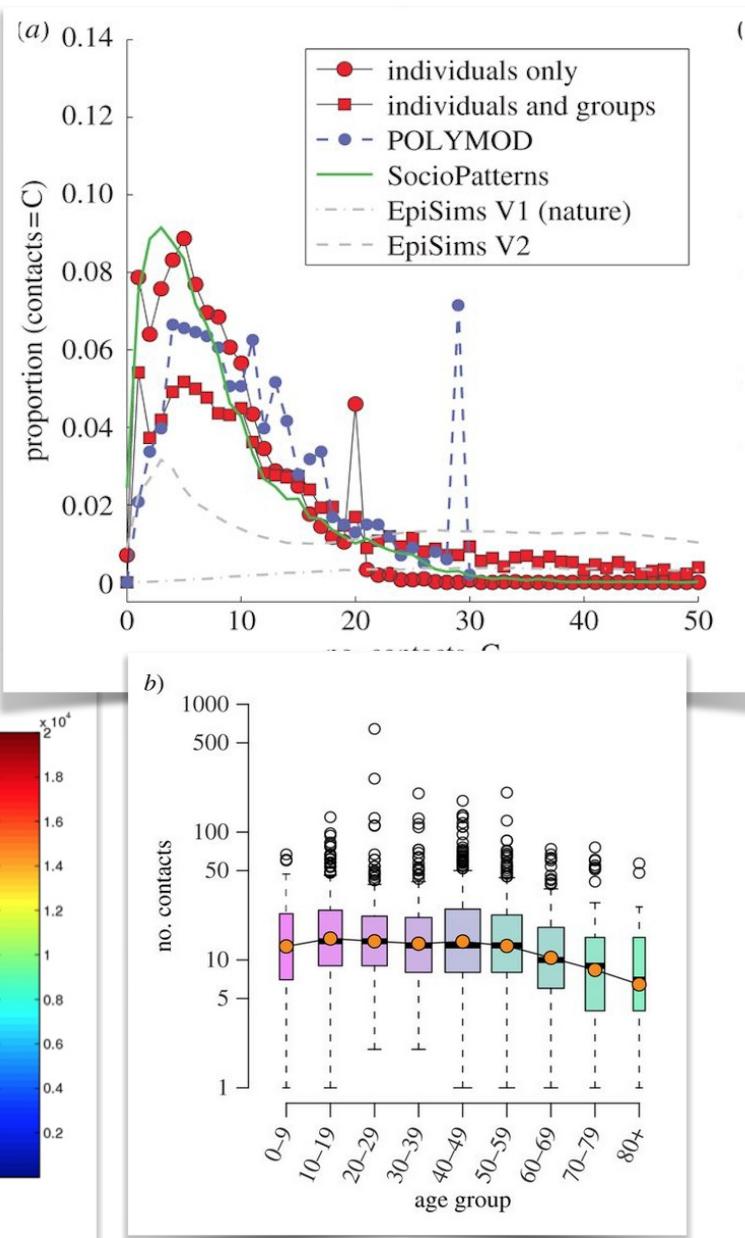
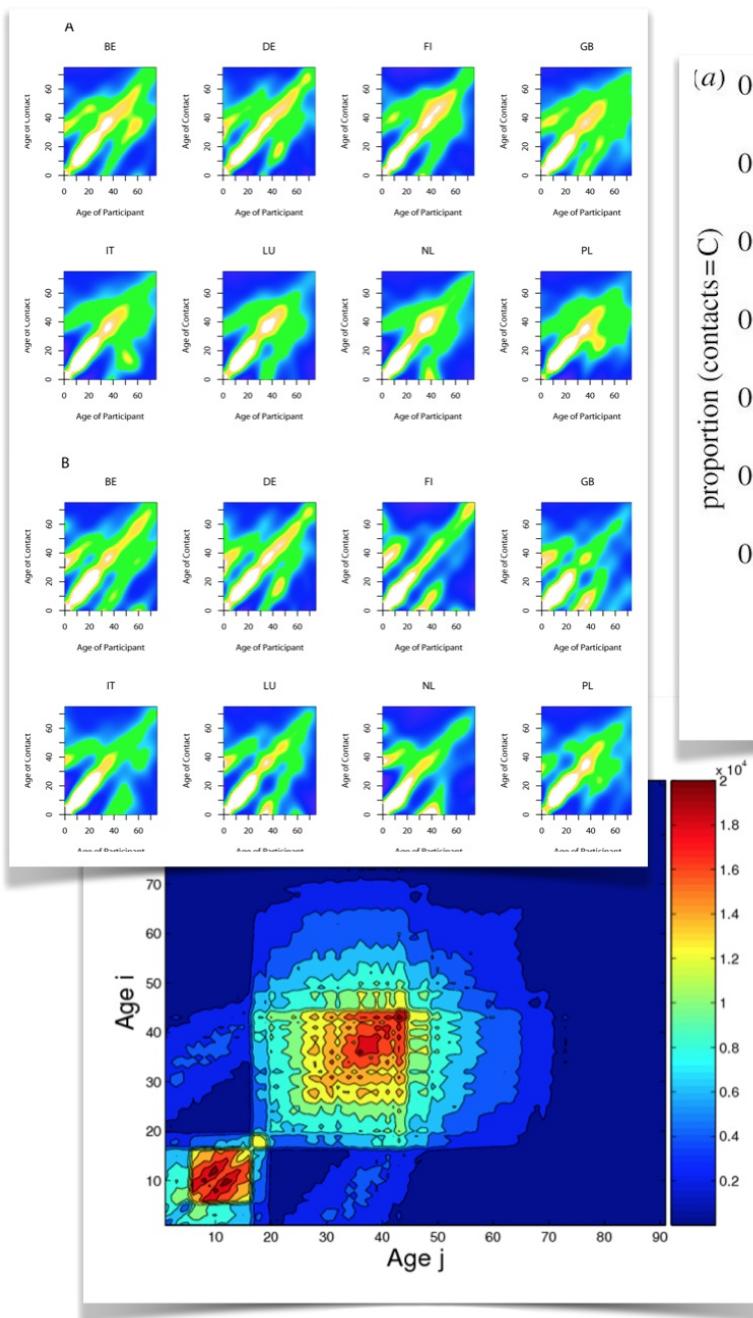


# Individual and collective dynamics of contact behaviour

Sebastian Funk  
18 May, 2017  
TRANSMID Workshop



## Questions

1. What is the relative importance of **individual** vs **collective** variation in contact behaviour?
2. How can we find out about **long-term changes** in collective contact behaviour

Individual vs. collective variation in  
contact behaviour

Flusurvey: Home

# Influzenæt

Influzenæt is a system to monitor the activity of influenza-like-illness (ILI) with the aid of volunteers via the internet

# flusurvey



London School of Hygiene & Tropical Medicine



Public Health England



Log in

Register

Forgot login details?

Home News Results Competitions FAQ The project What is flu? Contact Dashboard

## Welcome to Flusurvey 2015-6

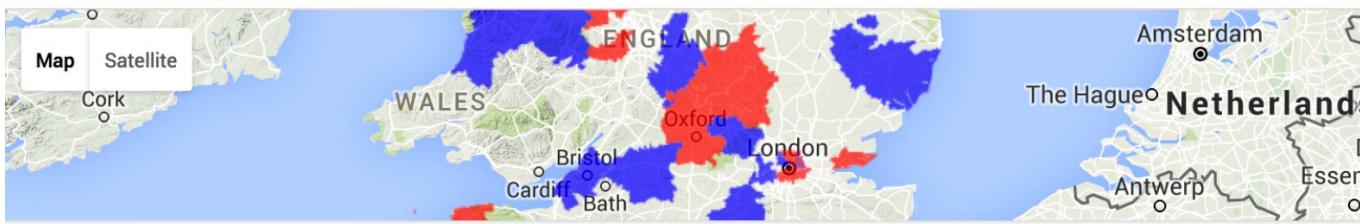
Flusurvey.org.uk is an online service that any member of the UK public can log onto to report flu like symptoms they may experience during the winter months. This data will be used by researchers at the London School of Hygiene and Tropical Medicine and Public Health England to monitor flu trends in the UK.

The UK Flusurvey was launched on 16<sup>th</sup> July 2009, in the middle of the swine flu epidemic, and is part of a Europe-wide initiative to monitor influenza-like illness (ILI) activity. We currently have more than 6,000 people, from all over the UK, participating in this survey and would like to increase this number to make our interpretations more meaningful. If you have participated in previous years please do so again this year.

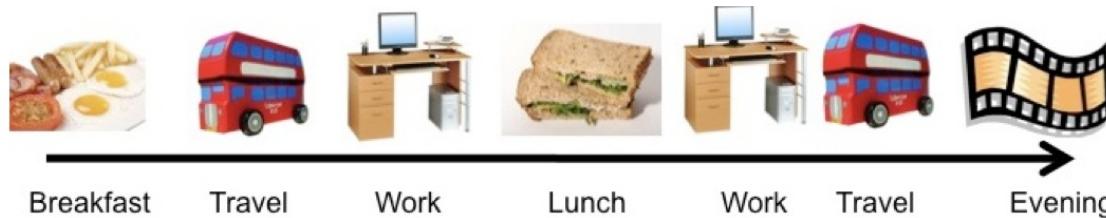
If you are new to this site please click on the 'Join the Survey' box on the right. Tell your friends about Flusurvey and be in with a chance to win a Google Nexus. See 'Competitions' tab for further information.

### Flu Like Illness Heatmap

Below see the amount of influenza like illness (ILI) reported around the UK right now. The map shows a gradient from no reported ILI (blue) to very high ILI (red). **Map updated every three minutes.**



[https://flusurvey.org.uk/ \[1/1\] 1%](https://flusurvey.org.uk/)



**Flu is spread via social contacts. Measuring how we meet each other helps understand and predict flu epidemics. Think about the all people you met yesterday and where you met them.**

**NOTE:** If you are filling this in on behalf of someone else, please answer all the questions as if you are that person

How many people did you have conversational contact with yesterday (talking face to face)? 

	0-4 years	5-18 years	19-44 years	45-64 years	65+ years
Home	0  	0  	0  	0  	0  
Work	0  	0  	0  	0  	0  
Other	0  	0  	0  	0  	0  

How many people did you have physical contact with yesterday (skin-to-skin contact, e.g. handshake, kiss)? 

	0-4 years	5-18 years	19-44 years	45-64 years	65+ years
Home	0  	0  	0  	0  	0  
Work	0  	0  	0  	0  	0  
Other	0  	0  	0  	0  	0  



## Article Navigation

### EDITOR'S CHOICE

## The Impact of Illness on Social Networks: Implications for Transmission and Control of Influenza FREE

Kim Van Kerckhove ✉, Niel Hens, W. John Edmunds, Ken T. D. Eames

Am J Epidemiol (2013) 178 (11): 1655-1662. DOI: <https://doi.org/10.1093/aje/kwt196>

Published: 07 October 2013   Article history ▾

 OPEN ACCESS  PEER-REVIEWED

RESEARCH ARTICLE

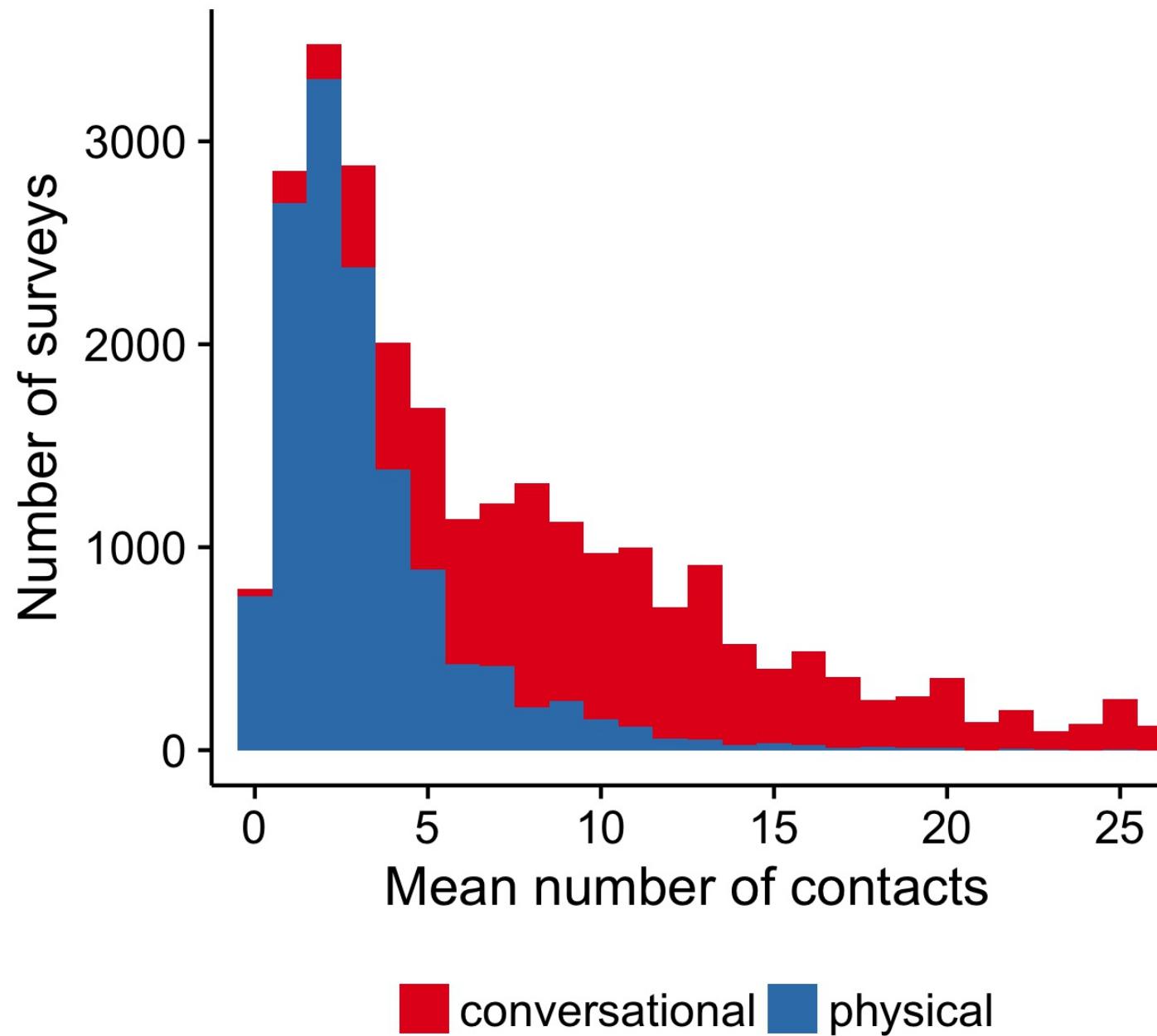
# Measured Dynamic Social Contact Patterns Explain the Spread of H1N1v Influenza

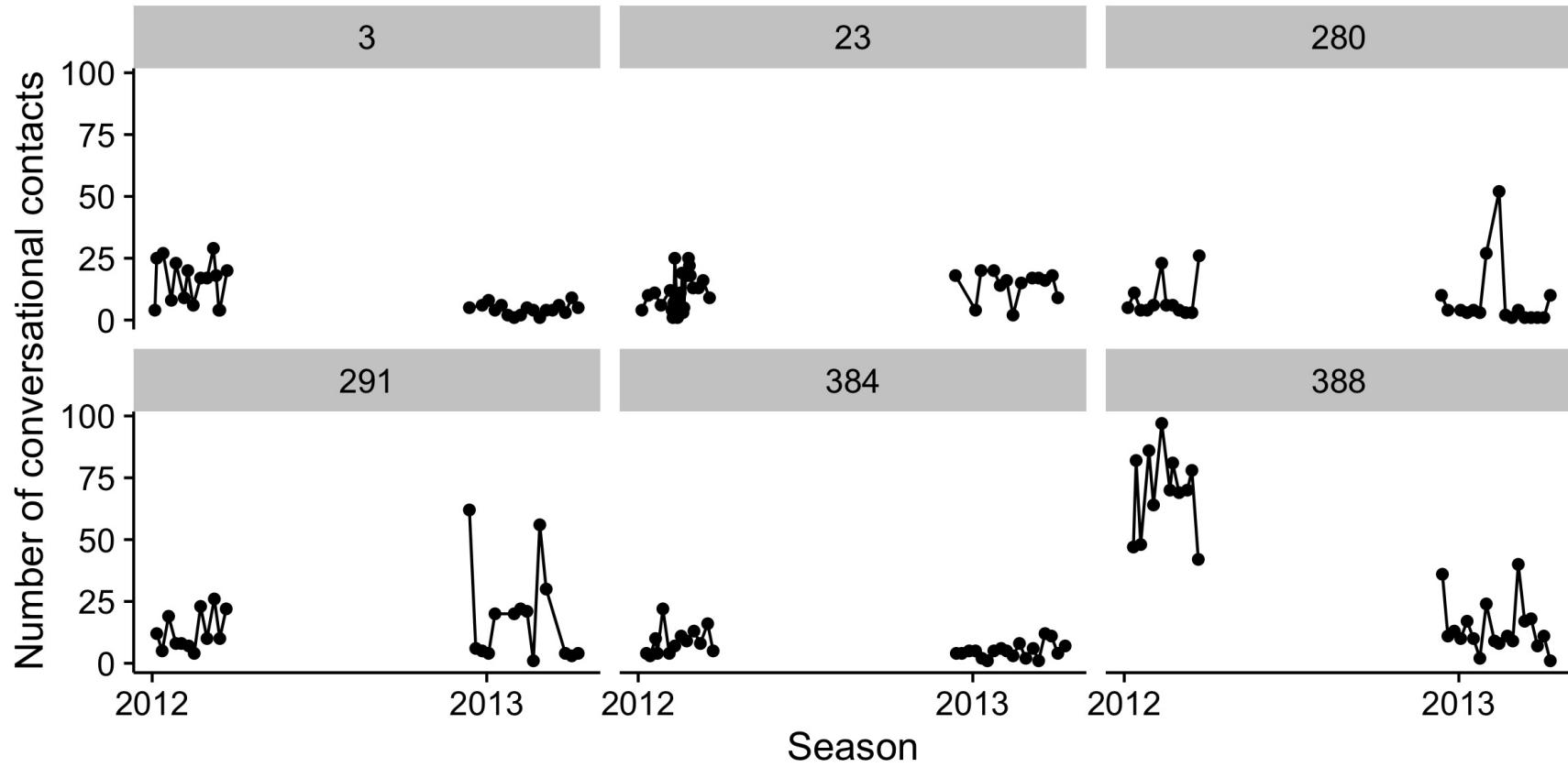
Ken T. D. Eames , Natasha L. Tilston, Ellen Brooks-Pollock, W. John Edmunds

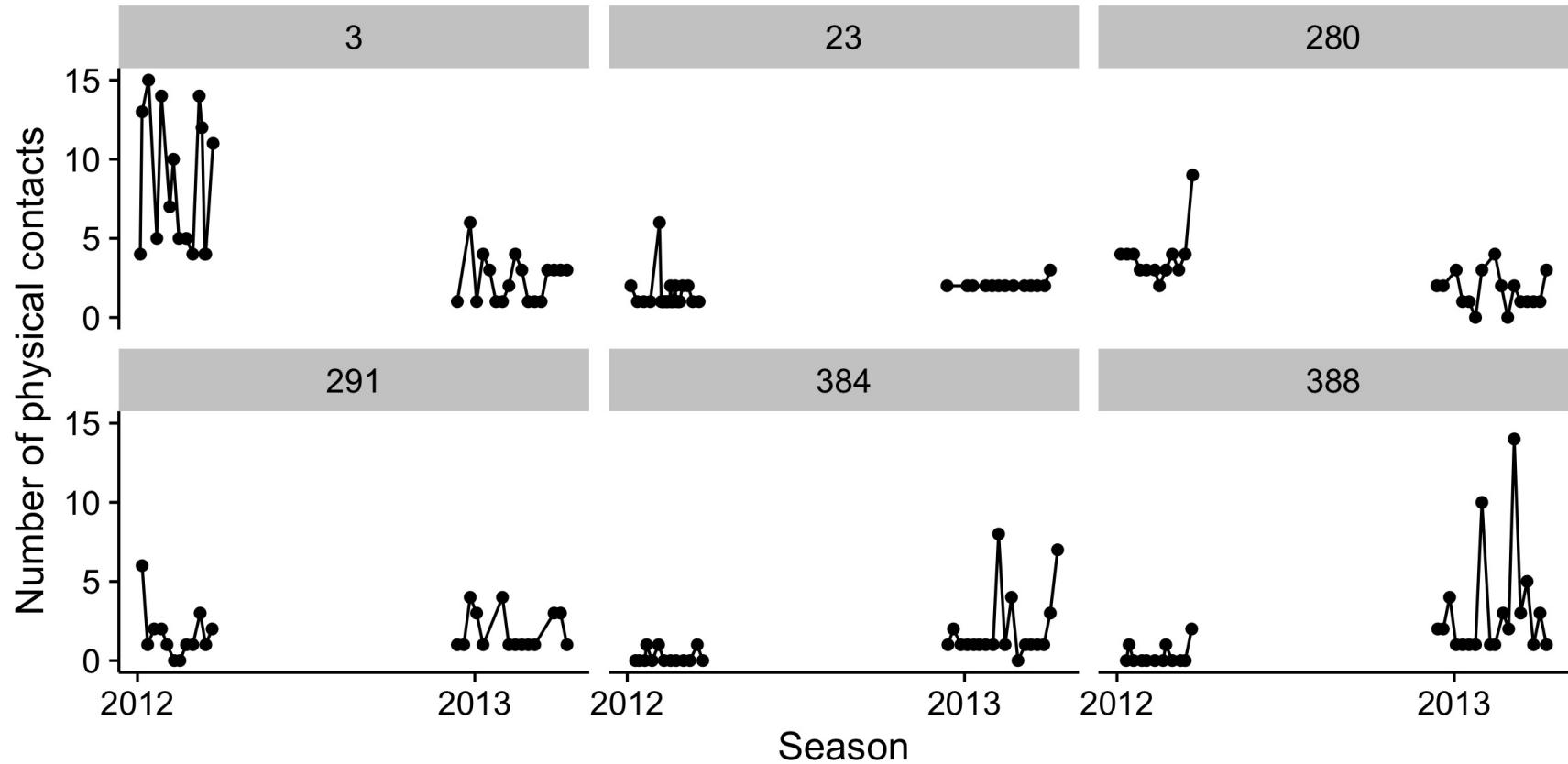
Published: March 8, 2012 • <https://doi.org/10.1371/journal.pcbi.1002425>

Article	Authors	Metrics	Comments	Related Content
				

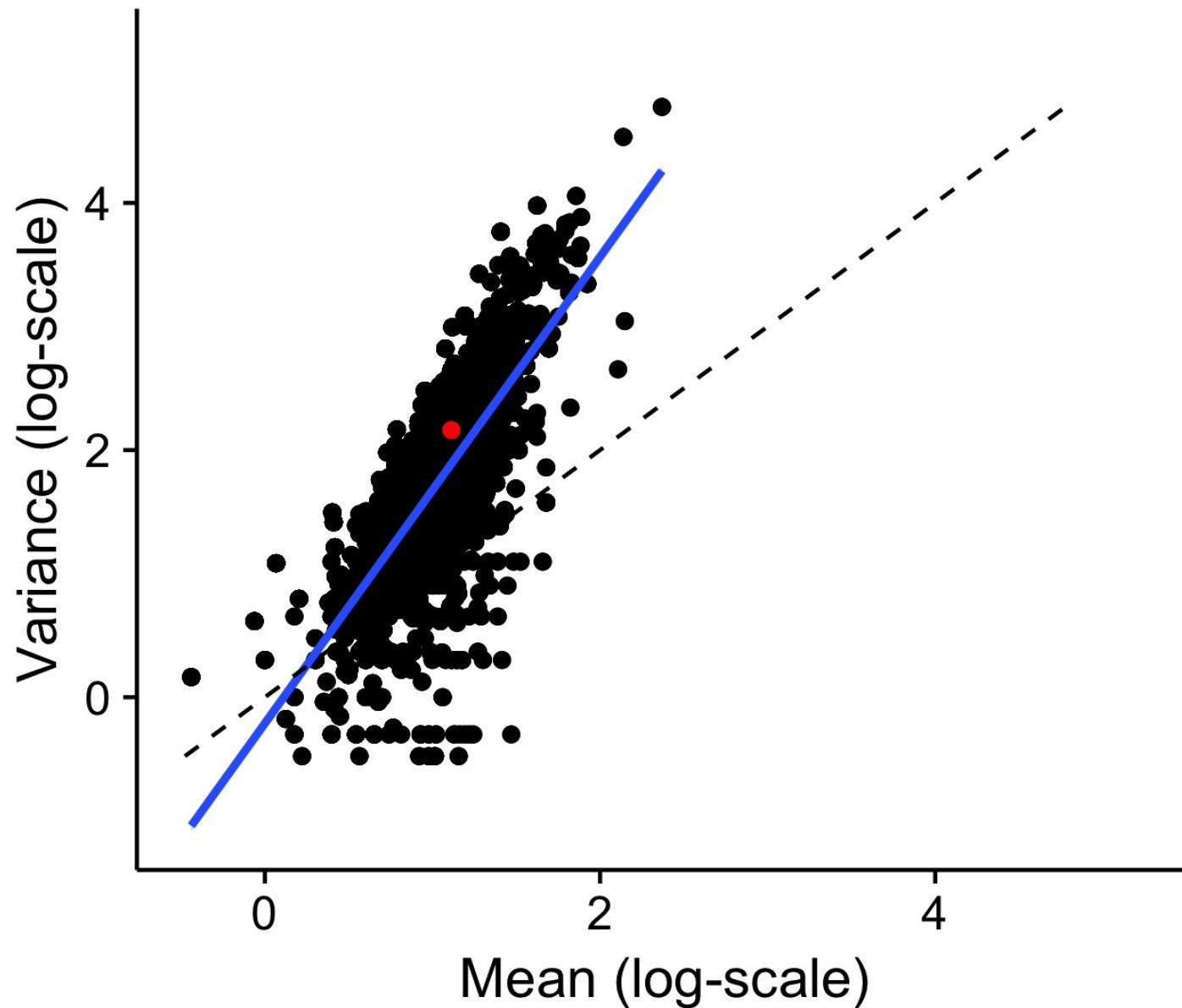
## Abstract







## Number of conversational contacts



## Longitudinal contact data

1. There is variation in the number of contacts both **within** and **between** individuals
2. The number of contacts is overdispersed both on the **individual** and the **collective** scales

## Are there high-contact individuals or high-contact days?

- Hierarchical model implemented in **stan**  
(<http://mc-stan.org>)
- Negative binomial model with **two parameters** vs negative binomial with two parameters **per person**, compared with Deviance Information Criterion (DIC)

## Model comparison

$\text{contacts} \sim \text{NegBin}(\mu, k)$

Model	@DIC
Collective	0
Individual	-5k

# Covariates

\* For whom are you filling in this survey?



- A member of my household
- Myself
- Someone else

\* What is your gender?



- Male
- Female

\* What is your date of birth (month and year)?



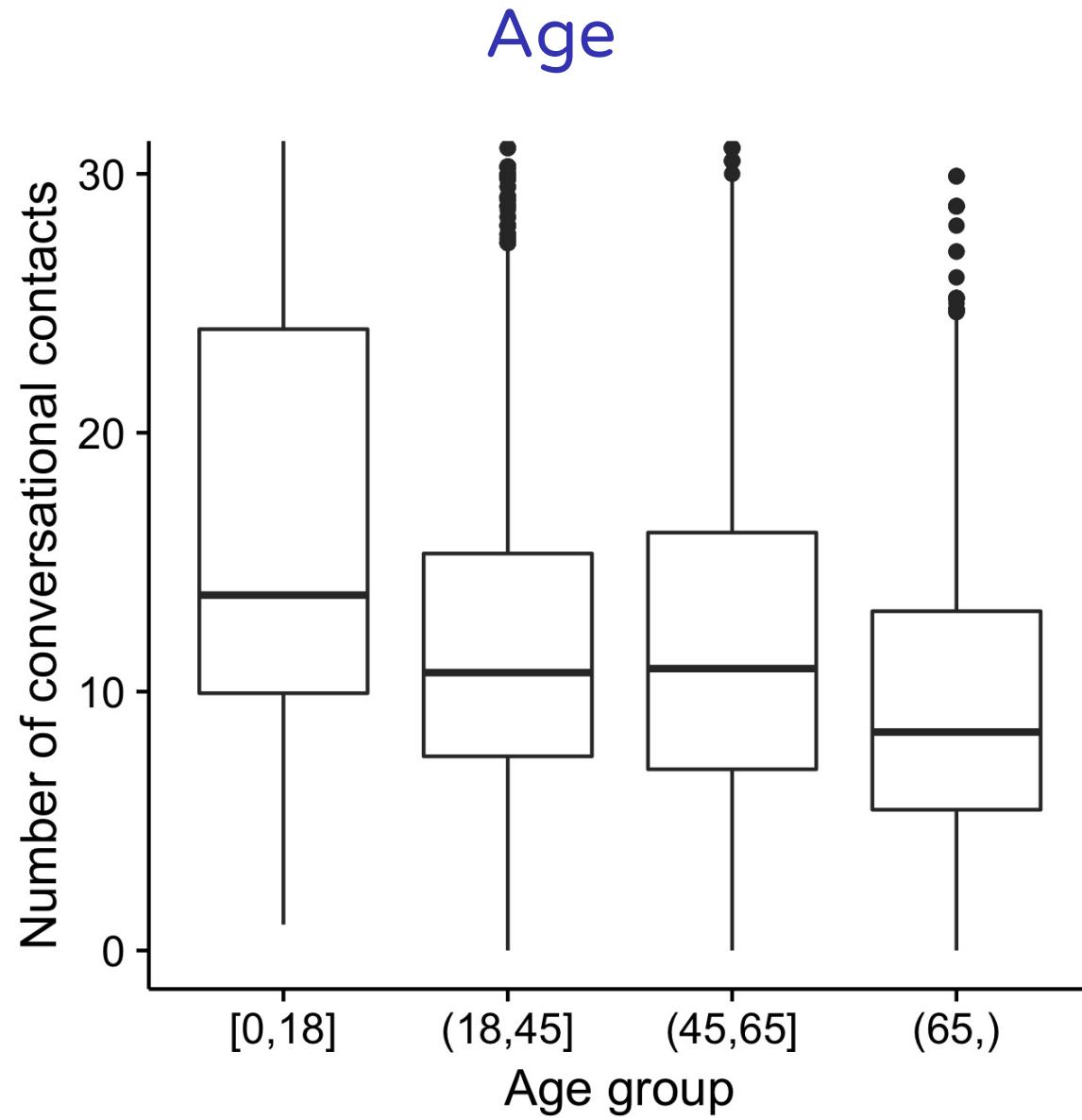
\* What is the first part of your home postcode (the part before the space)?



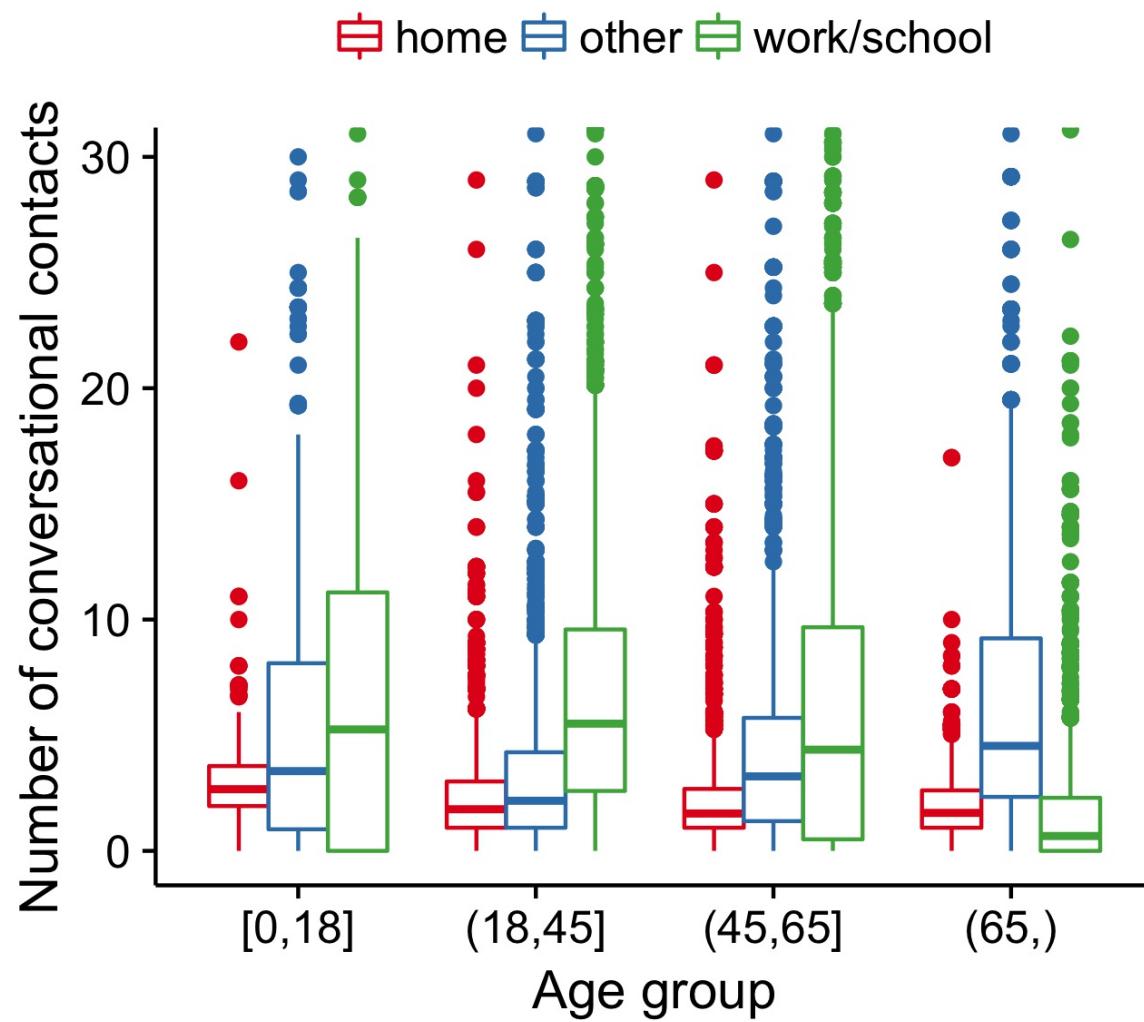
\* What is your main activity?



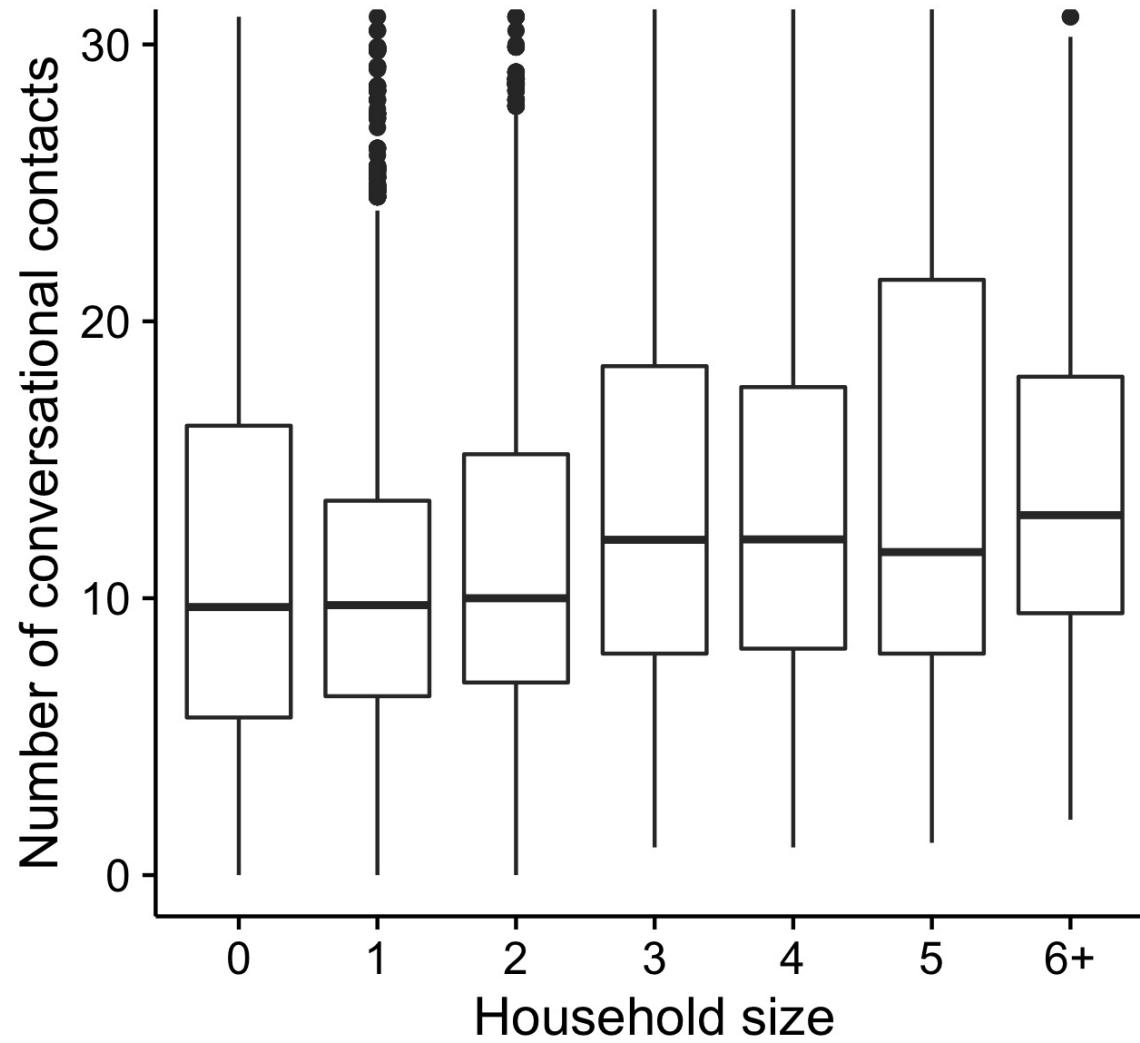
- Paid employment, full time
- Paid employment, part time
- Self-employed (businessman, farmer, tradesman, etc.)
- Attending daycare/school/college/university



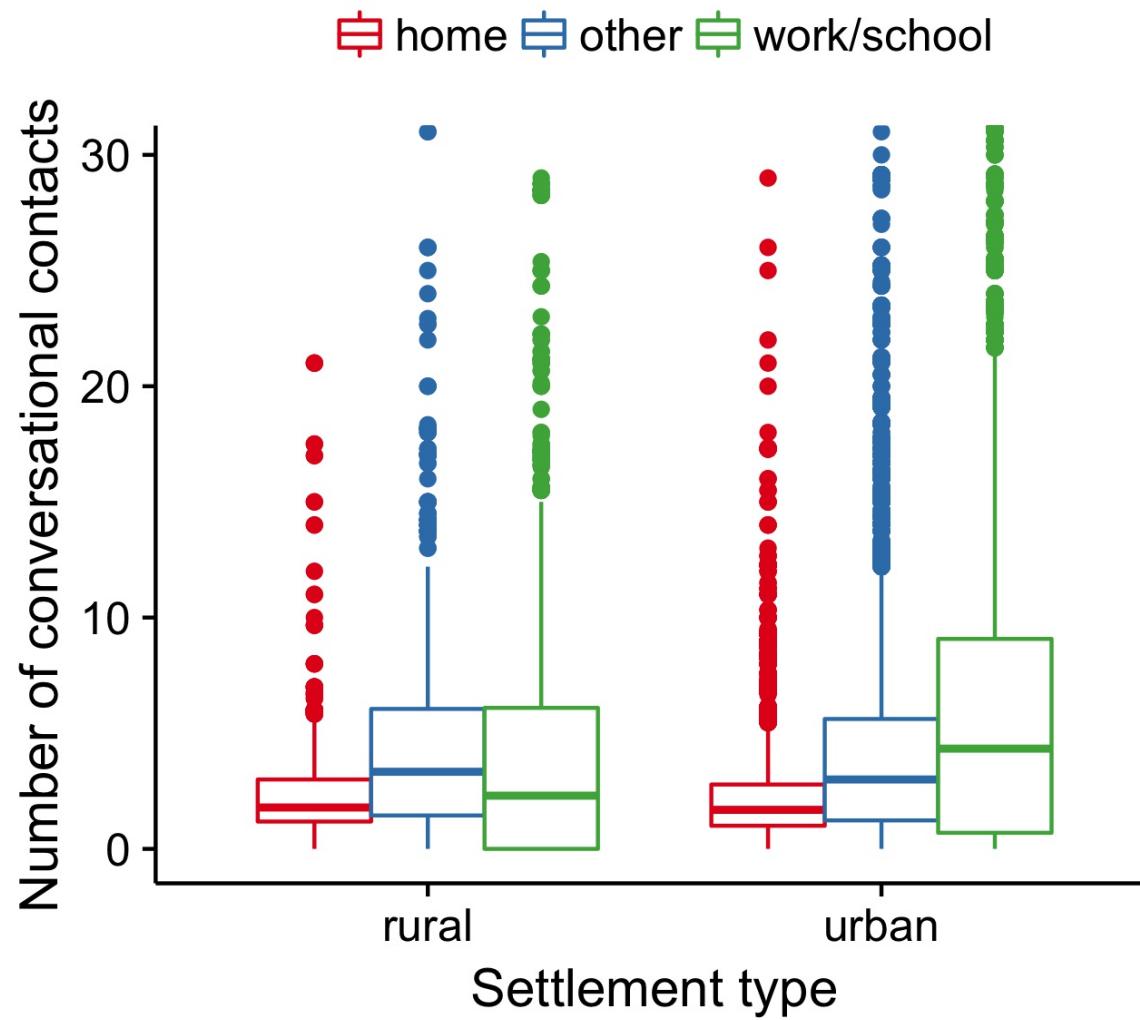
# Age



## Household size



# Urban/rural



## Covariate model

$\text{contacts} \sim \text{NegBin}(\mu, k)$

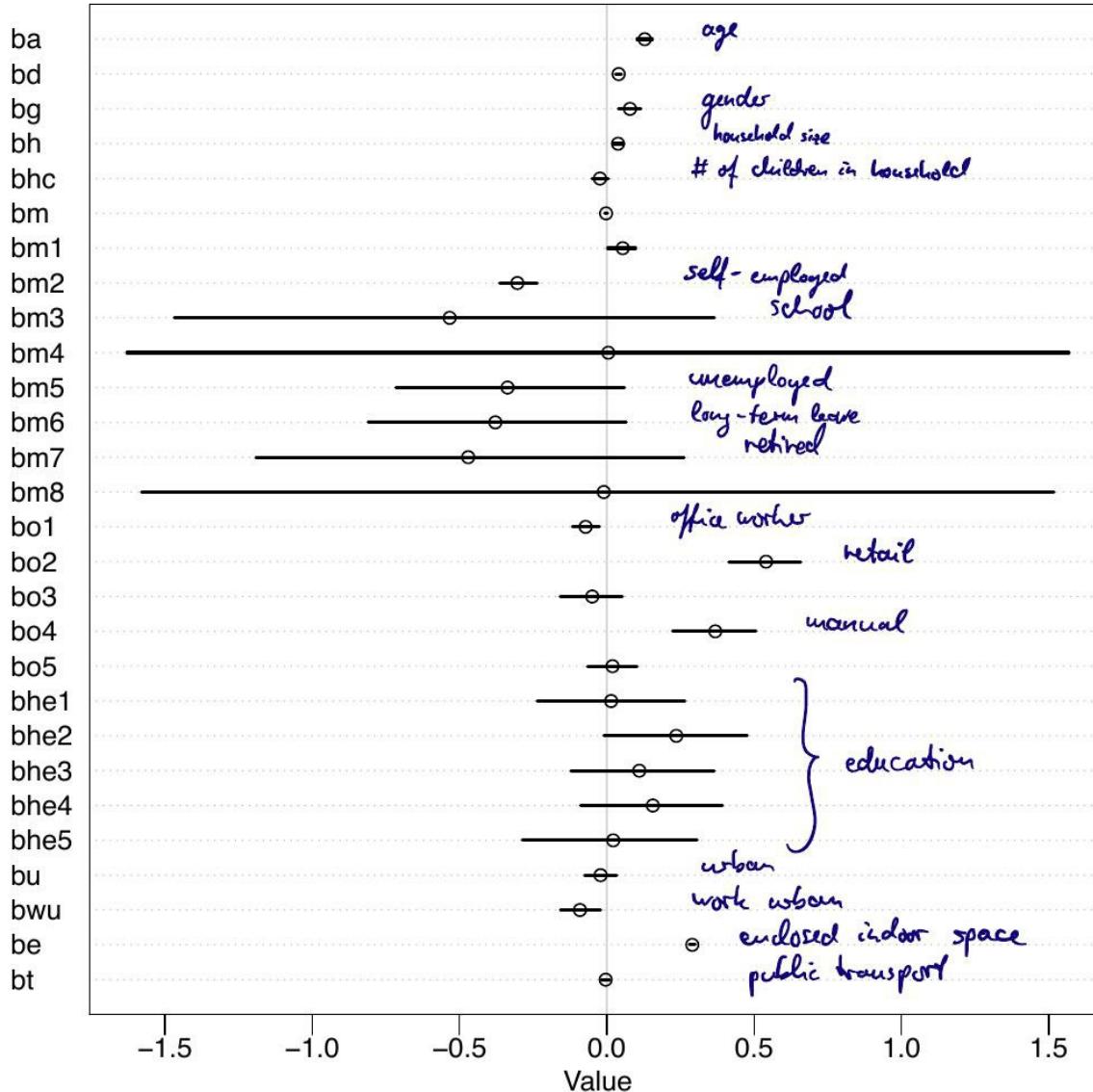
$$\log(\mu) = \alpha + \beta_a \cdot \text{age} + \dots$$

## Model comparison

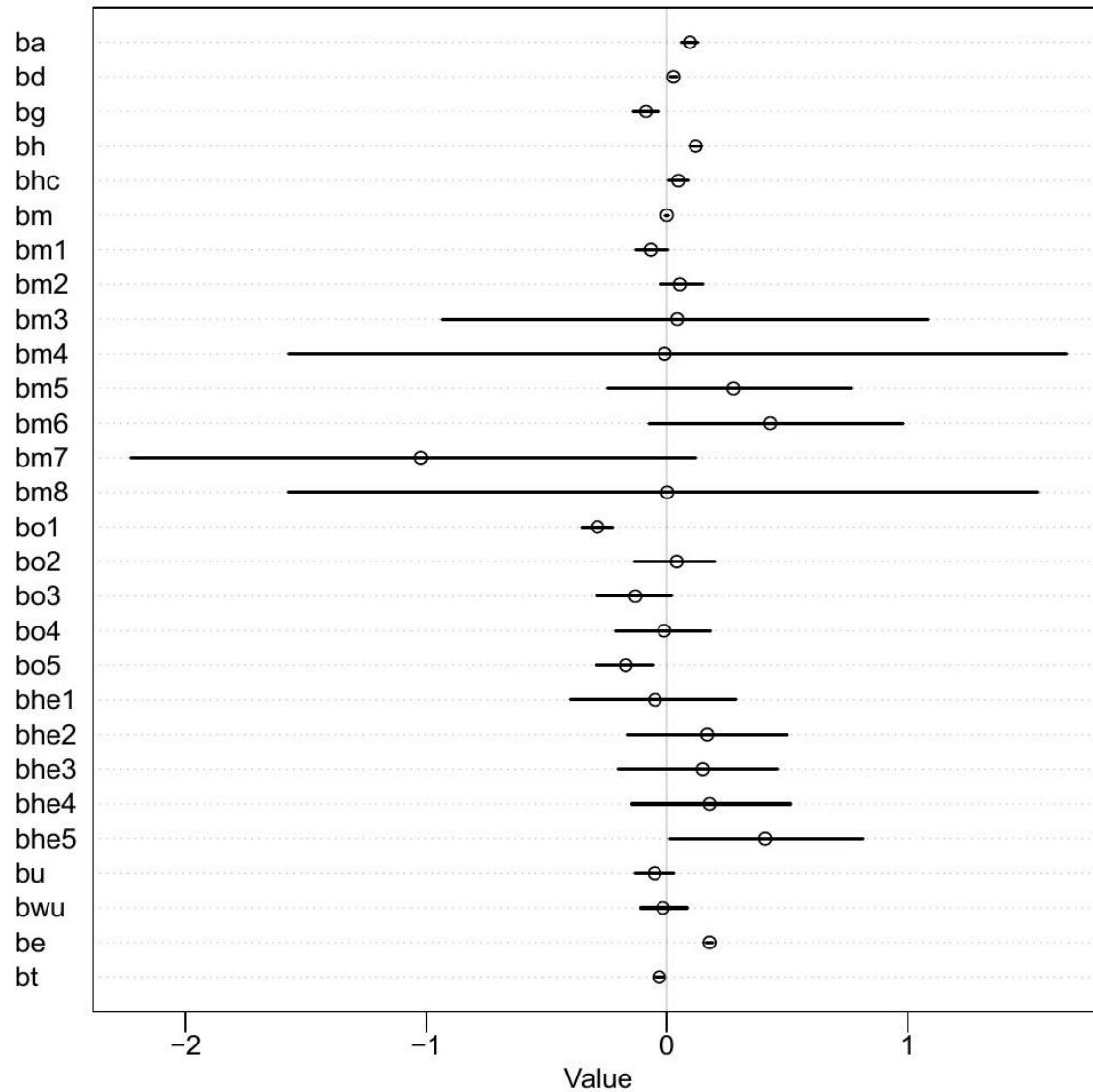
$\text{contacts} \sim \text{NegBin}(\mu, k)$

Model	@DIC
Collective	0
Individual	-5k
Covariate	-50k
Covariate individual	-52k

# Conversational contacts



# Physical contacts



# Symptoms

Weekly Questionnaire

- [My results](#)
- [My household](#)
- [Invite a friend](#)
- [Newsletter](#)
- [Account settings](#)
- [Log out](#)

You can add multiple people (i.e. from your household, class or company) through "My household". Each account can only have one **username** and **email address**. To leave feedback or get support, [contact us](#).

**NOTE: If you are filling this in on behalf of someone else, please answer all the questions as if you are that person**

\* Have you had any of the following symptoms since your last visit (or in the past weeks, if this is your first visit)? [i](#)

- No symptoms
- Fever
- Chills
- Runny or blocked nose
- Sneezing
- Sore throat
- Cough
- Shortness of breath
- Headache
- Muscle/joint pain
- Chest pain
- Feeling tired or exhausted (malaise)
- Loss of appetite
- Coloured sputum/phlegm
- Watery, bloodshot eyes
- Nausea

## Influenza-like illness

$$\text{ili} \sim \text{Binomial}(1, p)$$

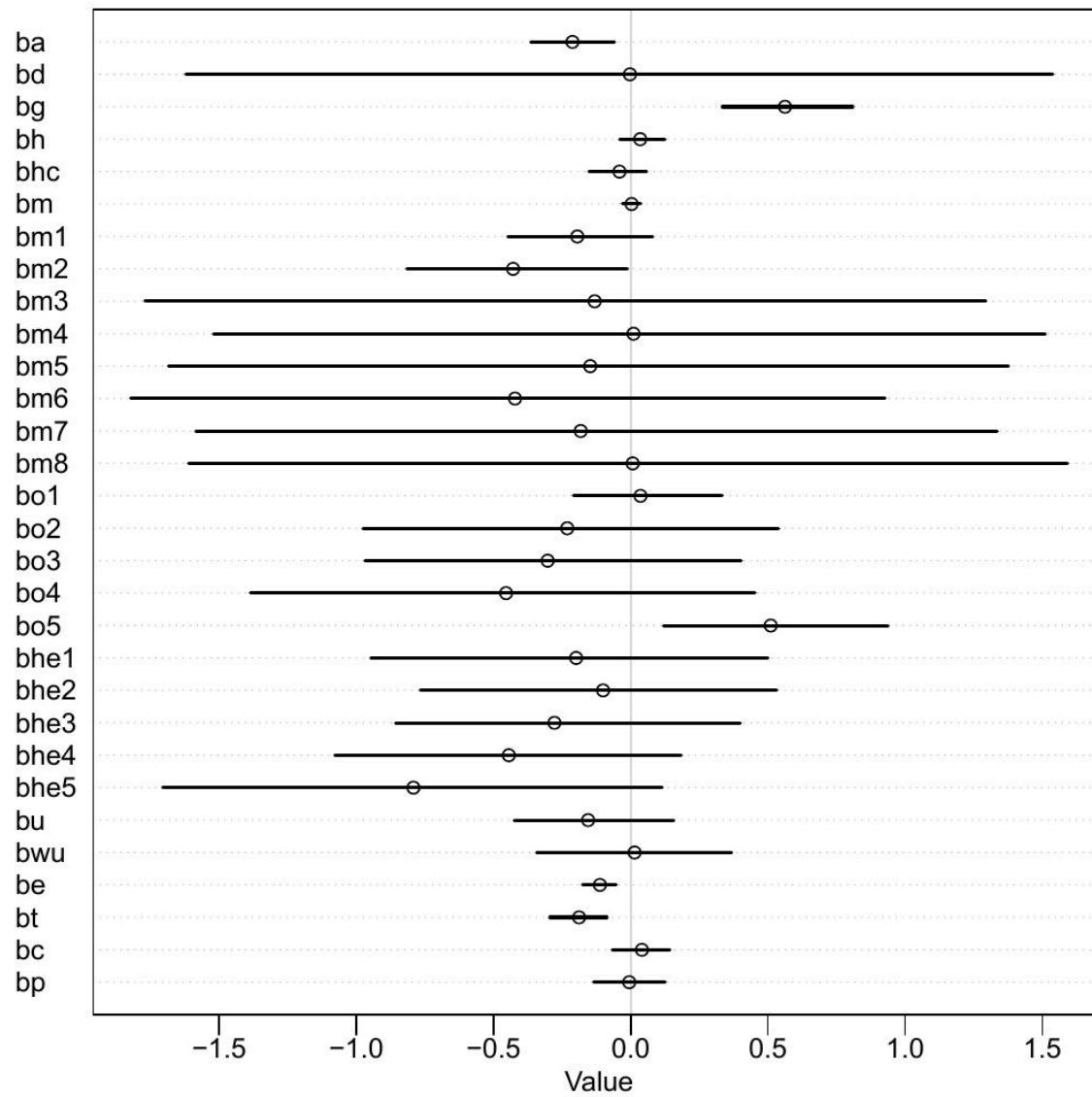
Model	@DIC
Collective	0
Collective + contacts	+4
Individual	+3k
Covariate	-21
Covariate individual	-42

## ILI covariate model

$$ili \sim \text{Binomial}(1, p)$$

$$\text{logit}(p) = \alpha + \beta_a \cdot \text{age} + \dots$$

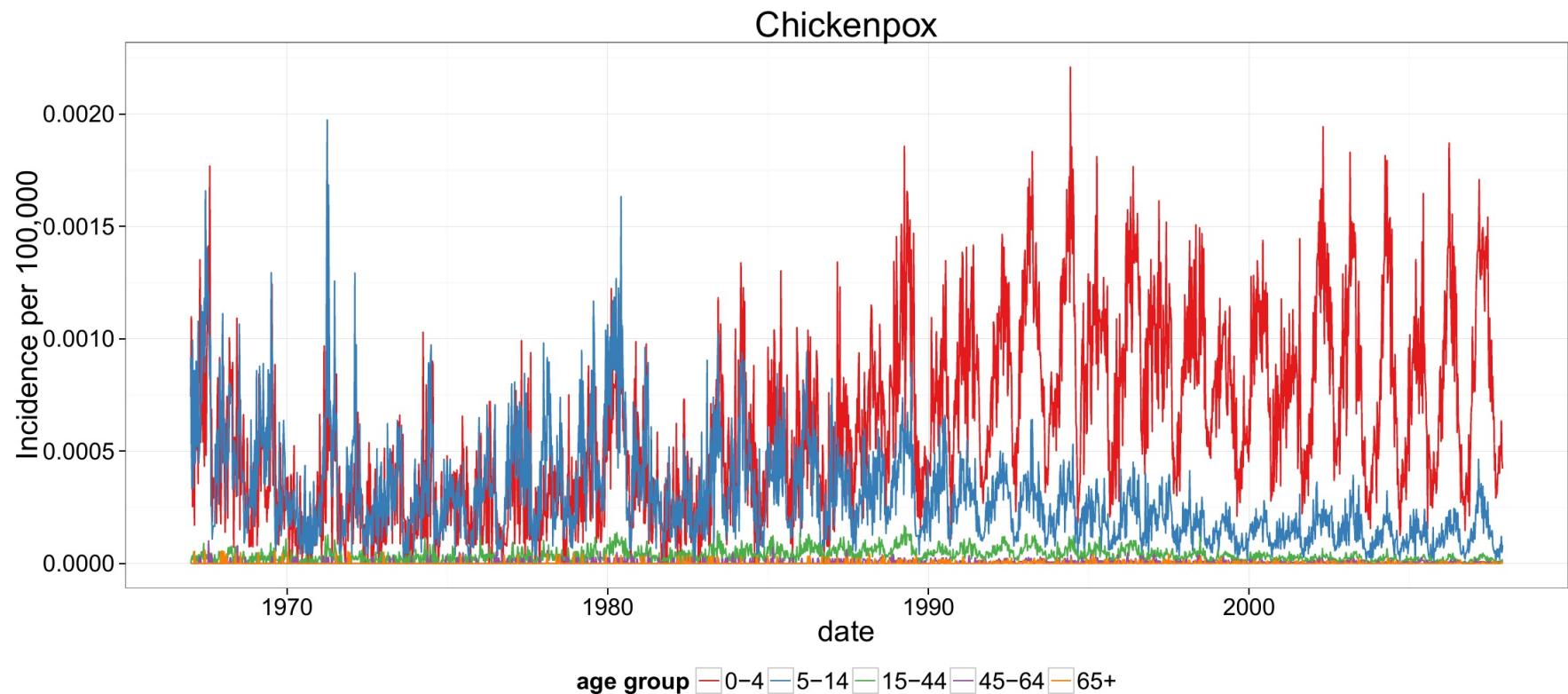
ILI

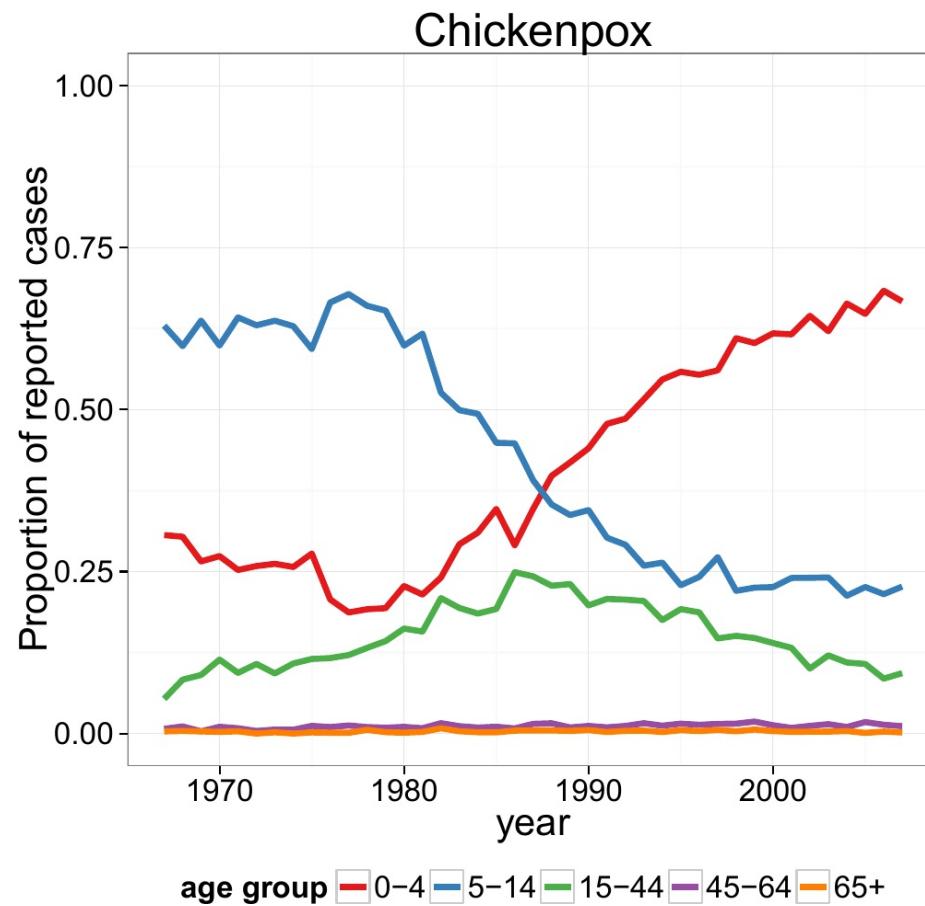


A photograph of a vibrant preschool or kindergarten classroom. The room is filled with natural light from large windows covered by red roller blinds. The walls are adorned with children's artwork and festive decorations, including a large blue fabric mobile hanging from the ceiling and a "HAPPY BIRTHDAY" banner. Several wooden tables and chairs are arranged throughout the room, with children sitting at them, engaged in various activities. A teacher is visible in the background, interacting with the students. The floor is carpeted in a light green color.

# Long-term collective dynamics in contact behaviour

# Age of infection of chickenpox in the UK



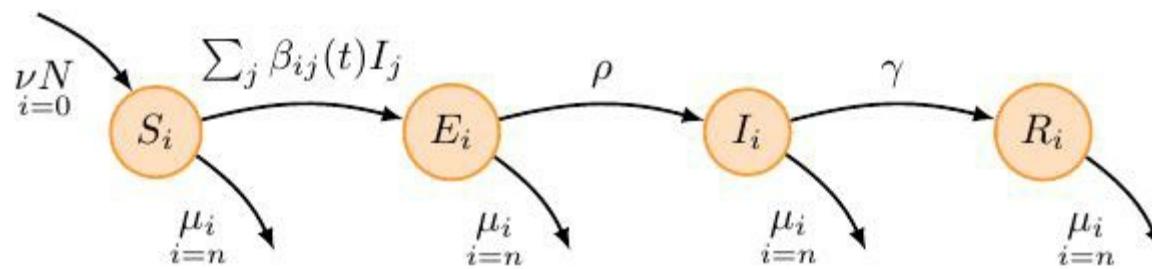


of varicella. Furthermore, an important shift in the age-specific incidence of infection has been observed in the United Kingdom. Interestingly, the shift in the age distribution of consultations in the United Kingdom coincides with a significant increase in children attending preschool [1, 42, 43]. Between 1970 and 1992 the number of children attending preschool has increased from 10 to 50 % [1]. In contrast, the

## Hypotheses

- Demographic change
- Change in social mixing
- Change in overall transmissibility

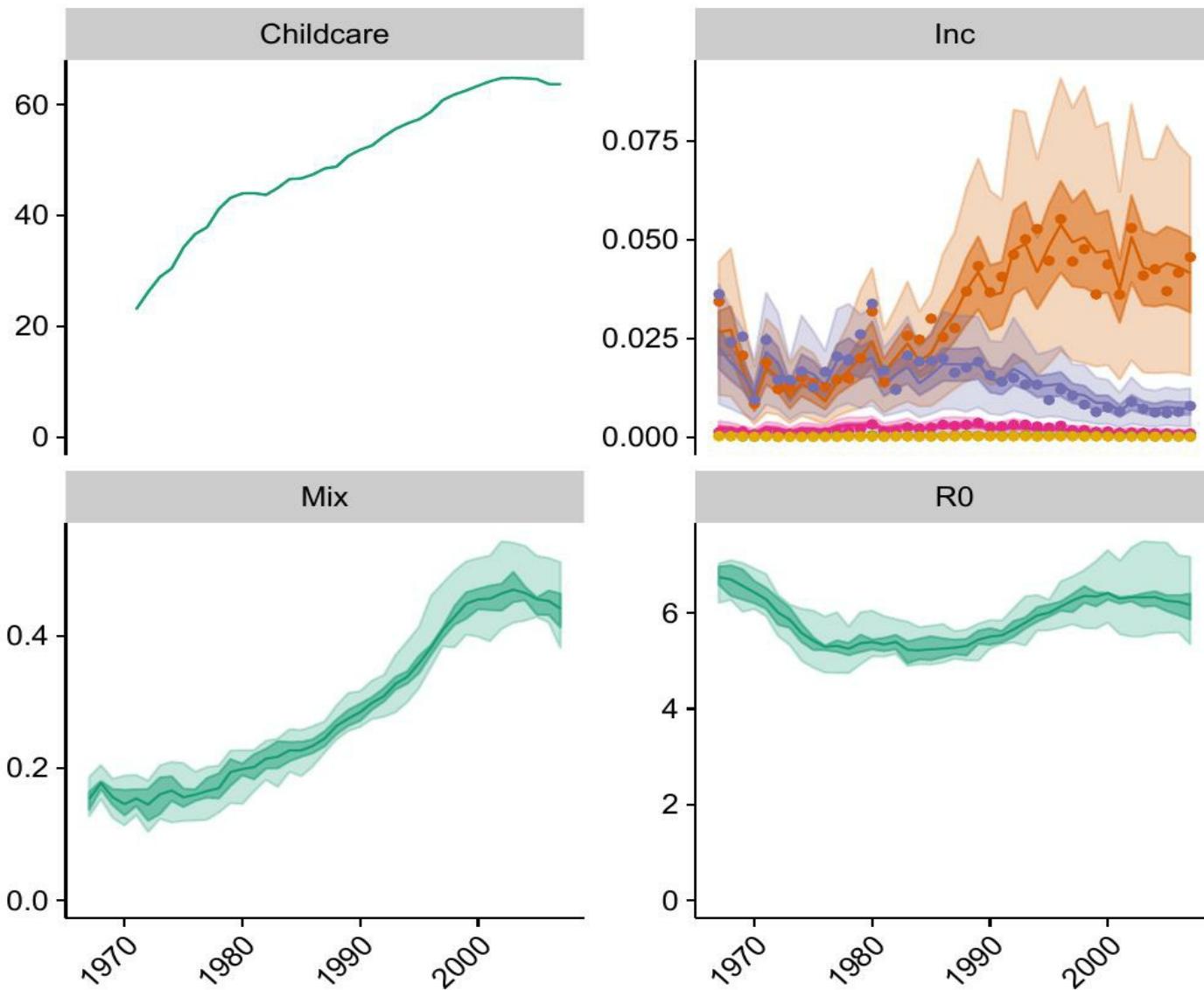
## An age-structured model for long-term chickenpox dynamics



$\beta_{ij}(t)$  varying stochastically, estimated as part of inference.

age

n/a	5-14	45-64
0-4	15-44	65+



# Summary & outlook

## Summary

- People are different in the amount of contact they make
- Number of contacts appears unrelated to risk of acquiring ILI
- Long-term changes in contact rates can be estimated by combining disease & demographic data



# Social mixing matrices for infectious disease modelling in R

build passing codecov 94%

[socialmixr](#) is an R package to derive social mixing matrices from survey data.

It contains:

- a function `contact_matrix` to sample contact matrices from diary data
- social mixing data sets

## Installation

The current development version can be installed using the `devtools` package

```
# install.packages("devtools")
library('devtools')
install_github("sbfnk/socialmixr")
```

RStudio

Project: (None)

Source

Console ~/ ↗

```
> library('socialmixr')
> m <- contact_matrix(survey = "POLYMOD", countries = "United Kingdom", age.limits = c(0, 1, 5, 15))
Using survey 'POLYMOD'. To cite this in a publication, use the output of survey_citation('POLYMOD'). To suppress this message, use 'quiet = TRUE'
Warning message:
In pop_age(survey.pop, ...) :
  Not all age groups represented in population data (5-year age band). Linearly estimating age group sizes from the 5-year bands.
> print(m)
$matrix
      [0,1)     [1,5)     [5,15)    [15,80)
[0,1)  0.4073569 0.1559723 0.07211548 0.05786058
[1,5)  0.6238890 1.9597565 0.52868347 0.33204521
[5,15) 0.7709980 1.4130597 8.01232854 1.10958138
[15,80) 4.1387838 5.9378225 7.42376767 9.45997032

$demography
  lower.age.limit population upper.age.limit year
1:           0       690312           1 2005
2:           1      2761248           5 2005
3:           5      7380235          15 2005
4:          15      49378217          80 2005

> survey_citation('POLYMOD')

To cite survey 'polymod' in publications use:

Mossong J, Hens N, Jit M, Beutels P, Auranen K, Mikolajczyk R, Massari M, Salmaso S, Tomba GS, Wallinga J, Heijne J, Sadkowska-Todys M and Edmunds WJ (2008). "Social Contacts and Mixing Patterns Relevant to the Spread of Infectious Diseases." PLoS Medicine, *5*(3). doi: 10.1371/journal.pmed.0050074 (URL: http://doi.org/10.1371/journal.pmed.0050074).
```

A BibTeX entry for LaTeX users is

## Acknowledgements

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The Flusurvey and Influenzanet teams and participants



**centre for the  
mathematical  
modelling of  
infectious diseases**

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SCHOOL of  
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& TROPICAL  
MEDICINE



<http://sbfnk.github.io>