

Kao group and COVID – lessons learned

Dr Anthony Wood

CERSE Meeting, Roslin Institute

31 May 2023

Me

- 2011 - 2015 **MSci Theoretical Physics** (Nottingham)
- 2015 - 2019 **PhD Theoretical Physics** (Edinburgh)
 - *Nonequilibrium statistical mechanics*
 - *Mathematica, MATLAB, pen and paper*
 - Learned: how to go about solving a problem
- 2019 - 2021 **Industry** (fintech)
 - Automating *reconciliation* of trading data from different sources (traders, banks, Bloomberg etc)
 - *SQL, Excel*
 - Learned: how to deal with high-freq/high-volume/messy/“real” data
- 2021 - **Postdoc @ Roslin, Kao group**
 - Applying data science to understand patterns in infectious diseases
 - *R*
 - Learned: how to pull insightful things from data

Kao group

Mix of vets, mathematicians, physicists, software engineers, computer scientists

Present

- Rowland Kao
- Anthony Wood
- Tijani Sulaimon
- Anna Gamza
- ★ Chris Banks
- Ewan Colman
- ★ Aeron Sanchez
- Muhammad Bilal

★ Software Engineers

Past

- Paul Bessell
- Anne-Sophie Ruget
- ★ Tom Doherty
- Sam Lycett
- Gianluigi Rossi
- Jess Enright
- Gavrila Puspitarani

Collaborators

- Anne Marie MacKintosh
- Martine Stead

Models of infectious disease transmission (often informed by “big” data)

- **Networks**
 - Derived from populations, trading patterns, sewers, commutes, Twitter...
- **Genetic sequences**
 - Comparing samples to infer who-infected whom

Current diseases

- Rift Valley fever
- Avian influenza
- Bovine viral diarrhoea
- “Rumours and behaviour”
- Bovine TB
- COVID-19

What happened in COVID-19?

Kao group

- **Early access to detailed data**
- Experience in disease modelling

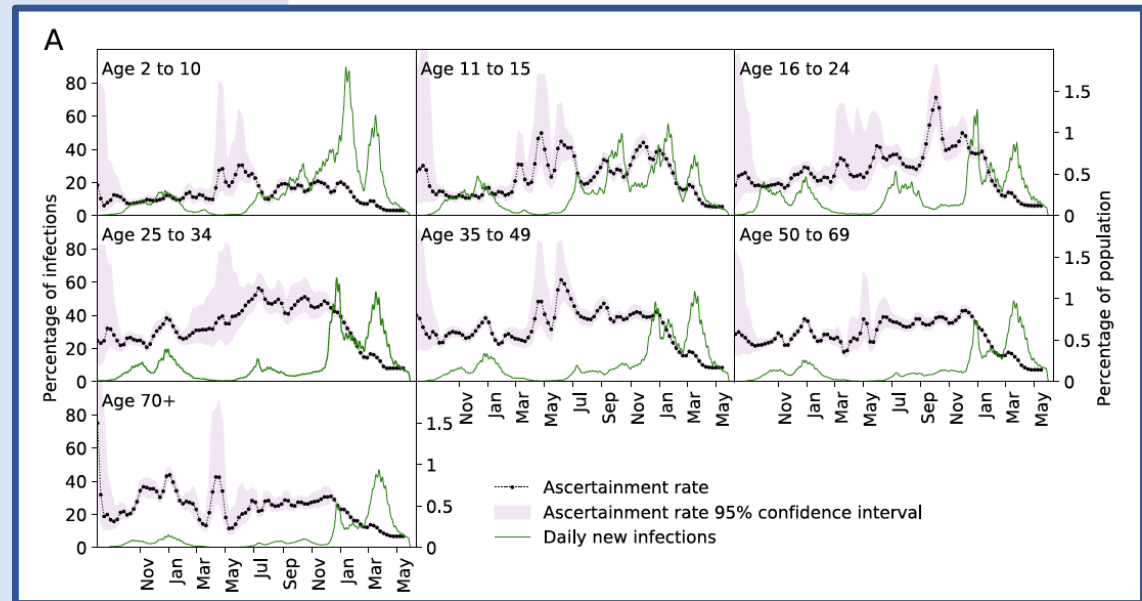
Kao group

- Early access to detailed data
- Experience in disease modelling

Modelling case ascertainment

Estimating true number of infections as opposed to cases

Colman et al. 2023
Journal of Theoretical Biology
<https://doi.org/10.1016/j.jtbi.2022.111333>



Kao group

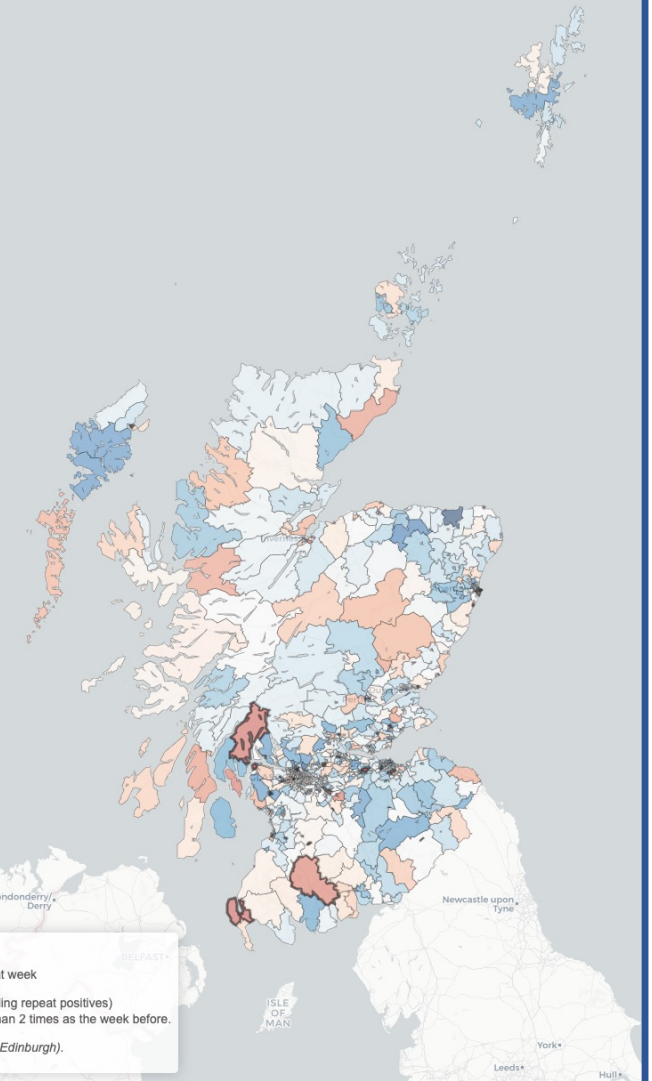
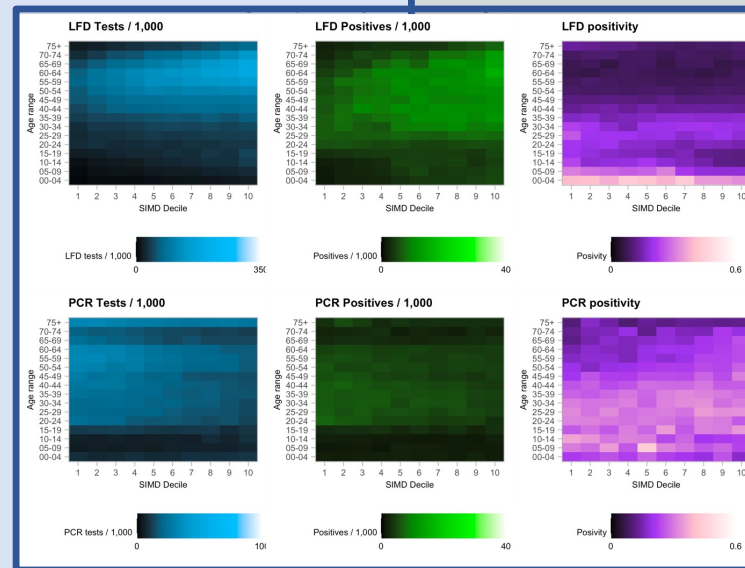
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Estimating true number of infections as opposed to cases

Real-time analysis of COVID-19 outcomes

Emphasis on variation with socioeconomic deprivation



Confirmed cases by IZ: 2022-07-06 - 2022-07-12
Tests: Total number of LFD tests reported, of any result, in that week
Cases: Total reported cases that week (including PCR, excluding repeat positives)
Highlighted spikes: IZs reporting at least 10 cases, and more than 2 times as the week before.
Created by Anthony Wood (The Roslin Institute, University of Edinburgh).

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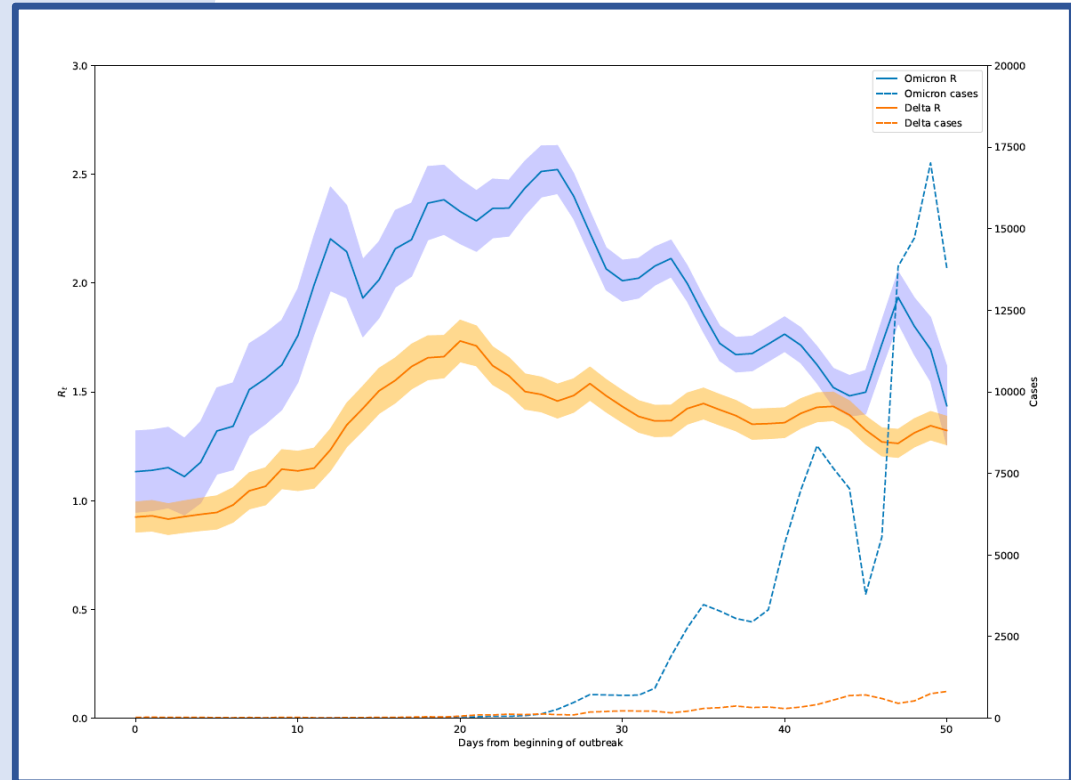
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Emphasis on variation with socioeconomic deprivation

R-value estimates

Using existing case numbers to estimate past + present R-value locally

Chris Banks, Aeron Sanchez



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Models of wastewater shedding

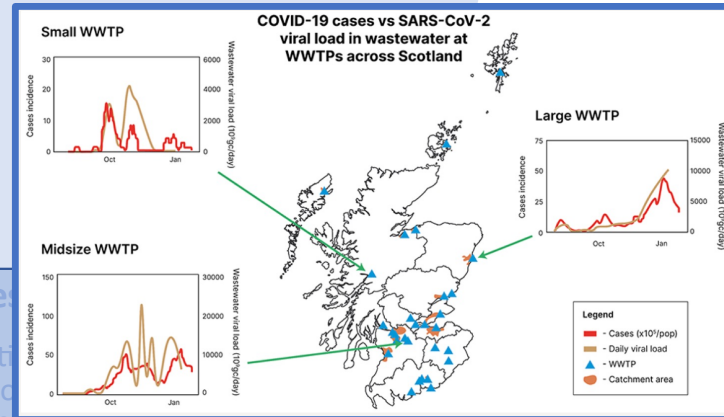
Prevalence vs shedding concentration

Optimal monitoring strategies with limited budget

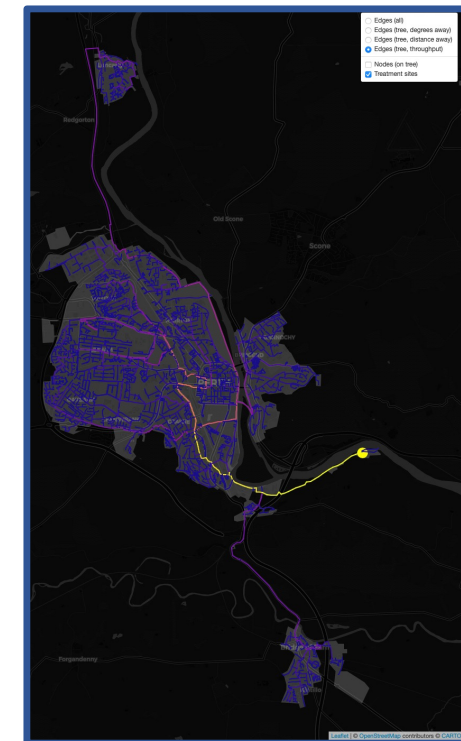
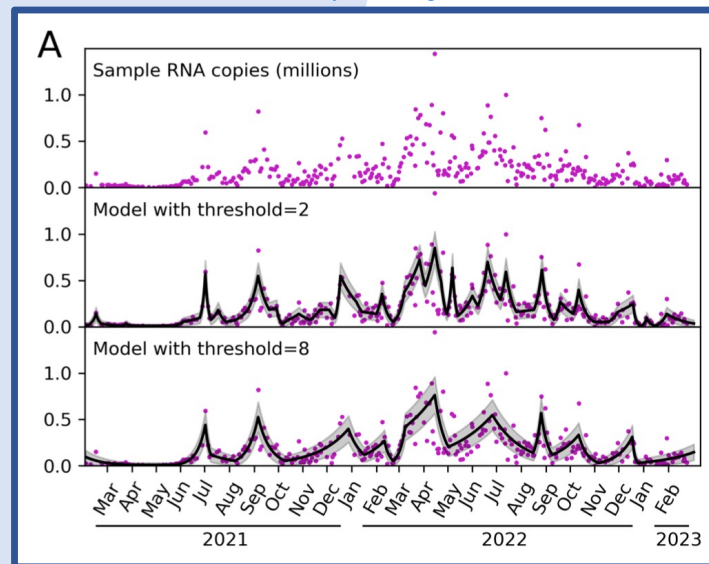
R-value estimation

Using existing numbers to estimate R-value locally

Fitzgerald, Rossi et al
Environmental Science & Technology
<https://doi.org/10.1021/acs.est.1c05029>



Colman, Kao 2022
Medrxiv preprint
<https://doi.org/10.1101/2023.03.07.23286904>



Anthony Wood, Jess Enright, Rowland Kao
Ongoing work

Kao group

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- Experience in disease modelling

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Real-time monitoring of vaccine uptake

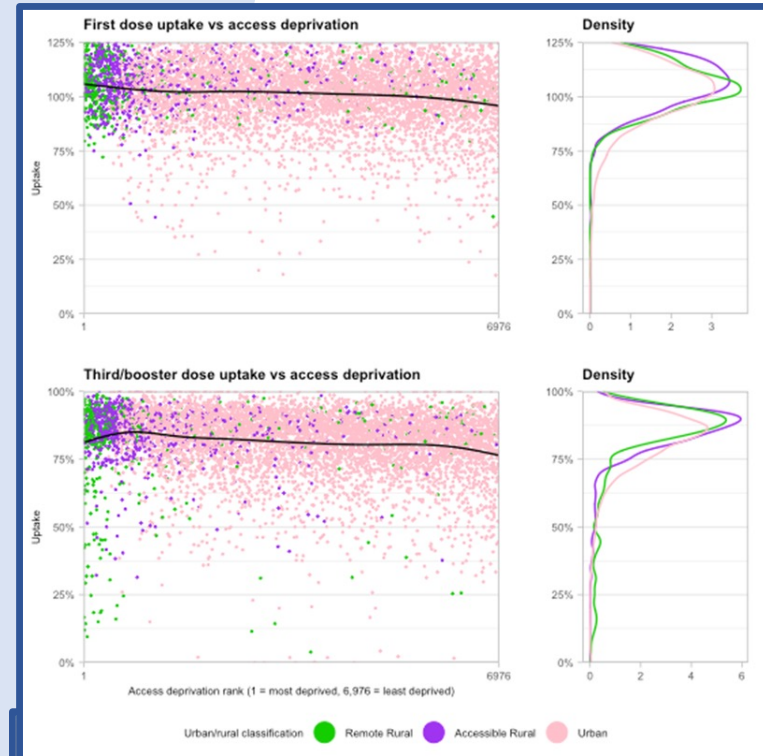
Highlighting regions of “low uptake” (hesitancy) and “slow uptake” (logistics)

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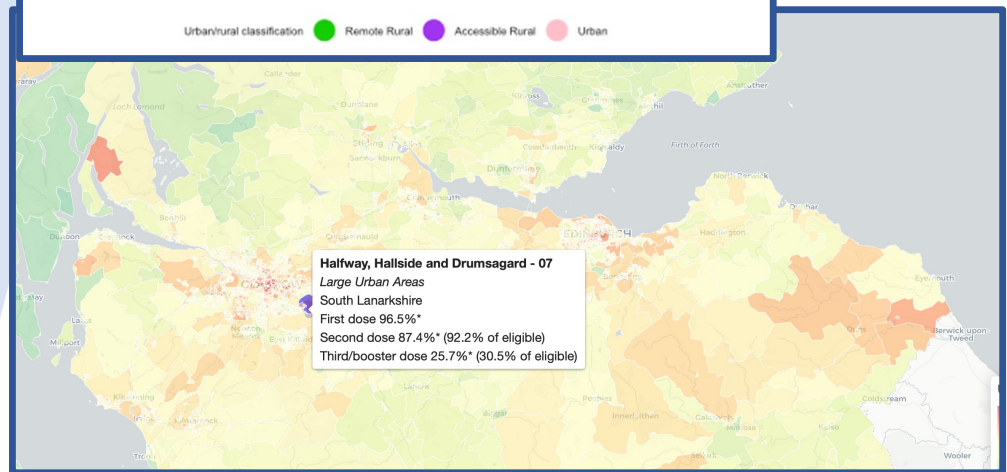
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Optimal monitoring strategies with limited budget

Anthony Wood



Anna Gamza (in prep.)



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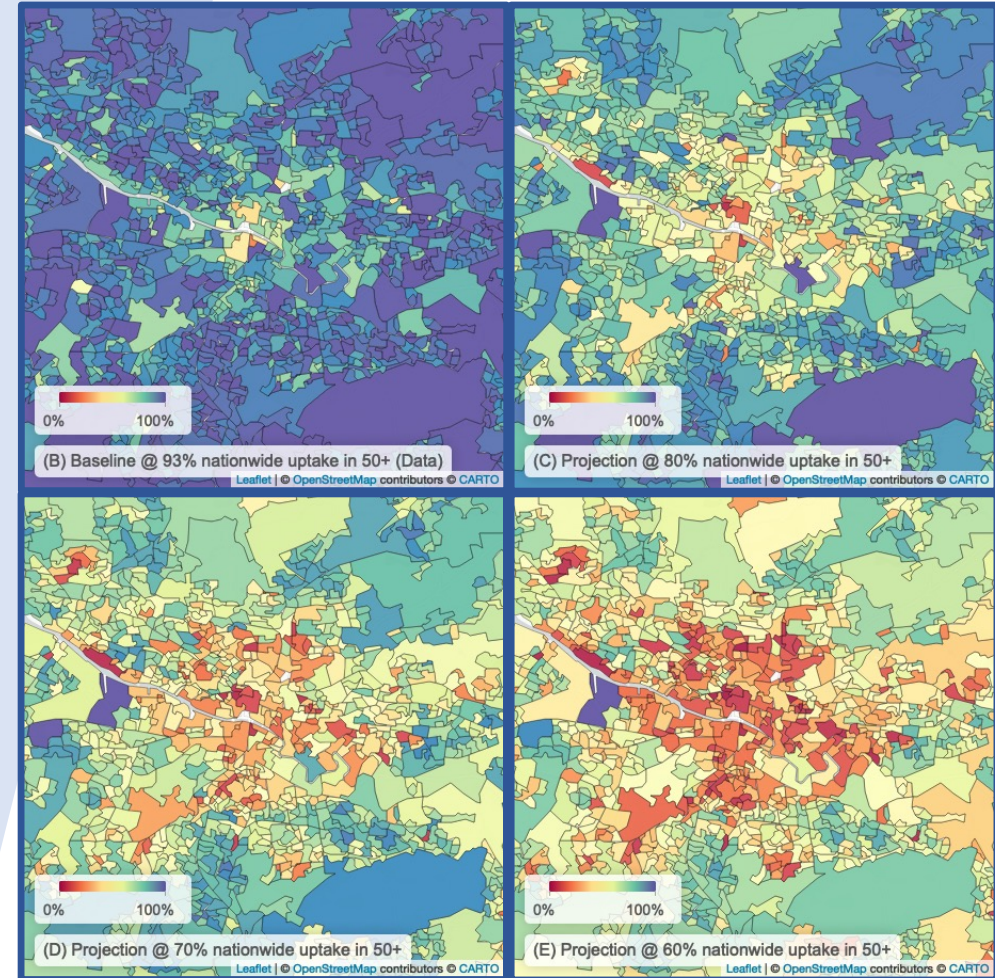
Predictive models of future vaccine uptake

Predicting variation in uptake “fall-off” with future boosters

Wood et al.

Medrxiv preprint

<https://doi.org/10.1101/2022.08.30.22279415>



Predicted vaccine uptake in Central Glasgow

Kao group

- Early access to detailed data
- Experience in disease modelling

SCoVMod: Scotland's Coronavirus Model

Individual-level model of disease spread across Scotland
Forecasts under different restrictions

Cattle disease model, rapidly adapted (early 2020) to COVID/humans by RSE

- Test driven development
- Paired programming

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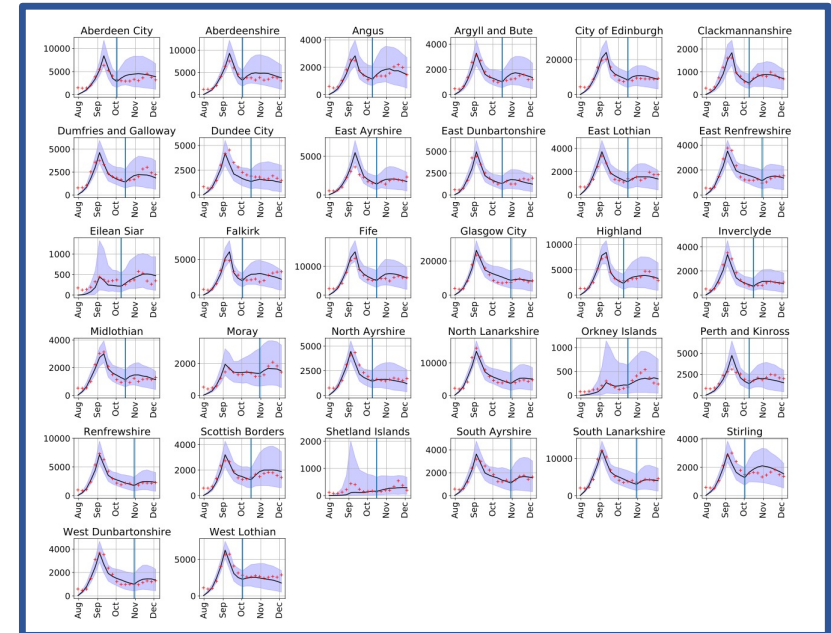
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Banks et al. 2022
Wellcome Open Research
<https://doi.org/10.21956%2Fwellcomeopenres.19604.r50789>

Banks et al. 2022
arXiv preprint
<https://doi.org/10.48550/arXiv.2211.13704>



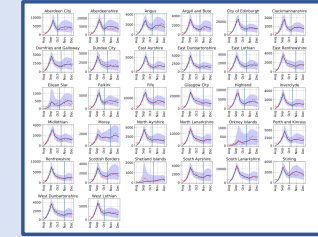
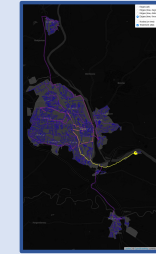
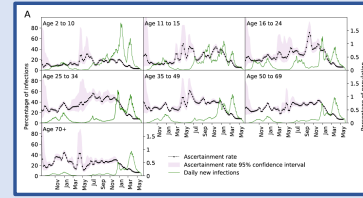
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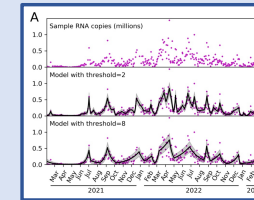
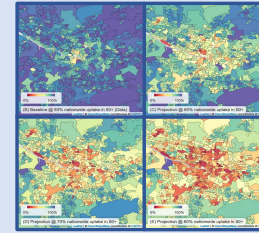
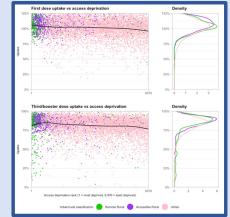
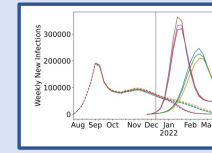
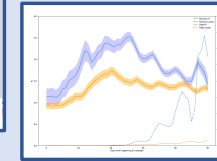
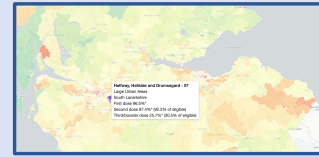
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Weekly
Daily
Ad-hoc

SPI-M / SAGE

Public Health Scotland

Scottish Government

Coronavirus lockdown 'avoided thousands of deaths' in Scotland

30 June 2020



By David Cowan
BBC Scotland

A study has suggested between 7,000 and 40,000 people could have died from coronavirus in Scotland if the country had not gone into lockdown.

Scientists have tried to estimate would have happened if Scotland had copied the approach taken in Sweden, where a lockdown was not imposed.

Rowland Kao, a professor of epidemiology and data science at Edinburgh University, led the team which carried out the research for BBC Scotland.

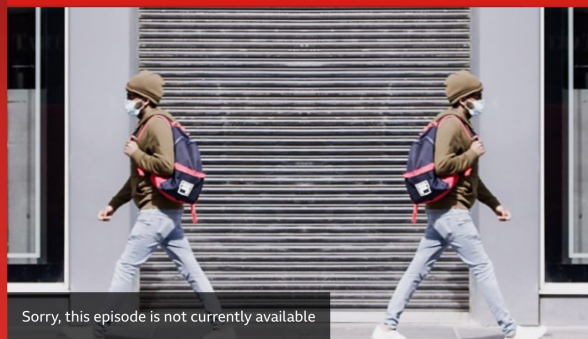
He said: "An obvious question to ask is if Scotland had done something similar to Sweden, would we have had a similar outcome without all the restrictions."

Although there was no lockdown, Sweden relied on voluntary social distancing, banning gatherings of more than 50 people and halting visits to elderly care homes.

"We took the relative amount of transmission going on in Sweden, translated that over to Scotland and looked at what the resultant number of deaths would have been had we taken that approach."

one Disclosure

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Sorry, this episode is not currently available

Scotland's Lockdown Series 2

Investigation into government handling of the Covid 19 pandemic. Reporter Mark Daly investigates the decisions made and asks whether Scotland could or should have locked down sooner. Disclosure speaks to scientists desperate to keep us safe and meets the families hardest hit by the virus.

29 minutes

Scottish Government
Riaghaidh na h-Alba

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Coronavirus (COVID-19): modelling the epidemic (Issue No. 107)

Published: 1 September 2022
From: Director-General Health and Social Care
Directorate: Constitution Directorate
Part of: Coronavirus in Scotland
ISBN: 9781804359105

Latest findings in modelling the COVID-19 epidemic in Scotland, both in terms of the spread of the disease through the population (epidemiological modelling) and of the demands it will place on the system, for example in terms of health care requirement.

This document is part of a collection

Supporting documents

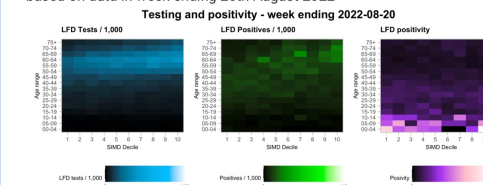
Summary of spatial analysis of Covid-19 spread in Scotland

Researchers at the Edinburgh Roslin Institute have conducted spatial analysis of COVID-19 Spread in Scotland. A summary of findings from data up to 25th August 2022 is included here.

Rates of LFD and PCR testing are stabilising, albeit at very low levels (1-2 LFD tests reported, per week, per 1,000).

The distribution of lateral flow/LFD tests being reported varies substantially by both age and deprivation status, with many fewer tests reported in younger adults across all deciles of deprivation, and for children in more deprived deciles. The high level of LFD positivity in the latter category is marked, and when compared to the high number of positives amongst the least deprived, suggests that ascertainment may be lower in younger people in deprived areas.

Figure 11: Variation in testing outcomes comparing Lateral Flow and PCR testing considering age and deprivation status of the data zone of record based on data in week ending 20th August 2022



My experience

Notable development in my programming

- from smaller, self-contained code to perform simpler tasks to
- “large”, complex scripts that
 - Are central to work that ends up in peer-review
 - Require extreme care with storage of data
 - Have spin-offs with short turnarounds
- Essential that the work is **reproducible**
 - My process for COVID was good *enough*, but very manual and caused some headaches later on

Resolutions

- At the start of a new project, take time to set up processes for **version control, sharing, standardising of code structure**
- Essential for my next project: The *aim* is to develop methods to be used by others!
- 2-3 days spent at the start of a project learning some basic git commands saves weeks later on!

```
1 # Script
2
3 # A stochastic_solutions.R
4
5
6 # Purpose
7 # - Initial exploration of master equations and trajectories for dual processes for epidemiology and substitution
8 # - This is the stochastic element - the analytic solution was in A_RFE_solutions.R, 2023-03-16: This no longer replicates the deterministic solution
9 # - and a new piece of code would need writing to verify A_RFE_solutions.R output
10
11 # - 2023-01-13: Addition of transmission trees
12 # - 2023-01-17: Removal of substitution (can be added later to the trees as an independent process), addition of heterogeneous infection rate
13 # - 2023-03-16: This no longer replicating the RFE solution
14
15 # Author
16 # - Anthony Wood, Roslin Institute (Kao group), University of Edinburgh
17
18 # Email
19 # - anthony.wood@ed.ac.uk
20
21 # Date created
22 # - 2022-10-31
23
24
25
26
27 # (0) Establish working directory, required packages, source files
28
29
30 # Working directory
31 setwd("~/Users/awood110/Desktop/btb")
32
33 # Required packages, and why I'm using them
34 library(tidyverse) # Tidyverse
35 options(dplyr.summarise.inform = FALSE) # Avoid message when summarising by multiple groups
36 library(RColorBrewer) # Colour palette
37 library(gtools) # For permutations with replacement
38 library(rop) # For rollups
39 library(crayon) # Print output text in different colours
40 library(igraph) # Network building
41 library(ggally) # Plot networks
42 library(gridExtra) # grid.arrange function
43
44 # Clear all vars
45 rm(list = ls())
46
47 # Source files (if required)
48 source("code/_state_details.R") # Function for pulling the details of all possible microstates - used in both the analytic and numerical code
49
50 # Full outer join function
51 full_outer_join = function(x,y, nameX = "x", nameY = "y"){tibble(x) %>% full_join
52
53
54
55 # (1) Defining parameters, and the state
56
```

The screenshot shows the GitHub interface for a repository named 'btb'. At the top, it displays 'Project ID: 9351', '103 Commits', '1 Branch', '0 Tags', '4.9 MB Files', and '4.9 MB Storage'. Below this, there are buttons for 'History', 'Find file', 'Web IDE', and 'Clone'. A commit by user 'awood310' is highlighted, with a commit message 'Small edits'. Below the commit list, there is a table of repository files and folders with their last commit details.

Name	Last commit	Last update
_bin	Further analysis on max likelihood algorithm	1 month ago
_template	Minor changes	4 months ago
mathematica	Small edits	6 days ago
parse_rawdata	Continuing application of likelihood work t...	1 week ago
.DS_Store	Saving mathematica file before fix	1 week ago
A_RFE_solutions.R	Exporting functional form of likelihood into R	1 month ago
A_WP_pair_likelihood.R	Small edits	6 days ago
A_fasta_exploration.R	Further work on KFE likelihoods. New file a...	2 weeks ago