## **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 NON

Curated data accessible to all contributors under strict publication embargo

# RESEARCH DATA:

ISARIC4C TIER 0/1/2 hospitalised (2,510):

host whole genome seq

serial: multiomics

serology

viral load

PHOSP clinical follow-up: (1,075)

host microarray genotype

serial: r

multiomics

serology

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

GenOMICC Host whole genome (18,076)

UK-CIC immunology

LINKED DATA:

Summary (non-disclosive) clinical data

Supervised exports of non-disclosive data

### LINKED RESEARCH DATA:

ISARIC4C TIER 0 (CO-CIN) (270,230)

ISARIC4C TIER 1/2 Multi-omics (2,510)

PHOSP clinical follow-up (1,075)

PHOSP TIER 1/2 multiomics

COG-UK Viral variant data (21,230)

GenOMICC Host variant data (18,076)

**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

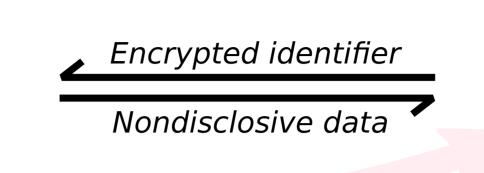
National immunisation database (NIMS)

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



API

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 academic instituions
NHS

Wellcome Sanger Institute

UK PHA

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