UK Outbreak data analysis platform

Flexible high-performance compute area for pseudonymised data with explicit consent

Safe haven research space for analysis of pseudonymised data without consent

EMBARGO AREA

Curated data accessible to all contributors under strict publication embargo

RESEARCH DATA:

ISARIC4C TIER 0/1/2 hospitalised (2,914):

host whole genome seq

serial: multiomics

THATCIOTHICS

serology

viral load

PHOSP clinical follow-up: (1,075)

serial: multiomics

serology

host microarray genotype

COG-UK Viral whole genome seq (550,000)

GenOMICC Host whole genome (19,328)

UK-CIC immunology

LINKED DATA:

Summary (non-disclosive) clinical data

Supervised exports of non-disclosive data

LINKED RESEARCH DATA:

ISARIC4C TIER 0 (CO-CIN) (303,251)

ISARIC4C TIER 1/2 Multi-omics (2,914)

PHOSP clinical follow-up (1,075)

PHOSP TIER 1/2 multiomics

COG-UK Viral variant data (21,230)

GenOMICC Host variant data (19,328)

UK-CIC immunology

LINKED DATA (available):

NHS Digital England &Wales In/outpatient

NHS Scotland (SMR00/01) In/outpatient

Death records (Scotland)

Critical care audit (SICSAG)

LINKED DATA (planned):

Critical care audit (ICNARC)

NHS England&Wales Inpatient/Outpatient

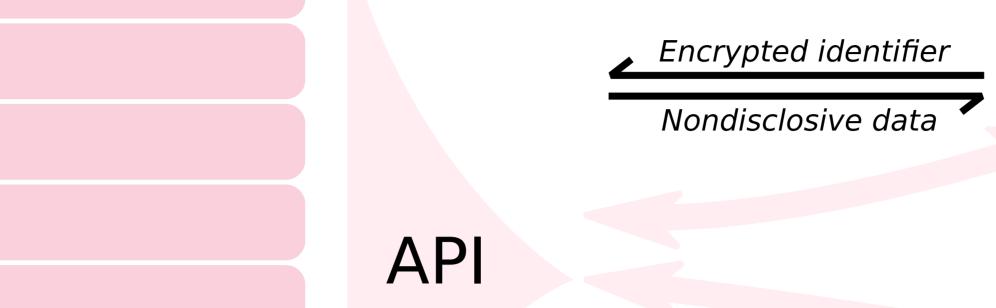
National immunisation database (NIMS)

Pillar 1/2 testing

NON-EMBARGO AREA

Curated data accessible to approved bona fide researchers for academic/commercial use

All data released by investigators at or before publication



UK Health Security Agency
Public Health England
Public Health Scotland
Public Health Wales
Public Health Nothern Ireland

Office for National Statistics

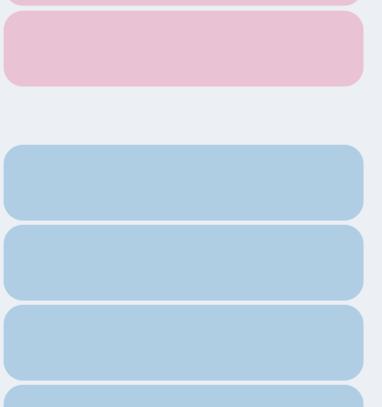
NHS Digital / OpenSafely

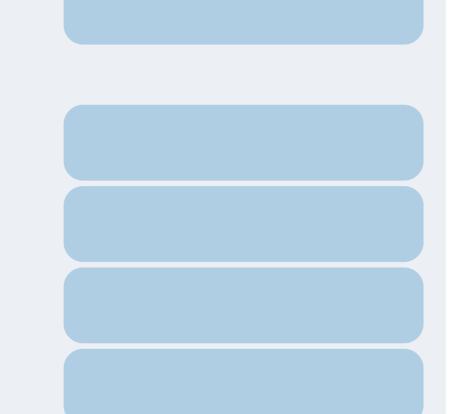
Other TREs

Supervised exports of non-disclosive data

All data released by investigators at or before publication







Public Health

England

Public Health Scotland Public Health Wales

Public Health NI Automated feed of viral genome data for clinical linkage

CLIMB COVID

UK PHA

UK academic instituions

NHS

Wellcome Sanger Institute

automated pipelines COG-UK Viral whole genome seq (550,000)

variant calling

viral evolution

phylogeny

automated deposit in open-access public databases UK Health Security Agency
Public Health England
Public Health Scotland
Public Health Wales
Public Health Nothern Ireland
International public databases

- GISAID
- ENA/INSDC