The Epidemiology of Scabies

Kylie Ainslie, Mariette Hooiveld, Jacco Wallinga

2024-07-31

Table of Contents

[Introduction 1](#_Toc173339779)

[Methods 2](#_Toc173339780)

[Data Sources 2](#_Toc173339781)

[Serial Interval 3](#_Toc173339782)

[Growth rate 3](#_Toc173339783)

[Reproduction Number 3](#_Toc173339784)

[Results 4](#_Toc173339785)

[Serial Interval 4](#_Toc173339786)

[Growth Rate 5](#_Toc173339787)

[Reproduction Number 6](#_Toc173339788)

[Discussion 7](#_Toc173339789)

[References 7](#_Toc173339790)

[Appendix 9](#_Toc173339791)

[Sensitivity Analyses 9](#_Toc173339792)

## Introduction

Scabies is a neglected tropical disease caused by infestation of the skin with a microscopic mite (Sarcoptes scabiei). Symptoms are characterized by itchiness and rash at the site of infestation. Scabies affects around 400 million people per year, and accounts for a large proportion of skin disease in many low- and middle-income countries7. A rise in scabies cases has been observed through out Europe in recent years8–13, putting pressure on local health services. Despite the considerable burden scabies poses annually, little is known about the disease dynamics of scabies transmission, such as the generation time (time between infection of an index case and a secondary case), serial interval (the time from onset of symptoms in an index case to the time of symptom onset in a secondary case), growth rate, and reproduction number (the average number of secondary cases resulting from one index case). A 1944 study by Mellanby14 forms much of the basis of our current understanding of scabies transmission; however, the study was carried out on a small number of healthy volunteers which, and may not be representative of the natural history of scabies in populations in which scabies in widespread.

In this work, we aim to estimate epidemiological parameters of scabies. It is critical to better understand the underlying disease dynamics of scabies to 1) assess current spread and 2) inform infection control policy. Some modelling work has been performed to study the potential impacts of intervention strategies, such as mass drug administration, on scabies transmission15–17; however, the values used to parameterise these models are based largely on Mellanby’s 1944 study and use information about the mite life-cycle to approximate quantities such as latent period and infectious period. However, this information doesn’t necessarily provide good estimates for transmission potential in reality. For example, Kinyanjui et al.15 assume a latent period of 7-14 days to allow for the time for the time it takes for a fertilised female mite to reproduce and incorporate it into a susceptible-exposed-infectious model of scabies transmission. However, this assumes an equal chance of infectiousness despite the number of mites inhabiting an infested indivual. Mellanby14 shows that the probability of onward transmission of scabies is rare when the number of mites on an individual is low and increases as the mite population grows. A better approximation of the disease process can be obtained using the generation time or serial interval; however, no such estimates exist for scabies.

Additionally, the growth rate and reproduction number are quantities that describe how fast an infectious disease spreads. They are also used to determine appropriate control measures to reduce the number of secondary infections so that an epidemic dies out. During the COVID-19 pandemic, many analyses were performed to determine what interventions were needed to “flatten the curve” [cite] whereby, measures of spread that govern the height of the curve, the effective reproduction number (and growth rate), were reduced to slow the spread of COVID-19. However, in the case of scabies, the basic reproduction number has never been described. This makes it immensely difficult to determine what level of control measures are needed to contain disease spread. As evidence continues to suggest that scabies is a growing problem, it is important to describe the epidemiological characteristics of scabies.

In this study, we use epidemic curves of scabies outbreaks from the literature to estimate the serial interval. We use data on weekly scabies cases in the Netherlands to estimate time-varying reproduction number and annual growth rate.

## Methods

### Data Sources

We used epidemic curves from previously published studies of scabies outbreaks (Table @ref(tab:data\_sources\_table)) to estimate the serial interval of scabies. When the original study data was not provided, we reconstructed the data from the published epidemic curves.

Data sources used to estimate serial interval.

| **Authors** | **Year** | **Country** | **Details** | **Reference** |
| --- | --- | --- | --- | --- |
| Kaburi et al. | 2019 | Ghana | Outbreak of scabies in a preschool | 1 |
| Ariza et al. | 2013 | Germany | Outbreak of scabies in a preschool | 2 |
| Akunzirwe et al. | 2023 | Uganda | Outbreak of scabies in a fishing community | 3 |
| Tjon-Kon-Fat et al. | 2021 | Netherlands | Outbreak of scabies in a nursing home | 4 |
| Larosa et al. | 2003 | Spain | Outbreak of scabies in a hospital | 5 |
| Division of Public and Behavioral Health | 2015 | USA | Outbreak of scabies in a long-term care facility | 6 |

### Serial Interval

Using the epidemic curves from six different studies of scabies outbreaks (Table \@ref(tab:data\_sources\_table)), we estimated the mean and standard deviation of the serial interval distribution using the method proposed by Vink et al.18. The method involves calculating the index case-to-case (ICC) interval for each person, where the person with the greatest value for number of days since symptom onset will be considered the index case. The rest of the individuals will have an ICC interval calculated as the number of days between their symptom onset and the index case. We assumed a Normal serial interval distribution. We performed a sensitivity analysis in which a Gamma distribution was assumed as the serial interval distribution [TODO!].

We also performed a Bayesian meta-analysis using the brms package in R19 to estimate the pooled mean serial interval. We used a Bayesian hierarchical random-effects model. We chose to use a random effects model because we assume that each study has its own “true” effect size, which has been sampled from an overarching distribution of true effect sizes20. We specified a prior distribution N(100, 50) for the true pooled effect size and Cauchy(0,1) for the between-study heterogeneity. We performed sensitivity analyses on our choices of prior distributions [TODO!].

### Growth rate

We estimated the annual growth rate of scabies cases by fitting an exponential growth model to annual incidence of scabies per 1000 people from 2011 to 2023 in the Netherlands21. Using the fitted exponential growth model and the estimated growth rate, we then determined the projected incidence of scabies per 1000 people until 2033 if no interventions are implemented. We used bootstrapping with 1000 samples to obtain 95% confidence bounds for the projected incidence of scabies per 1000 people.

### Reproduction Number

We obtained weekly reported cases of scabies from 2011 to 2023 in the Netherlands8,21. We performed spectral analysis on the time series of weekly scabies cases using a modified Daniell kernel (m = 2) for smoothing to identify typical frequencies within the time series. To estimate time-varying reproduction number, we first randomly assigned each reported case a date of symptom onset in the week in which the case was reported. Using the daily time series, we applied the method proposed by Wallinga and Teunis22 to estimate the time-varying reproduction number by determining the likelihood of an event occurring for every pair of time points23. The method requires the specification of the serial interval distribution. We assumed a Normal serial interval distribution with mean 91.2 and standard deviation 22.79, as estimated previously. To obtain confidence intervals on the daily reproduction number, we used bootstrapping.

All analyses were performed in R 4.4.024.

## Results

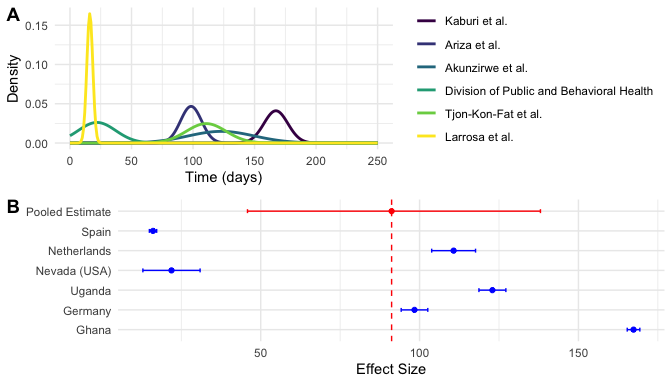
### Serial Interval

We estimated the mean and standard deviation of the serial interval using the epidemic curves from each study (Table \@ref(si\_results\_tab)). There was considerable variation between studies with the largest estimated mean serial interval of 167.34 (SD = 9.72) from data from Kaburi et al.1 which describes an outbreak in a preschool in Ghana. The smallest estimated mean serial interval was 16.11 (SD = 2.42), and was estimated from data from Larrosa et al.5 which describes an outbreak in a hospital in Spain.

Estimated mean and standard deviation (SD) of serial interval distribution for each study.

| **Study** | **Mean** | **SD** |
| --- | --- | --- |
| Kaburi et al. | 167.34 | 9.72 |
| Ariza et al. | 98.40 | 8.54 |
| Akunzirwe et al. | 122.92 | 26.92 |
| Tjon-Kon-Fat et al. | 110.71 | 16.14 |
| Larrosa et al. | 16.11 | 2.42 |
| Division of Public and Behavioral Health | 21.92 | 15.24 |

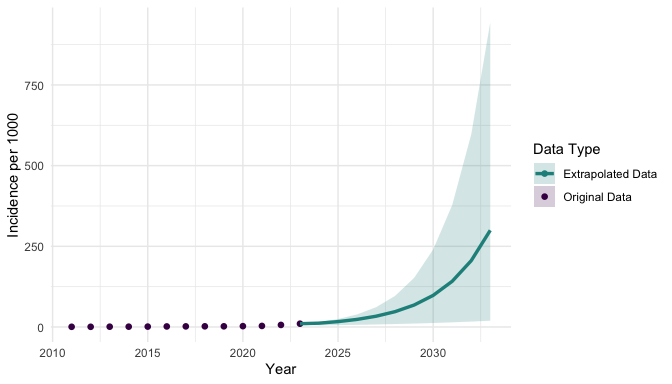
To obtain a pooled estimate of mean serial interval, we performed a Bayesian meta-analysis with random intercepts for each study. We estimated a pooled mean serial interval of 91.20 (95% CI: 45.84, 138.04) (Figure @ref(fsi\_multi-plot)B). As we saw with the individual study estimates (Table @ref(si\_results\_tab)), the meta-analysis provided further evidence of substantial heterogeneity among studies due to a large value of the standard deviation of the random intercepts (60.7). The large variation in the mean serial interval estimates can be visualised by plotting the estimated distributions of each study’s serial interval shown in Figure @ref(si\_multi-plot)A. A normal distribution is assumed, and is parameterized by the estimated mean and standard deviation of serial interval for each study.



A) Estimated serial interval distributions using data from epidemic curves from different scabies outbreaks. B) Forest plot of estimated mean serial interval and pooled mean.

### Growth Rate

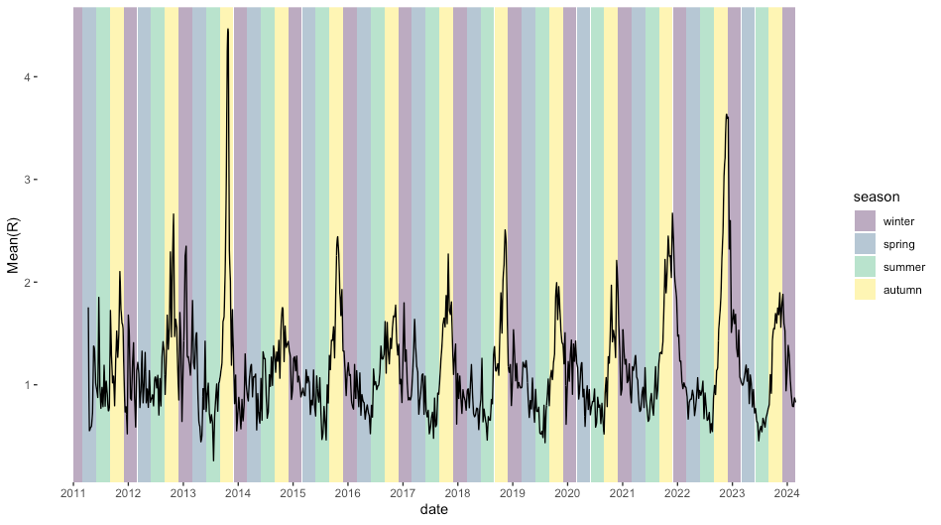
We estimated the annual growth rate of scabies cases by fitting an exponential growth model to annual incidence of scabies per 1000 people from 2011 to 2023 in the Netherlands21. We estimated an annual growth rate of 0.353 (95% CI: 0.152, 0.452). Using the fitted exponential growth model and the estimated growth rate, we then determined the projected incidence of scabies per 1000 people until 2033 if no interventions are implemented. We found that there could be a substantial increase in scabies incidence in the next 10 years in the Netherlands if no measures are taken to mitigate scabies spread (Figure @ref(fig:growth\_rate\_fig)).



Scabies incidence per 1000 people from 2011 to 2023 (points) and then projected scabies indcidence per 1000 people for 2024 to 2033 (line) using an exponential growth model with annual growth rate = 0.353. Shaded regions represent 95% confidence intervals for projected scabies incidence.

### Reproduction Number

We first performed a spectral analysis on the time series of weekly scabies cases in Netherlands from 2011 to 2023 using a modified Daniell kernel (m = 2) for smoothing. We found typical frequencies at 1/51.4 weeks and at 1/26.67 weeks (where 26.67 weeks is ~187 days). This suggests that there is a generation interval at 187 days and strong annual periodicity. We also estimated time-varying reproduction number and plotted it against season. It appears that peak transmissibility occurs in the autumn and in some years extend into winter (Figure \@ref(rt\_plot)).



Note: This is a place-holder figure.

# Discussion

Still need to flush this out.

Discuss time-series trends and population that it typically occurs in in NL (young adults/college students)

Discuss why estimates of mean serial interval across studies are so different (different populations and identification of symptom onset may be delayed).

Discuss limitations of the approach and caveats for interpretation.

# References

1. Kaburi, B. B. *et al.* Outbreak of scabies among preschool children, accra, ghana, 2017. *BMC Public Health* **19**, 746 (2019).

2. Ariza, L. *et al.* Investigation of a scabies outbreak in a kindergarten in constance, germany. *Eur. J. Clin. Microbiol. Infect. Dis.* **32**, 373–380 (2013).

3. An outbreak of scabies in a fishing community in hoima district, uganda, February−June, 2022. (2023).

4. Tjon-Kon-Fat, R. *et al.* Short report: The potential of PCR on skin flakes from bed linens for diagnosis of scabies in an outbreak. *PLoS Negl. Trop. Dis.* **15**, e0009485 (2021).

5. Larrosa, A. *et al.* Nosocomial outbreak of scabies in a hospital in spain. *Euro Surveill.* **8**, 199–203 (2003).

6. Division of Public and Behavioral Health. *Epidemiologic Investigation Summary, Scabies Outbreak Among Residents and Staff of a Long Term Care Facility in Clark County, Nevada, 2015*. vol. 2015 (2016).

7. Scabies.

8. Deursen, B. van *et al.* Increasing incidence of reported scabies infestations in the netherlands, 2011-2021. *PLoS One* **17**, e0268865 (2022).

9. Reichert, F., Schulz, M., Mertens, E., Lachmann, R. & Aebischer, A. Reemergence of scabies driven by adolescents and young adults, germany, 2009-2018. *Emerg. Infect. Dis.* **27**, 1693–1696 (2021).

10. Redondo-Bravo, L. *et al.* Scabies in spain? A comprehensive epidemiological picture. *PLoS One* **16**, e0258780 (2021).

11. Lugović-Mihić, L. *et al.* An increasing scabies incidence in croatia: A call for coordinated action among dermatologists, physicians and epidemiologists. *Zdr Varst* **59**, 264–272 (2020).

12. Amato, E. *et al.* Increase of scabies infestations, norway, 2006 to 2018. *Euro Surveill.* **24**, (2019).

13. Donà, M. G. *et al.* Increasing trend in confirmed scabies cases in the only public dermatological institute of scientific research and care in italy. *Eur. J. Dermatol.* **33**, 709–710 (2023).

14. Mellanby, K. [The development of symptoms, parasitic infection and immunity in human scabies](https://doi.org/10.1017/S0031182000021612). *Parasitology* **35**, 197–206 (1944).

15. Kinyanjui, T. *et al.* Scabies in residential care homes: Modelling, inference and interventions for well-connected population sub-units. *PLoS Comput. Biol.* **14**, e1006046 (2018).

16. Lydeamore, M. J. *et al.* A biological model of scabies infection dynamics and treatment informs mass drug administration strategies to increase the likelihood of elimination. *Math. Biosci.* **309**, 163–173 (2019).

17. Tellioglu, N. *et al.* Modelling mass drug administration strategies for reducing scabies burden in monrovia, liberia. *Epidemiol. Infect.* **151**, e153 (2023).

18. Vink, M. A., Bootsma, M. C. J. & Wallinga, J. Serial intervals of respiratory infectious diseases: A systematic review and analysis. *Am. J. Epidemiol.* **180**, 865–875 (2014).

19. Bürkner, P.-C. Brms: An R package for bayesian multilevel models using stan. *J. Stat. Softw.* **80**, 1–28 (2017).

20. Harrer, M., Cuijpers, P., Furukawa, T. A. & Ebert, D. D. Chapter 13 bayesian Meta-Analysis.

21. NIVEL. Cijfers ziekten per week in nederland.

22. Wallinga, J. & Teunis, P. Different epidemic curves for severe acute respiratory syndrome reveal similar impacts of control measures. *Am. J. Epidemiol.* **160**, 509–516 (2004).

23. Wallinga, J. & Lipsitch, M. How generation intervals shape the relationship between growth rates and reproductive numbers. *Proc. Biol. Sci.* **274**, 599–604 (2007).

24. R Core Team. [*R: A Language and Environment for Statistical Computing*](https://www.R-project.org). (R Foundation for Statistical Computing, Vienna, Austria, 2019).

# Appendix

## Sensitivity Analyses

TODO:

* add gamma distribution to Vink et al. method and re-run estimation
* re-run meta-analysis assuming gamma distribution
* potentially remove Uganda estimate from meta-analysis because it’s community transmission and not a confined setting (e.g., school, hospital, care home)
* check prior assumptions for meta-analysis
* more in-depth analysis of Rt