Covid in Georgia

Josephine Walker

31/07/2020

## Intro

Georgia reported their first confirmed case of Covid-19 on 26 February 2020. As of 2 July 2020, only 939 confirmed cases and 15 deaths have been reported. The success of Georgia’s limitation of spread of Covid-19 can be attributed to early non-pharmaceutical interventions including closing schools (early March), closing borders and mandatory quarantining of international arrivals, lockdown of individual affected areas (late March) and full lockdown throughout the country (30 March). Alongside this, they have implemented extensive contact tracing and testing, and all confirmed cases are treated in hospital. There is regular screening of key workers. As of 2 July 2020, 117,701 PCR tests for Covid-19 have been conducted, a rate of more than 30,000 tests per million population.

Here we use test data and contact tracing data collected by the National Center for Disease Control (NCDC) in Georgia to characterize the epidemic in Georgia. This includes demographics of those infected compared to the general population, symptom and death rates by age, and rates of transmission to different types of contacts. We also calculate the secondary attack rate for different types of contacts and overall number of secondary cases per primary case (observed reproductive number).

## Methods

### Data collection

* Types of test used, criteria for testing (case identification).
  + A variety of test types were used, here we present the results from antigen tests confirming current infection, primarily real time PCR tests. [In the database as confirmation test result]
  + Data exported on 24 June 2020 [match numbers in intro to data we have]
* More detail on policies - maybe in a figure
* Ethics waiver from NCDC and registered in Bristol

### Analysis

* De-identified personal IDs used to link contact tracing database to confirmed cases
* Data cut off date 24 June 2020
* Analysis conducted in R
* Can we compare demographics of infection to national demographics? geostat or other source?

## Results

##   
## Attaching package: 'lubridate'

## The following object is masked from 'package:base':  
##   
## date

##   
## Attaching package: 'dplyr'

## The following objects are masked from 'package:lubridate':  
##   
## intersect, setdiff, union

## The following objects are masked from 'package:stats':  
##   
## filter, lag

## The following objects are masked from 'package:base':  
##   
## intersect, setdiff, setequal, union

### Table of demographics of those infected (treated database)

Hospitalization data and comorbidities were available for 500 diagnosed patients with hospitalization dates ranging from to -. Could add more detail here on particular symptoms if of interest.

##   
## Attaching package: 'data.table'

## The following objects are masked from 'package:dplyr':  
##   
## between, first, last

## The following objects are masked from 'package:lubridate':  
##   
## hour, isoweek, mday, minute, month, quarter, second, wday, week,  
## yday, year

##   
## Attaching package: 'arsenal'

## The following object is masked from 'package:lubridate':  
##   
## is.Date

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Female (N=253) | Male (N=247) | Total (N=500) | p value |
| **Age (years)** |  |  |  | < 0.001 |
| Mean (SD) | 45.783 (19.503) | 39.615 (18.716) | 42.736 (19.347) |  |
| Median (Q1, Q3) | 47.000 (32.000, 59.000) | 39.000 (25.500, 52.000) | 44.000 (29.000, 56.250) |  |
| Min - Max | 2.000 - 90.000 | 0.000 - 86.000 | 0.000 - 90.000 |  |
| Missing | 0 | 0 | 0 |  |
| **Age group** |  |  |  | 0.154 |
| 0-14 | 18 (7.1%) | 22 (8.9%) | 40 (8.0%) |  |
| 15-19 | 9 (3.6%) | 11 (4.5%) | 20 (4.0%) |  |
| 20-29 | 27 (10.7%) | 40 (16.2%) | 67 (13.4%) |  |
| 30-59 | 137 (54.2%) | 134 (54.3%) | 271 (54.2%) |  |
| 60-69 | 37 (14.6%) | 22 (8.9%) | 59 (11.8%) |  |
| 70+ | 25 (9.9%) | 18 (7.3%) | 43 (8.6%) |  |
| Missing | 0 | 0 | 0 |  |
| **Intensive care** |  |  |  | 0.363 |
| No | 230 (90.9%) | 230 (93.1%) | 460 (92.0%) |  |
| Yes | 23 (9.1%) | 17 (6.9%) | 40 (8.0%) |  |
| Missing | 0 | 0 | 0 |  |
| **Disease severity** |  |  |  | 0.294 |
| critical | 13 (5.1%) | 10 (4.0%) | 23 (4.6%) |  |
| mild | 130 (51.4%) | 145 (58.7%) | 275 (55.0%) |  |
| moderate | 86 (34.0%) | 77 (31.2%) | 163 (32.6%) |  |
| Severe | 24 (9.5%) | 15 (6.1%) | 39 (7.8%) |  |
| Missing | 0 | 0 | 0 |  |
| **Length of hospital stay** |  |  |  | 0.449 |
| Mean (SD) | 22.249 (8.699) | 21.476 (8.420) | 21.868 (8.563) |  |
| Median (Q1, Q3) | 21.000 (16.000, 27.000) | 21.000 (16.000, 25.750) | 21.000 (16.000, 27.000) |  |
| Min - Max | 4.000 - 65.000 | 2.000 - 52.000 | 2.000 - 65.000 |  |
| Missing | 0 | 1 | 1 |  |
| **Outcome** |  |  |  | 0.173 |
| dead | 9 (3.6%) | 4 (1.6%) | 13 (2.6%) |  |
| recovered | 244 (96.4%) | 243 (98.4%) | 487 (97.4%) |  |
| Missing | 0 | 0 | 0 |  |
| **Diagnosis date** |  |  |  | 0.846 |
| Nmiss | 34 | 31 | 65 |  |
| median | 2020-04-13 | 2020-04-14 | 2020-04-13 |  |
| Min - Max | 2020-03-05 - 2020-05-02 | 2020-03-04 - 2020-05-02 | 2020-03-04 - 2020-05-02 |  |
| **Place of exposure** |  |  |  | 0.465 |
| American Samoa (AS0000) | 2 (0.9%) | 4 (1.9%) | 6 (1.4%) |  |
| Armenia (AM0000) | 0 (0.0%) | 1 (0.5%) | 1 (0.2%) |  |
| Austria (AT0000) | 0 (0.0%) | 1 (0.5%) | 1 (0.2%) |  |
| Azerbaijan (AZ0000) | 2 (0.9%) | 1 (0.5%) | 3 (0.7%) |  |
| Belarus (BY0000) | 0 (0.0%) | 2 (0.9%) | 2 (0.5%) |  |
| belgium (BE0000) | 0 (0.0%) | 1 (0.5%) | 1 (0.2%) |  |
| Brazil (BR0000) | 0 (0.0%) | 1 (0.5%) | 1 (0.2%) |  |
| British Virgin Islands(VG0000) | 0 (0.0%) | 1 (0.5%) | 1 (0.2%) |  |
| France (FR0000) | 2 (0.9%) | 5 (2.4%) | 7 (1.6%) |  |
| Georgia (GG0000) | 190 (87.6%) | 172 (81.1%) | 362 (84.4%) |  |
| Germany (DE0000) | 1 (0.5%) | 1 (0.5%) | 2 (0.5%) |  |
| Israel (IL0000) | 1 (0.5%) | 0 (0.0%) | 1 (0.2%) |  |
| Italy (IT0000) | 3 (1.4%) | 3 (1.4%) | 6 (1.4%) |  |
| Russia (RU0000) | 3 (1.4%) | 5 (2.4%) | 8 (1.9%) |  |
| Spain (ES0000) | 1 (0.5%) | 6 (2.8%) | 7 (1.6%) |  |
| Turkey (TR0000) | 7 (3.2%) | 5 (2.4%) | 12 (2.8%) |  |
| UK (UK0000) | 3 (1.4%) | 1 (0.5%) | 4 (0.9%) |  |
| United Arab Emirates (AE0000) | 2 (0.9%) | 1 (0.5%) | 3 (0.7%) |  |
| USA (US0000) | 0 (0.0%) | 1 (0.5%) | 1 (0.2%) |  |
| Missing | 36 | 35 | 71 |  |
| **Asymptomatic** |  |  |  | 0.371 |
| no | 174 (79.5%) | 173 (80.1%) | 347 (79.8%) |  |
| unknown | 2 (0.9%) | 0 (0.0%) | 2 (0.5%) |  |
| yes | 43 (19.6%) | 43 (19.9%) | 86 (19.8%) |  |
| Missing | 34 | 31 | 65 |  |

###Table of demographics of those tested (tested database)

A total of 96317 antigen (PCR) test results were available, with 67886 unique individual patient IDs recorded.

## [1] "2080-01-21"

## [1] "1902-01-01"

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | neg (N=94109) | pos SARS-CoV-2 (N=1947) | Suspicted (N=261) | Total (N=96317) | p value |
| **Age** |  |  |  |  | 0.713 |
| Mean (SD) | 41.961 (18.113) | 41.849 (19.992) | 42.969 (19.382) | 41.962 (18.156) |  |
| Median (Q1, Q3) | 41.000 (29.000, 55.000) | 43.000 (27.000, 57.000) | 43.000 (30.000, 56.000) | 41.000 (29.000, 55.000) |  |
| Min - Max | 0.000 - 102.000 | 0.000 - 91.000 | 0.000 - 90.000 | 0.000 - 102.000 |  |
| Missing | 88 | 1 | 0 | 89 |  |
| **Gender** |  |  |  |  | 0.004 |
| Female | 51047 (54.2%) | 1001 (51.4%) | 129 (49.4%) | 52177 (54.2%) |  |
| male | 43023 (45.7%) | 945 (48.5%) | 131 (50.2%) | 44099 (45.8%) |  |
| N/A | 39 (0.0%) | 1 (0.1%) | 1 (0.4%) | 41 (0.0%) |  |
| Missing | 0 | 0 | 0 | 0 |  |
| **Fever** |  |  |  |  | < 0.001 |
| No | 6650 (32.1%) | 87 (20.3%) | 14 (31.1%) | 6751 (31.9%) |  |
| Yes | 14037 (67.9%) | 342 (79.7%) | 31 (68.9%) | 14410 (68.1%) |  |
| Missing | 73422 | 1518 | 216 | 75156 |  |
| **Cough** |  |  |  |  | < 0.001 |
| No | 13454 (67.5%) | 196 (47.3%) | 32 (72.7%) | 13682 (67.1%) |  |
| Yes | 6486 (32.5%) | 218 (52.7%) | 12 (27.3%) | 6716 (32.9%) |  |
| Missing | 74169 | 1533 | 217 | 75919 |  |
| **Risk Group** |  |  |  |  | < 0.001 |
| 53/5000 | 1 (0.0%) | 0 (0.0%) | 0 (0.0%) | 1 (0.0%) |  |
| Ambulance driver | 7478 (8.9%) | 4 (0.2%) | 9 (3.7%) | 7491 (8.7%) |  |
| Being on dialysis | 342 (0.4%) | 0 (0.0%) | 1 (0.4%) | 343 (0.4%) |  |
| Beneficiary of a fever or COVID clinic | 13397 (15.9%) | 1338 (69.2%) | 85 (35.0%) | 14820 (17.1%) |  |
| Contact of Confirmed case | 5485 (6.5%) | 158 (8.2%) | 24 (9.9%) | 5667 (6.6%) |  |
| Defined by the standard definition of accident | 1 (0.0%) | 0 (0.0%) | 0 (0.0%) | 1 (0.0%) |  |
| Dialysis staff | 17 (0.0%) | 0 (0.0%) | 0 (0.0%) | 17 (0.0%) |  |
| Employee of COVID Clinic | 5431 (6.4%) | 12 (0.6%) | 3 (1.2%) | 5446 (6.3%) |  |
| Employee of other hospitals | 13483 (16.0%) | 11 (0.6%) | 12 (4.9%) | 13506 (15.6%) |  |
| Employees of the customs and border checkpoint | 3569 (4.2%) | 3 (0.2%) | 9 (3.7%) | 3581 (4.1%) |  |
| Epidemiologist of the NCDC and / or PHC Centers | 560 (0.7%) | 0 (0.0%) | 0 (0.0%) | 560 (0.6%) |  |
| Fever and respiratory disease | 7024 (8.3%) | 107 (5.5%) | 17 (7.0%) | 7148 (8.3%) |  |
| Justice and MIA Customs Services | 59 (0.1%) | 0 (0.0%) | 0 (0.0%) | 59 (0.1%) |  |
| Other Risk groups | 2217 (2.6%) | 6 (0.3%) | 1 (0.4%) | 2224 (2.6%) |  |
| Patients from other hospitals | 1095 (1.3%) | 1 (0.1%) | 1 (0.4%) | 1097 (1.3%) |  |
| PCR Lab staff | 157 (0.2%) | 0 (0.0%) | 0 (0.0%) | 157 (0.2%) |  |
| PHC staff | 40 (0.0%) | 0 (0.0%) | 0 (0.0%) | 40 (0.0%) |  |
| Pneumonia | 1103 (1.3%) | 10 (0.5%) | 3 (1.2%) | 1116 (1.3%) |  |
| psshemtkhvevis st’andart’uli ganmart’ebit gansazghvruli | 1 (0.0%) | 0 (0.0%) | 0 (0.0%) | 1 (0.0%) |  |
| Psychiatric clininc staff | 98 (0.1%) | 0 (0.0%) | 1 (0.4%) | 99 (0.1%) |  |
| Public Transport staff | 115 (0.1%) | 0 (0.0%) | 0 (0.0%) | 115 (0.1%) |  |
| Quarantine zone beneficiaries | 14031 (16.7%) | 143 (7.4%) | 54 (22.2%) | 14228 (16.5%) |  |
| Quarantine zone staff | 1243 (1.5%) | 2 (0.1%) | 6 (2.5%) | 1251 (1.4%) |  |
| Self isolated | 1743 (2.1%) | 108 (5.6%) | 5 (2.1%) | 1856 (2.1%) |  |
| Shelter Beneficiary | 1306 (1.6%) | 0 (0.0%) | 1 (0.4%) | 1307 (1.5%) |  |
| Shelter Staff | 879 (1.0%) | 0 (0.0%) | 1 (0.4%) | 880 (1.0%) |  |
| Standard case definition | 2550 (3.0%) | 5 (0.3%) | 5 (2.1%) | 2560 (3.0%) |  |
| TB confirmed case | 131 (0.2%) | 0 (0.0%) | 0 (0.0%) | 131 (0.2%) |  |
| TB staff | 25 (0.0%) | 0 (0.0%) | 0 (0.0%) | 25 (0.0%) |  |
| Truck drivers | 661 (0.8%) | 25 (1.3%) | 5 (2.1%) | 691 (0.8%) |  |
| Missing | 9867 | 14 | 18 | 9899 |  |
| **IsForeigner** |  |  |  |  | < 0.001 |
| FALSE | 6602 (79.7%) | 721 (94.4%) | 29 (69.0%) | 7352 (80.9%) |  |
| TRUE | 1683 (20.3%) | 43 (5.6%) | 13 (31.0%) | 1739 (19.1%) |  |
| Missing | 85824 | 1183 | 219 | 87226 |  |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | neg (N=66966) | pos SARS-CoV-2 (N=763) | Suspicted (N=157) | Total (N=67886) | p value |
| **Age** |  |  |  |  | 0.061 |
| Mean (SD) | 41.277 (18.929) | 42.733 (19.786) | 42.815 (20.116) | 41.297 (18.942) |  |
| Median (Q1, Q3) | 40.000 (28.000, 55.000) | 44.000 (28.000, 57.000) | 41.000 (29.000, 58.000) | 40.000 (28.000, 55.000) |  |
| Min - Max | 0.000 - 102.000 | 0.000 - 91.000 | 0.000 - 90.000 | 0.000 - 102.000 |  |
| Missing | 9 | 0 | 0 | 9 |  |
| **Gender** |  |  |  |  | 0.502 |
| Female | 34567 (51.6%) | 389 (51.0%) | 74 (47.1%) | 35030 (51.6%) |  |
| male | 32399 (48.4%) | 374 (49.0%) | 83 (52.9%) | 32856 (48.4%) |  |
| Missing | 0 | 0 | 0 | 0 |  |
| **Fever** |  |  |  |  | 0.006 |
| No | 6004 (32.6%) | 30 (21.1%) | 7 (21.9%) | 6041 (32.5%) |  |
| Yes | 12412 (67.4%) | 112 (78.9%) | 25 (78.1%) | 12549 (67.5%) |  |
| Missing | 48550 | 621 | 125 | 49296 |  |
| **Cough** |  |  |  |  | 0.827 |
| No | 12230 (68.9%) | 87 (66.4%) | 21 (67.7%) | 12338 (68.8%) |  |
| Yes | 5532 (31.1%) | 44 (33.6%) | 10 (32.3%) | 5586 (31.2%) |  |
| Missing | 49204 | 632 | 126 | 49962 |  |
| **Risk Group** |  |  |  |  | < 0.001 |
| Ambulance driver | 1983 (3.4%) | 0 (0.0%) | 2 (1.4%) | 1985 (3.4%) |  |
| Being on dialysis | 332 (0.6%) | 0 (0.0%) | 1 (0.7%) | 333 (0.6%) |  |
| Beneficiary of a fever or COVID clinic | 10867 (18.7%) | 604 (79.6%) | 41 (28.7%) | 11512 (19.5%) |  |
| Contact of Confirmed case | 4060 (7.0%) | 50 (6.6%) | 13 (9.1%) | 4123 (7.0%) |  |
| Dialysis staff | 16 (0.0%) | 0 (0.0%) | 0 (0.0%) | 16 (0.0%) |  |
| Employee of COVID Clinic | 2209 (3.8%) | 1 (0.1%) | 0 (0.0%) | 2210 (3.8%) |  |
| Employee of other hospitals | 8380 (14.4%) | 5 (0.7%) | 6 (4.2%) | 8391 (14.2%) |  |
| Employees of the customs and border checkpoint | 1882 (3.2%) | 3 (0.4%) | 6 (4.2%) | 1891 (3.2%) |  |
| Epidemiologist of the NCDC and / or PHC Centers | 253 (0.4%) | 0 (0.0%) | 0 (0.0%) | 253 (0.4%) |  |
| Fever and respiratory disease | 6323 (10.9%) | 25 (3.3%) | 14 (9.8%) | 6362 (10.8%) |  |
| Justice and MIA Customs Services | 58 (0.1%) | 0 (0.0%) | 0 (0.0%) | 58 (0.1%) |  |
| Other Risk groups | 2056 (3.5%) | 5 (0.7%) | 0 (0.0%) | 2061 (3.5%) |  |
| Patients from other hospitals | 1000 (1.7%) | 1 (0.1%) | 1 (0.7%) | 1002 (1.7%) |  |
| PCR Lab staff | 65 (0.1%) | 0 (0.0%) | 0 (0.0%) | 65 (0.1%) |  |
| PHC staff | 39 (0.1%) | 0 (0.0%) | 0 (0.0%) | 39 (0.1%) |  |
| Pneumonia | 1013 (1.7%) | 1 (0.1%) | 3 (2.1%) | 1017 (1.7%) |  |
| Psychiatric clininc staff | 69 (0.1%) | 0 (0.0%) | 1 (0.7%) | 70 (0.1%) |  |
| Public Transport staff | 114 (0.2%) | 0 (0.0%) | 0 (0.0%) | 114 (0.2%) |  |
| Quarantine zone beneficiaries | 11541 (19.9%) | 43 (5.7%) | 42 (29.4%) | 11626 (19.7%) |  |
| Quarantine zone staff | 915 (1.6%) | 2 (0.3%) | 4 (2.8%) | 921 (1.6%) |  |
| Self isolated | 989 (1.7%) | 10 (1.3%) | 2 (1.4%) | 1001 (1.7%) |  |
| Shelter Beneficiary | 848 (1.5%) | 0 (0.0%) | 1 (0.7%) | 849 (1.4%) |  |
| Shelter Staff | 542 (0.9%) | 0 (0.0%) | 1 (0.7%) | 543 (0.9%) |  |
| Standard case definition | 1851 (3.2%) | 4 (0.5%) | 5 (3.5%) | 1860 (3.2%) |  |
| TB confirmed case | 121 (0.2%) | 0 (0.0%) | 0 (0.0%) | 121 (0.2%) |  |
| TB staff | 7 (0.0%) | 0 (0.0%) | 0 (0.0%) | 7 (0.0%) |  |
| Truck drivers | 469 (0.8%) | 5 (0.7%) | 0 (0.0%) | 474 (0.8%) |  |
| Missing | 8964 | 4 | 14 | 8982 |  |
| **IsForeigner** |  |  |  |  | 0.515 |
| FALSE | 4323 (99.5%) | 253 (100.0%) | 8 (100.0%) | 4584 (99.5%) |  |
| TRUE | 22 (0.5%) | 0 (0.0%) | 0 (0.0%) | 22 (0.5%) |  |
| Missing | 62621 | 510 | 149 | 63280 |  |

## Contact networks

Index cases summary

contacts$missingPatID <- is.na(contacts$`Patient unique ID`)  
contacts$missingPatID[contacts$missingPatID] <- 1:sum(contacts$missingPatID)  
contacts$newPatID <- ifelse(is.na(contacts$`Patient unique ID`),paste("missingP",contacts$missingPatID,sep=""),contacts$`Patient unique ID`)  
  
contacts$missingCID <- is.na(contacts$`Contact ID`)  
contacts$missingCID[contacts$missingCID] <- 1:sum(contacts$missingCID)  
contacts$newCID <- ifelse(is.na(contacts$`Contact ID`),paste("missingC",contacts$missingCID,sep=""),contacts$`Contact ID`)  
  
contacts$case <- as.factor(contacts$`Confirmed Case`)  
levels(contacts$case) <- c(FALSE,NA,TRUE)  
  
contacts$Age[contacts$Age=="\*"] <- NA  
contacts$Age <- as.numeric(contacts$Age)  
contacts$Gender[contacts$Gender=="male"] <- "Male"  
# rate of transmission by type of contact  
  
contactsType <- contacts %>% filter(`Contact type`!="unknown")  
contactsType$Coworker <- contactsType$`Contact type`=="Co-worker"  
contactsType$Family <- contactsType$`Contact type`=="Family member"  
contactsType$Friend <- contactsType$`Contact type`=="Friend"  
contactsType$Medical <- contactsType$`Contact type`=="Medical Personnel"  
contactsType$Neighbour <- contactsType$`Contact type`=="Neighbour"  
  
mType <- glm(data=contactsType,case ~ `Contact type`,family=binomial)  
summary(mType)

##   
## Call:  
## glm(formula = case ~ `Contact type`, family = binomial, data = contactsType)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.9628 -0.9628 -0.7306 1.4084 2.1964   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -1.1844 0.1185 -9.995 < 2e-16 \*\*\*  
## `Contact type`Family member 0.6560 0.1283 5.112 3.19e-07 \*\*\*  
## `Contact type`Friend -0.2709 0.2410 -1.124 0.261   
## `Contact type`Medical Personnel -15.3816 302.3142 -0.051 0.959   
## `Contact type`Neighbour -1.1338 0.2681 -4.230 2.34e-05 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 3191.3 on 2585 degrees of freedom  
## Residual deviance: 3032.8 on 2581 degrees of freedom  
## AIC: 3042.8  
##   
## Number of Fisher Scoring iterations: 15

mType2 <- glm(data=contactsType,case ~ Family,family=binomial)  
summary(mType2)

##   
## Call:  
## glm(formula = case ~ Family, family = binomial, data = contactsType)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.9628 -0.9628 -0.6119 1.4084 1.8802   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -1.58045 0.09281 -17.03 <2e-16 \*\*\*  
## FamilyTRUE 1.05207 0.10507 10.01 <2e-16 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 3191.3 on 2585 degrees of freedom  
## Residual deviance: 3078.7 on 2584 degrees of freedom  
## AIC: 3082.7  
##   
## Number of Fisher Scoring iterations: 4

mType3 <- glm(data=contactsType,case ~ Coworker,family=binomial)  
summary(mType3)

##   
## Call:  
## glm(formula = case ~ Coworker, family = binomial, data = contactsType)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.8794 -0.8794 -0.8794 1.5082 1.7037   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -0.75058 0.04579 -16.391 < 2e-16 \*\*\*  
## CoworkerTRUE -0.43385 0.12704 -3.415 0.000638 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 3191.3 on 2585 degrees of freedom  
## Residual deviance: 3179.0 on 2584 degrees of freedom  
## AIC: 3183  
##   
## Number of Fisher Scoring iterations: 4

mType4 <- glm(data=contactsType,case ~ Friend,family=binomial)  
summary(mType4)

##   
## Call:  
## glm(formula = case ~ Friend, family = binomial, data = contactsType)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.8692 -0.8692 -0.8692 1.5208 1.8248   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -0.77869 0.04361 -17.854 <2e-16 \*\*\*  
## FriendTRUE -0.67660 0.21436 -3.156 0.0016 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 3191.3 on 2585 degrees of freedom  
## Residual deviance: 3180.0 on 2584 degrees of freedom  
## AIC: 3184  
##   
## Number of Fisher Scoring iterations: 4

mType5 <- glm(data=contactsType,case ~ Medical,family=binomial)  
summary(mType5)

##   
## Call:  
## glm(formula = case ~ Medical, family = binomial, data = contactsType)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.87 -0.87 -0.87 1.52 1.52   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -0.77638 0.04286 -18.116 <2e-16 \*\*\*  
## MedicalTRUE -15.78969 302.31422 -0.052 0.958   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 3191.3 on 2585 degrees of freedom  
## Residual deviance: 3144.3 on 2584 degrees of freedom  
## AIC: 3148.3  
##   
## Number of Fisher Scoring iterations: 15

mType6 <- glm(data=contactsType,case ~ Neighbour,family=binomial)  
summary(mType6)

##   
## Call:  
## glm(formula = case ~ Neighbour, family = binomial, data = contactsType)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.8898 -0.8898 -0.8898 1.4954 2.1964   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -0.72236 0.04375 -16.509 < 2e-16 \*\*\*  
## NeighbourTRUE -1.59590 0.24434 -6.532 6.51e-11 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 3191.3 on 2585 degrees of freedom  
## Residual deviance: 3128.4 on 2584 degrees of freedom  
## AIC: 3132.4  
##   
## Number of Fisher Scoring iterations: 4

####  
# age and gender of index case  
mAS <- glm(data=contacts,case ~ Age + Gender, family=binomial)  
summary(mAS)

##   
## Call:  
## glm(formula = case ~ Age + Gender, family = binomial, data = contacts)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.9192 -0.8914 -0.8190 1.4782 1.6140   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -0.857966 0.111157 -7.718 1.18e-14 \*\*\*  
## Age -0.001415 0.002191 -0.646 0.5186   
## GenderMale 0.217877 0.086238 2.526 0.0115 \*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 3191.3 on 2585 degrees of freedom  
## Residual deviance: 3183.9 on 2583 degrees of freedom  
## (296 observations deleted due to missingness)  
## AIC: 3189.9  
##   
## Number of Fisher Scoring iterations: 4

mA <- glm(data=contacts,case ~ Age , family=binomial)  
summary(mA)

##   
## Call:  
## glm(formula = case ~ Age, family = binomial, data = contacts)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.8883 -0.8645 -0.8465 1.5139 1.5847   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -0.724045 0.096973 -7.466 8.24e-14 \*\*\*  
## Age -0.002181 0.002164 -1.008 0.314   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 3191.3 on 2585 degrees of freedom  
## Residual deviance: 3190.2 on 2584 degrees of freedom  
## (296 observations deleted due to missingness)  
## AIC: 3194.2  
##   
## Number of Fisher Scoring iterations: 4

mS <- glm(data=contacts,case ~ Gender, family=binomial)  
summary(mS)

##   
## Call:  
## glm(formula = case ~ Gender, family = binomial, data = contacts)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -0.9005 -0.9005 -0.8195 1.4823 1.5840   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -0.91881 0.05936 -15.478 < 2e-16 \*\*\*  
## GenderMale 0.22566 0.08540 2.642 0.00823 \*\*   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 3191.3 on 2585 degrees of freedom  
## Residual deviance: 3184.3 on 2584 degrees of freedom  
## (296 observations deleted due to missingness)  
## AIC: 3188.3  
##   
## Number of Fisher Scoring iterations: 4

### merge contacts with screening data  
testsub <- testingU %>% filter(!is.na(PersonalID)) %>% select(PersonalID,Gender,Age)  
  
contact.merge <- left\_join(contacts,testsub,by=c("Contact ID"="PersonalID"))  
contactsType.m <- contact.merge %>% filter(`Contact type`!="unknown")  
contactsType.m$Coworker <- contactsType.m$`Contact type`=="Co-worker"  
contactsType.m$Family <- contactsType.m$`Contact type`=="Family member"  
contactsType.m$Friend <- contactsType.m$`Contact type`=="Friend"  
contactsType.m$Medical <- contactsType.m$`Contact type`=="Medical Personnel"  
contactsType.m$Neighbour <- contactsType.m$`Contact type`=="Neighbour"  
  
  
m2 <- glm(data=contact.merge,case ~ Age.x + Age.y,family=binomial)  
summary(m2)

##   
## Call:  
## glm(formula = case ~ Age.x + Age.y, family = binomial, data = contact.merge)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.2137 -0.9912 -0.9148 1.3314 1.5574   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -0.8627037 0.1377223 -6.264 3.75e-10 \*\*\*  
## Age.x -0.0001186 0.0023316 -0.051 0.959   
## Age.y 0.0100557 0.0023839 4.218 2.46e-05 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 2617.7 on 1964 degrees of freedom  
## Residual deviance: 2599.8 on 1962 degrees of freedom  
## (917 observations deleted due to missingness)  
## AIC: 2605.8  
##   
## Number of Fisher Scoring iterations: 4

m3 <- glm(data=contact.merge,case ~ Age.x + Age.y + Gender.x + Gender.y + `Contact type`,family=binomial)  
summary(m3)

##   
## Call:  
## glm(formula = case ~ Age.x + Age.y + Gender.x + Gender.y + `Contact type`,   
## family = binomial, data = contact.merge)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.3702 -1.0302 -0.7399 1.2217 2.1265   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -1.298071 0.201073 -6.456 1.08e-10 \*\*\*  
## Age.x -0.000796 0.002400 -0.332 0.740136   
## Age.y 0.011147 0.002429 4.590 4.43e-06 \*\*\*  
## Gender.xMale 0.165445 0.096839 1.708 0.087551 .   
## Gender.ymale -0.097878 0.096604 -1.013 0.310968   
## `Contact type`Family member 0.661155 0.142294 4.646 3.38e-06 \*\*\*  
## `Contact type`Friend -0.357527 0.260216 -1.374 0.169454   
## `Contact type`Medical Personnel -14.785542 229.003543 -0.065 0.948521   
## `Contact type`Neighbour -1.026411 0.286574 -3.582 0.000341 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 2617.7 on 1964 degrees of freedom  
## Residual deviance: 2467.4 on 1956 degrees of freedom  
## (917 observations deleted due to missingness)  
## AIC: 2485.4  
##   
## Number of Fisher Scoring iterations: 14

m4 <- glm(data=contactsType.m,case ~ Age.x + Age.y + Gender.x + Gender.y + Coworker + Family + Friend + Medical + Neighbour,family=binomial)  
summary(m4)

##   
## Call:  
## glm(formula = case ~ Age.x + Age.y + Gender.x + Gender.y + Coworker +   
## Family + Friend + Medical + Neighbour, family = binomial,   
## data = contactsType.m)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.3702 -1.0302 -0.7399 1.2217 2.1265   
##   
## Coefficients: (1 not defined because of singularities)  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -2.324482 0.303711 -7.654 1.95e-14 \*\*\*  
## Age.x -0.000796 0.002400 -0.332 0.740136   
## Age.y 0.011147 0.002429 4.590 4.43e-06 \*\*\*  
## Gender.xMale 0.165445 0.096839 1.708 0.087551 .   
## Gender.ymale -0.097878 0.096604 -1.013 0.310968   
## CoworkerTRUE 1.026411 0.286574 3.582 0.000341 \*\*\*  
## FamilyTRUE 1.687566 0.260557 6.477 9.37e-11 \*\*\*  
## FriendTRUE 0.668884 0.340006 1.967 0.049152 \*   
## MedicalTRUE -13.759132 229.003649 -0.060 0.952090   
## NeighbourTRUE NA NA NA NA   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 2617.7 on 1964 degrees of freedom  
## Residual deviance: 2467.4 on 1956 degrees of freedom  
## (621 observations deleted due to missingness)  
## AIC: 2485.4  
##   
## Number of Fisher Scoring iterations: 14

m5 <- glm(data=contactsType.m,case ~ Age.y + Coworker + Family + Friend + Medical,family=binomial)  
summary(m5)

##   
## Call:  
## glm(formula = case ~ Age.y + Coworker + Family + Friend + Medical,   
## family = binomial, data = contactsType.m)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.3595 -1.0406 -0.7553 1.2169 2.1194   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)   
## (Intercept) -2.349784 0.276941 -8.485 < 2e-16 \*\*\*  
## Age.y 0.011352 0.002416 4.700 2.61e-06 \*\*\*  
## CoworkerTRUE 1.050510 0.286128 3.671 0.000241 \*\*\*  
## FamilyTRUE 1.701196 0.260359 6.534 6.40e-11 \*\*\*  
## FriendTRUE 0.707672 0.339148 2.087 0.036923 \*   
## MedicalTRUE -13.690541 229.082275 -0.060 0.952345   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 2617.7 on 1964 degrees of freedom  
## Residual deviance: 2471.7 on 1959 degrees of freedom  
## (621 observations deleted due to missingness)  
## AIC: 2483.7  
##   
## Number of Fisher Scoring iterations: 14

Rates of transmission by type of contact, gender and age of index case - table as in Bi

Contact by age groups and type of contact

##   
## 0-9 10-19 20-29 30-39 40-49 50-59 60-69  
## 0-9 0.8461538 0.2857143 0.2105263 0.5555556 0.4117647 0.3636364 0.5000000  
## 10-19 0.2666667 0.4242424 0.3684211 0.3939394 0.6486486 0.5151515 0.4642857  
## 20-29 0.4000000 0.3750000 0.1785714 0.1481481 0.1750000 0.4074074 0.3500000  
## 30-39 0.3414634 0.3333333 0.3714286 0.3797468 0.2439024 0.3902439 0.4285714  
## 40-49 0.2500000 0.3939394 0.4444444 0.3863636 0.4411765 0.5600000 0.4545455  
## 50-59 0.3636364 0.4583333 0.2857143 0.2698413 0.4193548 0.5000000 0.5625000  
## 60-69 0.2500000 0.3333333 0.3750000 0.2750000 0.4000000 0.3750000 0.3571429  
## 70+ 0.3684211 0.4000000 0.3888889 0.2307692 0.2631579 0.5600000 0.3636364  
##   
## 70+  
## 0-9 0.4285714  
## 10-19 0.6000000  
## 20-29 0.2142857  
## 30-39 0.3750000  
## 40-49 0.4285714  
## 50-59 0.5500000  
## 60-69 0.6000000  
## 70+ 0.7000000

Transmission by age groups and type of contact

Total number of secondary cases per primary case

##   
## FALSE TRUE   
## 1791 795

Plot of contact network

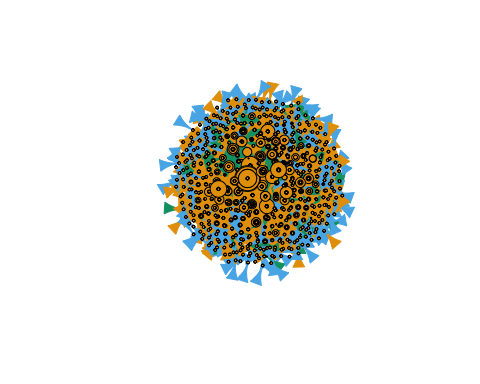
##   
## Attaching package: 'igraph'

## The following objects are masked from 'package:dplyr':  
##   
## as\_data\_frame, groups, union

## The following objects are masked from 'package:lubridate':  
##   
## %--%, union

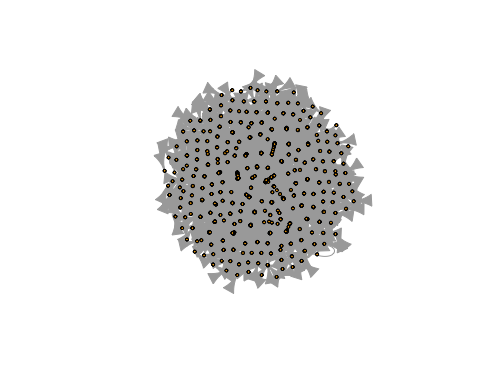
## The following objects are masked from 'package:stats':  
##   
## decompose, spectrum

## The following object is masked from 'package:base':  
##   
## union



##   
## 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 21   
## 417 110 102 99 66 43 20 11 16 2 5 10 3 1 2 1 2 2 1 2   
## 22 23 30   
## 1 2 3

##   
## 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 21   
## 417 110 102 99 66 43 20 11 16 2 5 10 3 1 2 1 2 2 1 2   
## 22 23 30   
## 1 2 3



## Discussion

* main outcomes
* limitations of study
* comparison to other contact tracing studies (Bi, etc.)
* comparison to other countries in the region
* understanding how and why the response was able to be so strong (eg HCV testing and treatment infrastructure)