

Endemic-epidemic modelling with surveillance

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```
library("surveillance")
```

Some background:

- Michael Höhle had worked on statistical methods for **outbreak detection** and published a first version of surveillance on CRAN in *November 2005*
- Back then, we had R 2.2.0 and only about 600 packages on CRAN.
- Since 2011, surveillance additionally provides three classes of **regression models for infectious disease surveillance data**



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

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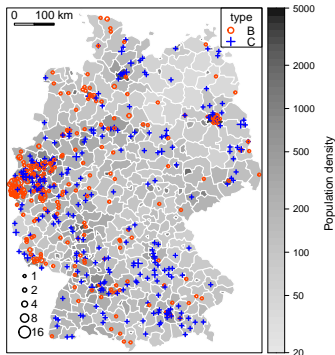
Abstract

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:

Two types of supported surveillance data

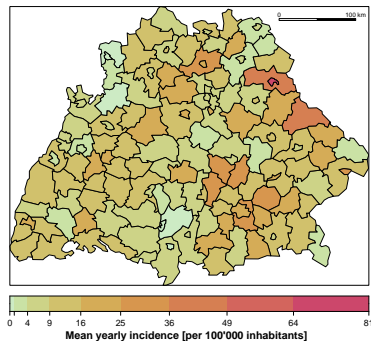
Individual-level data

```
coordinates time sex agegrp ...
1 (4112, 3203) 1 male [3,19) ...
2 (4123, 3077) 1 male [3,19) ...
3 (4412, 2916) 6 female [19,Inf) ...
[....]
```

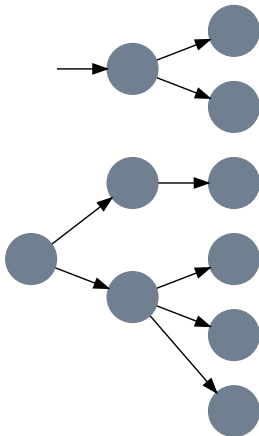


Count time series

```
09162 09184 09179 09174 ...
2005-W01 7 0 0 1 ...
2005-W02 2 1 0 0 ...
2005-W03 1 4 0 0 ...
[....]
```



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Endemic-epidemic modelling frameworks in surveillance

	twinstim	hhh4	twinSIR
Data	individual events in continuous space-time	event counts aggregated in space and time	individual SI[R][S] history of a fixed population
Example	case reports of IMD, Germany, 2002–2008	week × district counts of measles, Weser-Ems region, 2001–2002	measles outbreak among households, Hagelloch, 1861
Model	spatio-temporal PP	multivariate NegBin time series	multivariate temporal PP
Rate = Endemic + Epidemic	$\lambda(s, t)$ $V[s][t] \rho[s][t]$ $\sum_{j: t_j < t} \eta_j f(\ s - s_j\) g(t - t_j)$	μ_{it} $V_{it} e_{it}$ $\lambda_{it} Y_{i,t-1} + \phi_{it} \sum_{j \neq i} w_{ji} Y_{j,t-1}$	$\lambda_i(t) \mid \{i \in S(t)\}$ $v_i(t) \lambda_0(t)$ $\sum_{j \in I(t)} f(\ s_i - s_j\)$

visualization

model assessment

likelihood inference

simulation

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: a joint model of all three data dimensions

g : social mixing patterns between age groups

r : spatial dynamics through human travel

t : temporal dependencies inherent to communicable diseases

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

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

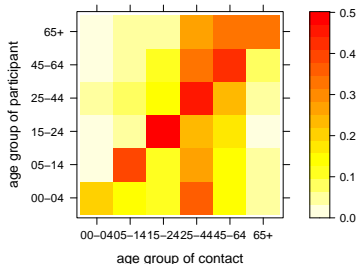
$$\mu_{grt} = v_{grt} + \phi_{grt} \sum_{g', r'} c_{g'g} w_{r'r} Y_{g', r', t-1}$$

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

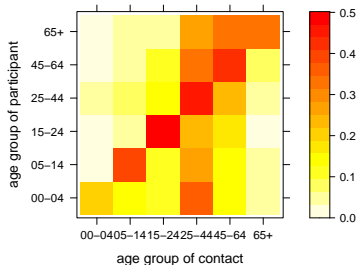


An age-stratified, spatio-temporal, endemic-epidemic model

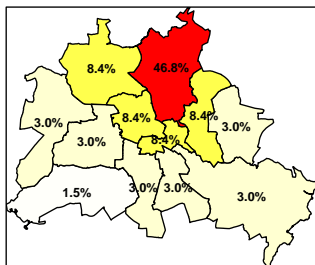
$$Y_{grt} | Y_{\cdot, \cdot, t-1} \sim \text{NegBin}(\mu_{grt}, \psi_{gr})$$

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

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



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

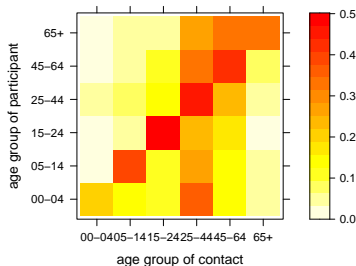


An age-stratified, spatio-temporal, endemic-epidemic model

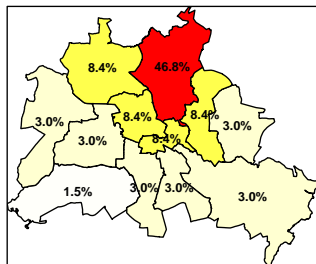
$$Y_{grt} | Y_{\cdot, \cdot, t-1} \sim \text{NegBin}(\mu_{grt}, \psi_{gr})$$

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

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

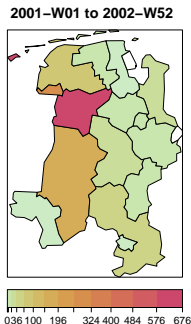


Log-linear
predictors
 v_{grt} and ϕ_{grt}

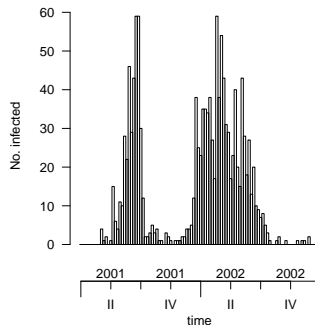
- Population
- Seasonality
- Group-specific susceptibility
- (Covariates)

A simple example: data("measlesWeserEms")

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



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



Following slides: univariate model for the (right-hand) overall time series

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

Univariate hhh4() model

Number of cases at time t

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

Endemic-Epidemic decomposition of disease risk:

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

Seasonality via sine-cosine terms in v_t :

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

```
(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")
measlesFit <- hhh4(measles1, control = measlesModel)
summary(measlesFit, amplitudeShift = TRUE, idx2exp = TRUE)
```

Call:

```
hhh4(stsObj = measles1, control = measlesModel)
```

Coefficients:

	Estimate	Std. Error
ar.1	-0.09456	0.10125
end.1	-0.09826	0.22934
end.A(2 * pi * t/52)	1.43597	0.37315
end.s(2 * pi * t/52)	-0.77073	0.19739
overdisp	0.34459	0.07951

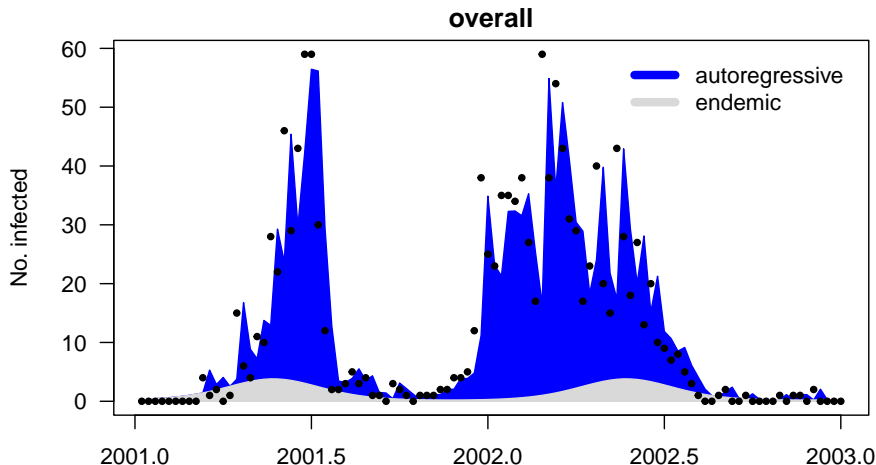
Log-likelihood: -271.32

AIC: 552.64

BIC: 565.82

Fitted mean components

```
plot(measlesFit, type = "fitted")
```



Methods for "hhh4" objects

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		