

# Endemic-epidemic modelling with surveillance

Sebastian Meyer

Institute of Medical Informatics, Biometry, and Epidemiology

Friedrich-Alexander-Universität Erlangen-Nürnberg, Erlangen, Germany

9 September 2024



## library("surveillance"): Temporal and Spatio-Temporal Modeling and Monitoring of Epidemic Phenomena

How it all started:

- **Michael Höhle** works on statistical methods for outbreak detection
- November 2005: first version on CRAN (among 600 packages, for R 2.2.0)
- **Held, Höhle, Hofmann (2005)** create an *endemic-epidemic* regression oriented model for multivariate infectious disease surveillance counts
- September 2006: initial release, much extended by **Michaela Paul** until 2012
- **Meyer et al. (2012)** develop an endemic-epidemic point process model

Meanwhile, surveillance is listed in four CRAN Task Views:  
 "Environmetrics", "Epidemiology", "SpatioTemporal", "TimeSeries"



---

# *Journal of Statistical Software*

April 2017, Volume 77, Issue 11.

doi:10.18637/jss.v077.i11

---

## Spatio-Temporal Analysis of Epidemic Phenomena Using the R Package `surveillance`

Sebastian Meyer  
Friedrich-Alexander-Universität  
Erlangen-Nürnberg

Leonhard Held  
University of Zurich

Michael Höhle  
Stockholm University

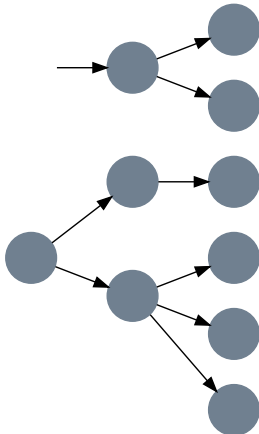
---

### Abstract

The availability of geocoded health data and the inherent temporal structure of communicable diseases have led to an increased interest in statistical models and software for spatio-temporal data with epidemic features. The open source R package `surveillance` can handle various levels of aggregation at which infective events have been recorded:

## Basic modelling concept

### Stochastic branching process with immigration



- Decomposed disease risk:
  - **Endemic:** background risk driven by seasonality, demographics, ...
  - $\oplus$
  - **Epidemic:** force of infection by previously infected individuals
- Force of infection may depend on social mixing and spatial/temporal distance to infective

## Endemic-epidemic modelling frameworks in surveillance

	twinstim	hhh4	twinSIR
<b>Data</b>	individual infections in continuous space-time	time series of counts stratified by region	individual SI[R][S] history of a fixed population
<b>Model</b>	spatio-temporal PP	conditional NegBin	multivariate temporal PP
<b>Rate</b> = <b>Endemic</b> + <b>Epidemic</b>	$\lambda(s, t)$ $V_{[s][t]} \rho_{[s][t]}$ $\sum_{j:t_j < t} \eta_j f(\ s - s_j\ ) g(t - t_j)$	$\mu_{it}$ $v_{it} e_{it}$ $\lambda_{it} Y_{i,t-1} + \phi_{it} \sum_{j \neq i} w_{ji} Y_{j,t-1}$	$\lambda_i(t)   \{i \in S(t)\}$ $v_i(t) \lambda_0(t)$ $\sum_{j \in I(t)} f(\ s_i - s_j\ )$

visualization

model assessment

likelihood inference

simulation

## EE in the wild

[https://surveillance.r-forge.r-project.org/applications\\_EE.html](https://surveillance.r-forge.r-project.org/applications_EE.html)

The endemic-epidemic modelling frameworks implemented in the R package **surveillance** have proven useful in a wide range of applications.

Show  entries Search:

Model	Disease	Location	Period	Journal	Year	URL
hhh4	COVID-19	France, Czechia, Italy	2020-2023	BMC Infectious Diseases	2024	<a href="https://doi.org/10.1186/s12879-024-08986-x">https://doi.org/10.1186/s12879-024-08986-x</a>
hhh4	highly pathogenic avian influenza	Europe	2016-2022	Scientific Reports	2023	<a href="https://doi.org/10.1038/s41598-023-42660-7">https://doi.org/10.1038/s41598-023-42660-7</a>
hhh4	pertussis	King	2010-	Epidemics	2023	<a href="https://doi.org/10.1016/j.epidem.2023.100689">https://doi.org/10.1016/j.epidem.2023.100689</a>

Model	Freq
hhh4	31
twinstim	6
twinSIR	1

## EE in the wild

[https://surveillance.r-forge.r-project.org/applications\\_EE.html](https://surveillance.r-forge.r-project.org/applications_EE.html)

The endemic-epidemic modelling frameworks implemented in the R package **surveillance** have proven useful in a wide range of applications.

Show  entries

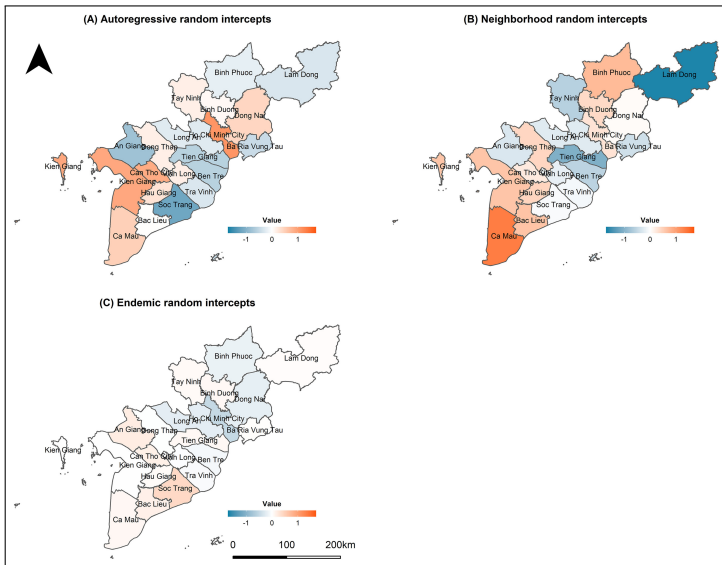
Search:

Model	Disease	Location	Period	Journal	Year	URL
hhh4	COVID-19	France, Czechia, Italy	2020-2023	BMC Infectious Diseases	2024	<a href="https://doi.org/10.1186/s12879-024-08986-x">https://doi.org/10.1186/s12879-024-08986-x</a>
hhh4	highly pathogenic avian influenza	Europe	2016-2022	Scientific Reports	2023	<a href="https://doi.org/10.1038/s41598-023-42660-7">https://doi.org/10.1038/s41598-023-42660-7</a>
hhh4	pertussis	King	2010-	Epidemics	2023	<a href="https://doi.org/10.1016/j.epidem.2023.100689">https://doi.org/10.1016/j.epidem.2023.100689</a>

Model	Freq
hhh4	31
twinstim	6
twinSIR	1

Diseases (hhh4)	Freq
COVID-19	11
measles	5
campylobacteriosis	3
dengue	2
pertussis	2
cutaneous leishmaniasis	1
hand, foot and mouth disease	1
invasive pneumococcal disease	1
norovirus gastroenteritis	1
SFTS	1
visceral leishmaniasis	1

# Nguyen et al. (2022): Understanding the transmission dynamics of a large-scale measles outbreak in Southern Vietnam





# Kjær et al. (2023): Early warning system for avian influenza

<https://www.enigmahpai.org/>



ENIGMA HPAI model version 1.0



2024-09-07 Select Date Range (needs to be within 27/09/2021 and 31/08/2024, see model description for details about date range).

27/09/2021

to

31/08/2024

Select:

- Map of detections
- Timeseries
- Model fit
- Forecasting

Select country (only countries with > 50 detections total are shown)

Summed all countries

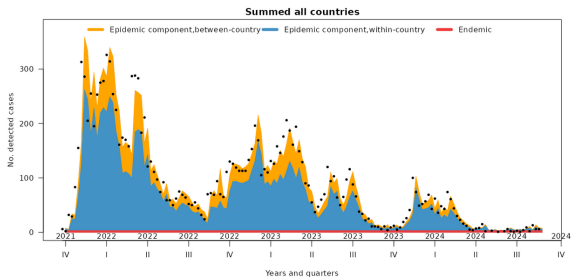
The purpose of this webpage is to show the predictions of the ENIGMA HPAI model. This model has been developed during research at the University of Copenhagen in the [ENIGMA project, 2021-2024](#). The ENIGMA project is based in the [Avian Influenza Epidemiology Subgroup](#) at the University of Copenhagen and is part of the [Danish Veterinary Contingency Consortium \(DKVET\)](#) funded by the Danish Food and Veterinary Administration. R code and data used for the ENIGMA HPAI model is available at [GitHub](#).

*Disclaimer: The model and data reflects the state of knowledge available on the date of dispatch. The University of*

Model output

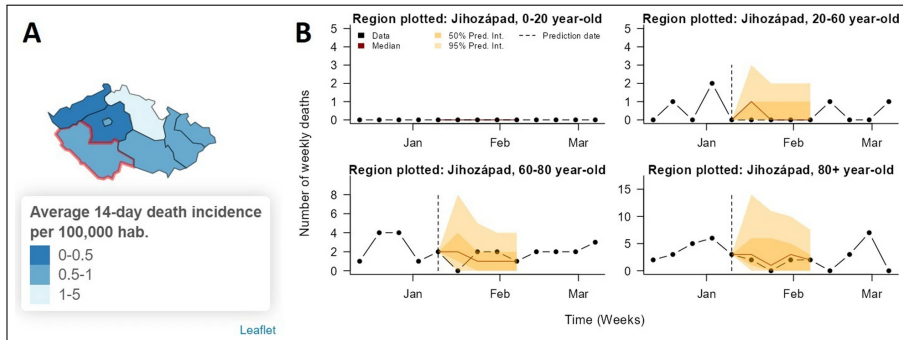
Model description

Download



Overall model fit aggregated over all the 37 countries shown for 27/09/2021 to 31/08/2024. The plot shows the relative contribution of model components based on the final multivariate time-series model in Kjær et al. (2023). Dots show the actual counts of reported highly pathogenic avian influenza (H5 subtype) detections in domestic and wild birds. Note that zero/missing detections have been omitted.

# Robert et al. (2024): Predicting subnational incidence of COVID-19 cases and deaths in EU countries (*R Shiny App*)



## Starting point for hhh4()

We have:

- Public health surveillance **counts**  $Y_{grt}$  indexed by [group,] [region,] time
- Maybe a **social contact matrix**  $C = (c_{g'g})$
- Maybe additional **covariates**: vaccination coverage, climate, socio-demographics, ...

We want: an easy-to-fit regression-like model coping with all dimensions

$g$ : social mixing patterns between age groups

$r$ : spatial dynamics through human travel

$t$ : temporal dependencies inherent to communicable diseases, including occasional outbreaks

## An age-stratified, spatio-temporal, endemic-epidemic model

$$Y_{grt} | Y_{\cdot, \cdot, t-1} \sim \text{NegBin}(\mu_{grt}, \psi_{gr})$$

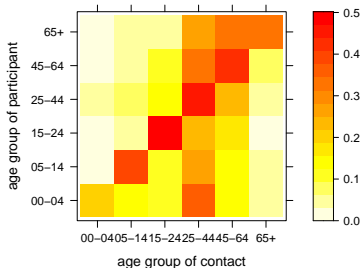
$$\mu_{grt} = v_{grt} + \phi_{grt} \sum_{g', r'} c_{g'g} w_{r'r} Y_{g', r', t-1}$$

## An age-stratified, spatio-temporal, endemic-epidemic model

$$Y_{grt} | Y_{\cdot, \cdot, t-1} \sim \text{NegBin}(\mu_{grt}, \Psi_{gr})$$

$$\mu_{grt} = \nu_{grt} + \phi_{grt} \sum_{g', r'} c_{g'g} w_{r'r} Y_{g', r', t-1}$$

Contact matrix ( $c_{g'g}$ ) for  $g' \rightarrow g$ ,  
for example from POLYMOD

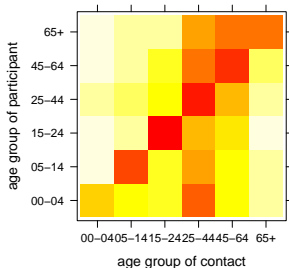


## An age-stratified, spatio-temporal, endemic-epidemic model

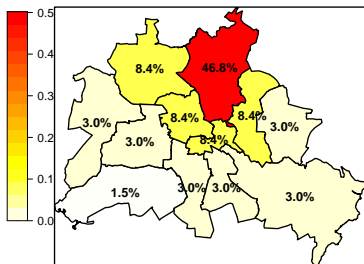
$$Y_{grt} | Y_{\cdot, \cdot, t-1} \sim \text{NegBin}(\mu_{grt}, \Psi_{gr})$$

$$\mu_{grt} = \nu_{grt} + \phi_{grt} \sum_{g', r'} c_{g'g} \boxed{w_{r'r}} Y_{g', r', t-1}$$

Contact matrix ( $c_{g'g}$ ) for  $g' \rightarrow g$ ,  
for example from POLYMOD



Spatial weights for  $r' \rightarrow r$ , e.g.,  
power-law decay  $w_{r'r} = (o_{r'r} + 1)^{-\rho}$

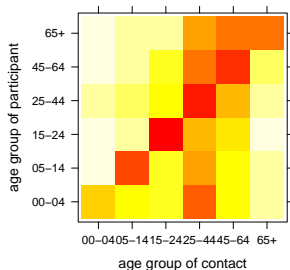


## An age-stratified, spatio-temporal, endemic-epidemic model

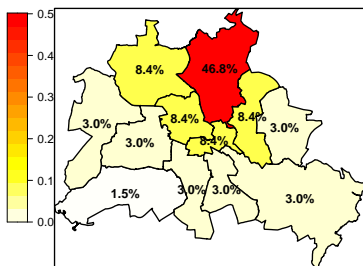
$$Y_{grt} | Y_{\cdot, \cdot, t-1} \sim \text{NegBin}(\mu_{grt}, \Psi_{gr})$$

$$\mu_{grt} = v_{grt} + \phi_{grt} \sum_{g', r'} c_{g'g} w_{r'r} Y_{g', r', t-1}$$

Contact matrix ( $c_{g'g}$ ) for  $g' \rightarrow g$ ,  
for example from POLYMOD



Spatial weights for  $r' \rightarrow r$ , e.g.,  
power-law decay  $w_{r'r} = (o_{r'r} + 1)^{-\rho}$



Log-linear  
predictors  
 $v_{grt}$  and  $\phi_{grt}$

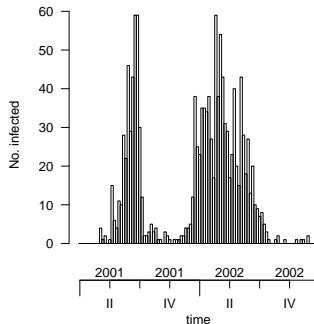
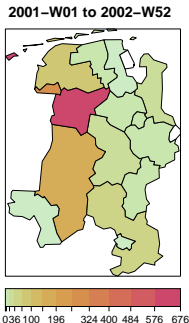
- Population
- Seasonality
- Group-specific susceptibility
- (Covariates)

## A simple example

```
library("surveillance")
data("measlesWeserEms") # of class "sts" (surveillance time series)
```

```
plot(measlesWeserEms,
     type = observed ~ unit)
```

```
plot(measlesWeserEms,
     type = observed ~ time)
```





## Univariate hhh4() model

For the overall count time series  $Y_t$ , aggregated over all districts:

```
measles1 <- aggregate(measlesWeserEms, by = "unit")
```

Endemic-Epidemic decomposition of disease risk:

$$Y_t | Y_{t-1} \sim \text{NegBin}(\mu_t, \psi)$$

$$\mu_t = \nu_t + \lambda Y_{t-1}$$

Yearly seasonality via sine-cosine terms in log-linear predictor  $\nu_t$ :

$$\log(\nu_t) = \alpha + \gamma \sin(2\pi t/52) + \delta \cos(2\pi t/52)$$

Equivalent R formula for this model component:

```
(endemic <- addSeason2formula(~1))  
~1 + sin(2 * pi * t/52) + cos(2 * pi * t/52)
```

## Univariate hhh4() model

```

measlesModel <- list(end = list(f = endemic), # "nu"
                    ar = list(f = ~1),      # "lambda"
                    family = "NegBin1")
  
```

## Univariate hhh4() model

```
measlesModel <- list(end = list(f = endemic), # "nu"
                    ar = list(f = ~1),      # "lambda"
                    family = "NegBin1")
```

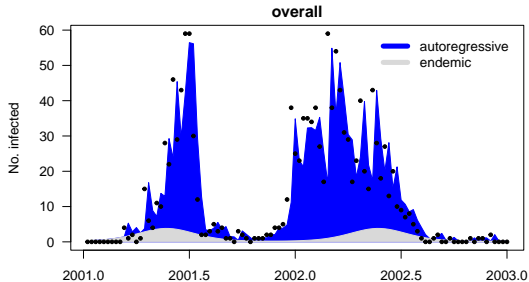
```
measlesFit <- hhh4(measles1, measlesModel)
```

## Univariate hhh4() model

```
measlesModel <- list(end = list(f = endemic), # "nu"  
                    ar = list(f = ~1),      # "lambda"  
                    family = "NegBin1")
```

```
measlesFit <- hhh4(measles1, measlesModel)
```

```
plot(measlesFit)
```



## methods(class = "hhh4")

Display	Extract	Modify	Other
print	nobs	update	predict
summary	coef		simulate
plot	fixef		pit
	ranef		scores
	vcov		calibrationTest
	confint		all.equal
	coeflist		oneStepAhead
	logLik		
	residuals		
	terms		
	formula		
	getNEweights		