Computational modelling of influenza outbreaks as a tool to predict the impact of epidemics

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Purpose

- ❑ Rapid identification of influenza virus infection is crucial during epidemics[1], allowing:
  - Hospital epidemiology interventions.
  - Rapid management of patient treatment (antivirals).
- ❑ However, classical surveillance models can only describe the status quo of an outbreak and do not allow predicting the future dynamics.
- ❑ The basic reproduction (R_0) number describes how many people are infected by a single infected individual e.g. $R_0 = 2$, indicates that 2 people are subsequently infected.

Datasets

University Hospital Basel, Influenza seasons 2013 – 2016

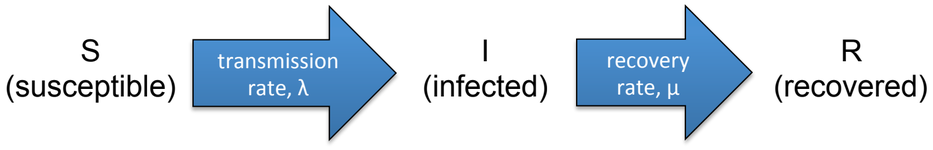
- ❑ All PCR confirmed cases (A+B) from the Hospital were included (**Figure 1**).
- ❑ PCR diagnostics was based on GeneXpert (Cepheid®).

Federal dataset of PCR-confirmed influenza cases reported in Switzerland

- ❑ All cases of Influenza have to be reported by law to the Federal Office of Health (**Figure 2**).
- ❑ Cases reported from 2007 to 2014 across age groups were available.
- ❑ We included all data from the cities Basel, Bern, and Zurich.

Methods

- ❑ A classic transmission-recovery model describes the spread.



- ❑ A statistical method was developed to estimate lambda and mu, and thus R0=lambda/mu.
- ❑ Assumption: Epidemics starts at week 0 with one case.
- ❑ In both datasets, the first six weeks were used for the R_0 calculation.

References

1 Miller MR, Peters TR et al J Infect Diseases 2015

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Results

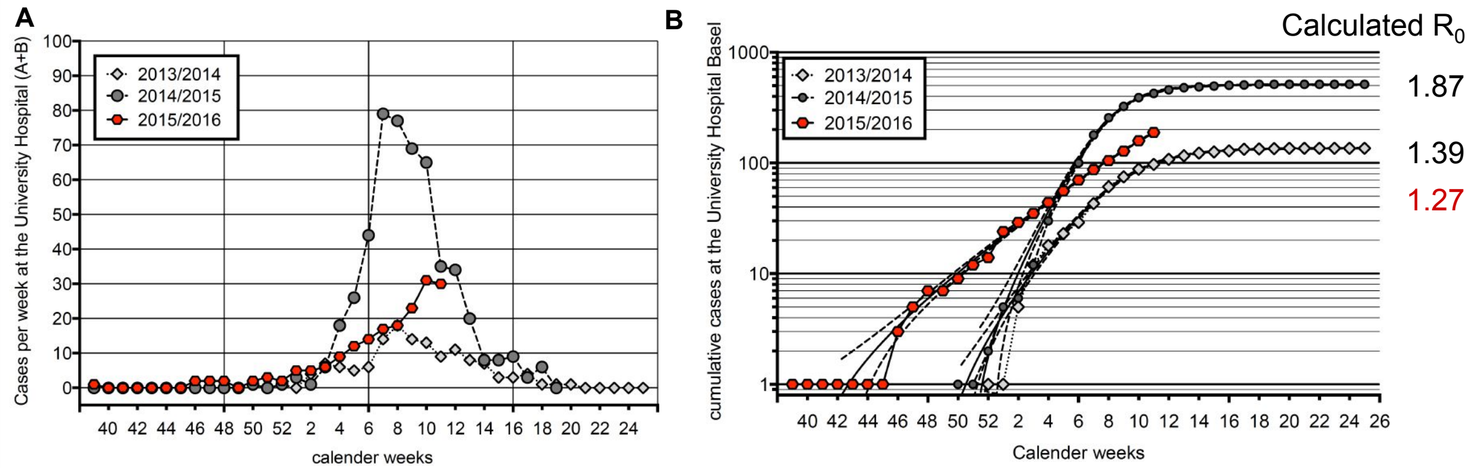

Figure 1. Absolute (**A**) and cumulative (**B**) cases of Influenza at the University Hospital Basel are shown. Based on the first six weeks, the R_0 was predicted using the computer algorithm.

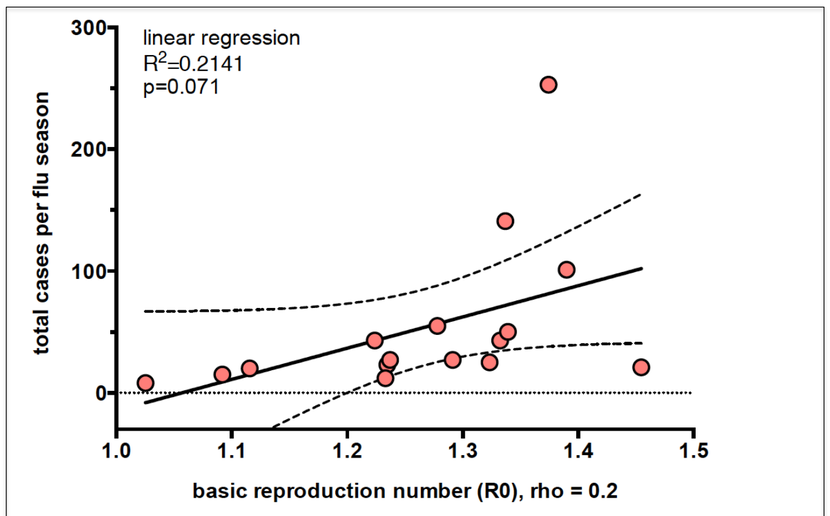

Figure 2. Correlation of total cases per flu season and predicted R_0 value are shown. Data of the Federal Office of Health from three major Swiss cities were used.

Outlook of the project:

- Comparison of different algorithms to predict the basic reproduction number.
- Prospective validation of the algorithm over the next years.
- Comparison of R_0 between age groups.
- Implementation into epidemic management.

Summary and Conclusions

- ❑ The basic reproduction number (R_0) can be calculated 4-6 weeks after the first detection of an influenza case.
- ❑ The R_0 correlates with the cumulative amount of cases per season.
- ❑ In the near future such prediction algorithm based on real time influenza data can provide valuable information for epidemic management e.g. public health authorothies.