will be indexed and publicly accessible in NCBI and eLwazi
- Persistent repositories such as DockerHub, Terra and GitHub will store tools for public use.
- Data and findings will be published in Scientific Papers
- Data will be formatted in commonly found standards within their fields (OMOP, NCBI templates etc.)
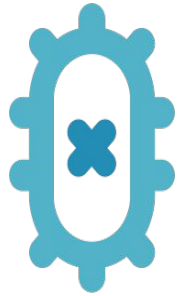
Links

- **WEBSITE:**
  https://camra.acegid.org/

- **Github:**
  https://github.com/JCVenterInstitute/CAMRA

- **Docker Images:**
  https://hub.docker.com/u/danylmb

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Thank you

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