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School on Modelling Tools and Capacity Building in Climate and Public Health

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Beyond linearity: Using GAMs for modelling dengue and malaria data

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What we wanted to know

- Are there significant relationships between occurrence and weather?
- What is the functional form of those relationships?
- Are there any thresholds?
- Other determinants showing a statistically significant effect?



Theoretical relationships

- Temperature and precipitation regulate many aspects of the ecology of vector-borne diseases
 - Temperature: Extrinsic incubation period (EIP), vector survival, biting frequency, mosquito size, changes in host behaviour
 - Very low or very high temperatures may hamper the ecology of the disease
 - Rainfall: creation or wash out of breeding sites
 - Dengue: preference for man-made containers
 - Malaria: sunlit shallow pools, edges of rivers, swamps, lake edges



But....

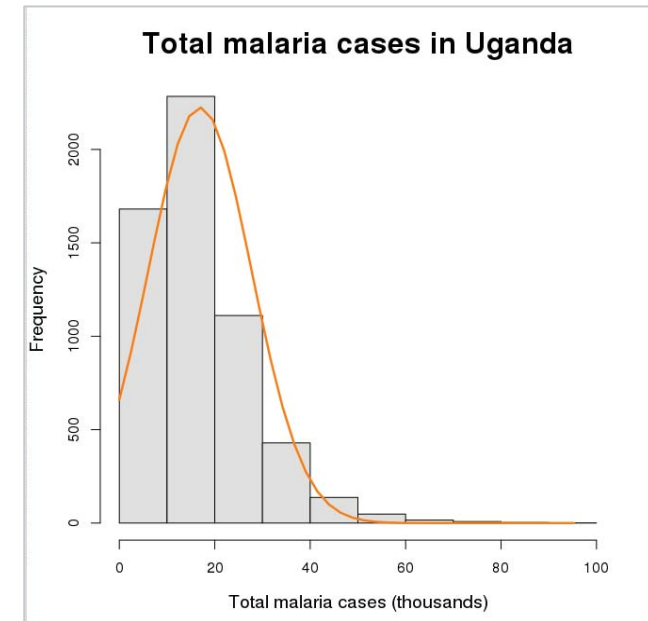
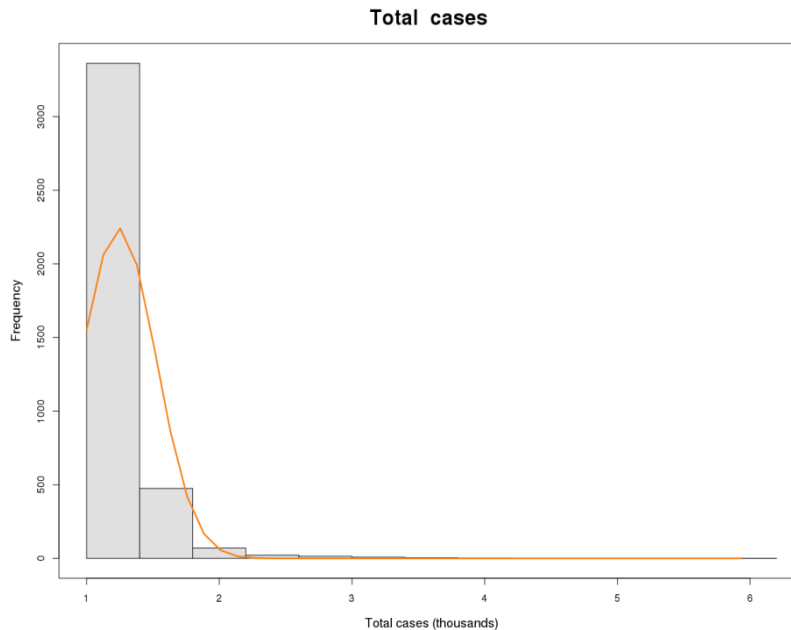
- These relationships are largely confounded by other factors:
 - Access to protective measures
 - Sheltering in sealed buildings
 - Control measures
 - Immunity
 - Urbanisation
 - Increased travelling and transportation



The need for a semi-parametric approach

- Epidemiological data
 - Dengue: 276 months of province-specific lab confirmed dengue reports ($n = 32$)
 - Malaria: 108 months of district-specific suspected cases ($n = 56$)
- Weather-related variables
 - Mexico: Tmin, Tmax, rainfall (station data)
 - Uganda: Air temperature, water fraction, soil moisture, mean temperature, rainfall (satellite and reanalyses data)
- Socioeconomic data
 - Usually yearly or decadal information

Data distribution



Quasi-Poisson models do not assume a particular probability distribution and relax the assumption of *variance* (σ^2) = *mean* (μ)

Model

- Poisson GAM:

$$g(\mu_{ti}) = \eta(t') + \sum_{j=1}^J \eta(X_{jti}) + \sum_{k=1}^K \beta_k(Z_{kti}) + \log(\xi_{ti}) + d_i + \alpha$$

$g(\cdot)$ is a log-link function that ensures that the fitted values are **always** non-negative

Model

- Poisson GAM:

$$g(\mu_{ti}) = \eta(t') + \sum_{j=1}^J \eta(X_{jti}) + \sum_{k=1}^K \beta_k(Z_{kti}) + \log(\xi_{ti}) + d_i + \alpha$$

μ is the **rate parameter** (expected number of new disease cases at time t and administrative unit i)

Model

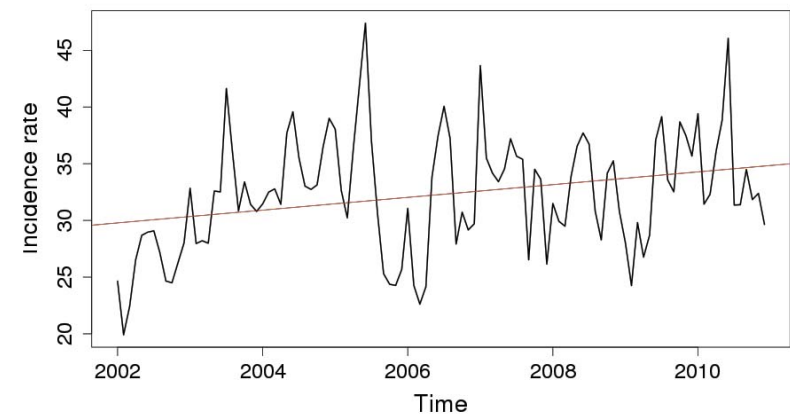
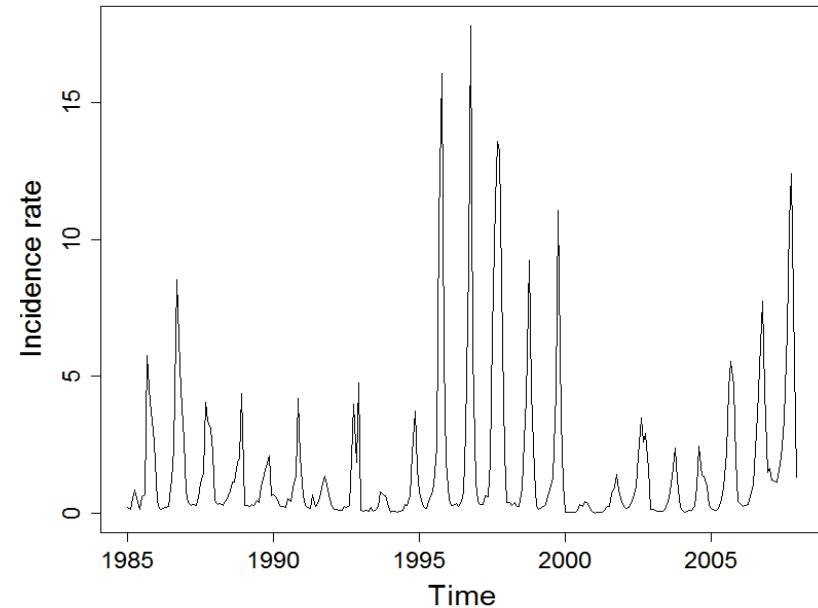
- Poisson GAM:

$$g(\mu_{ti}) = \mathbf{s}(t') + \sum_{j=1}^J \mathbf{s}(X_{jti}) + \sum_{k=1}^K \beta_k(Z_{kti}) + \log(\xi_{ti}) + d_i + \alpha$$

$\mathbf{s}(\cdot)$ indicates a **smooth function** (spline) for the time variable $1, \dots, n$ (months) with q degrees of freedom per year

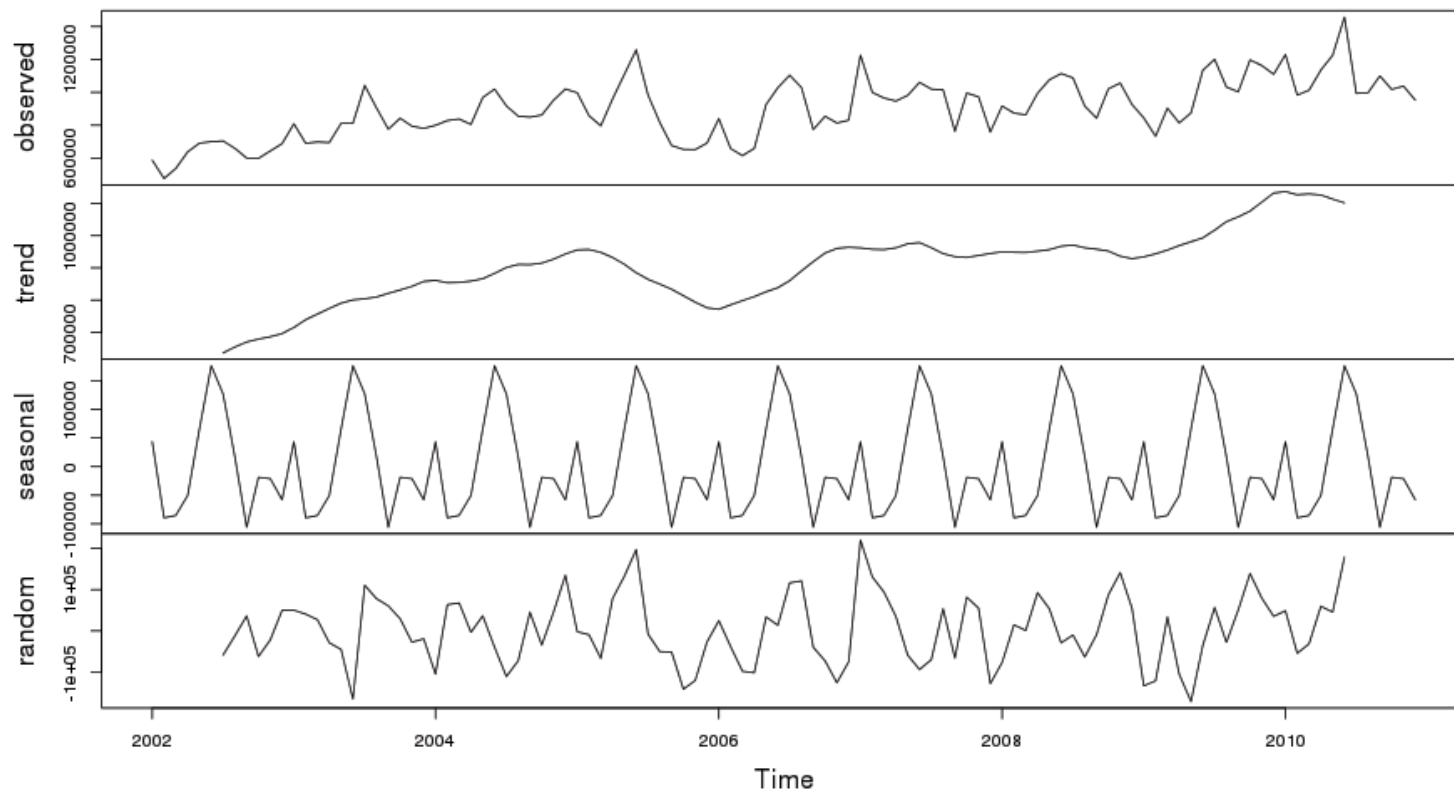
Annual cycle and inter-annual variability

- Holidays, seasonal water storage, seasonal migration
- New diagnostic techniques, micro-evolutionary changes, policy implementation



Malaria time series decomposition

Decomposition of additive time series



Model

- Poisson GAM:

$$g(\mu_{ti}) = \alpha(t') + \sum_{j=1}^J \alpha(X_{jti}) + \sum_{k=1}^K \beta_k(Z_{kti}) + \log(\xi_{ti}) + d_i + \alpha$$

Nonlinear effect of the climate variables (X) at time t and administrative unit i

In the model

- Univariate smooth functions for j climate variables

$$\sum_{j=1}^J s(X_{jti})$$
$$s_1(Tmin_{tj}) + s_2(Tmax_{tj}) + s_3(Rain_{tj})$$

In the model

- Univariate smooth functions for j climate variables

$$\sum_{j=1}^J s(X_{jti})$$

$$s_1(Tmin_{ti}) + s_2(Tmax_{ti}) + s_3(Rain_{ti})$$

In the model

- Univariate smooth functions for j climate variables

$$\sum_{j=1}^J s(X_{jti})$$
$$s_1(Tmin_{ti}) + s_2(Tmax_{ti}) + s_3(Rain_{ti})$$

Model

- Poisson GAM:

$$g(\mu_{ti}) = \mathfrak{s}(t') + \sum_{j=1}^J \mathfrak{s}(X_{jti}) + \sum_{k=1}^K \beta_k(Z_{kti}) + \log(\xi_{ti}) + d_i + \alpha$$

Effect of non-climatic predictors in a linear fashion $\beta_1 Z_1 + \beta_2 Z_2 + \dots \beta_K Z_K$

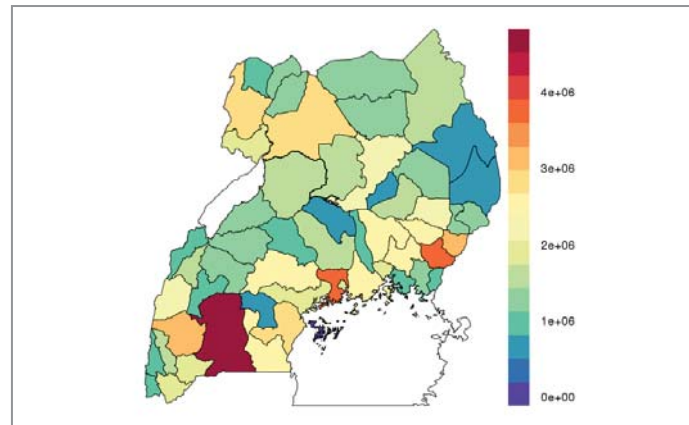
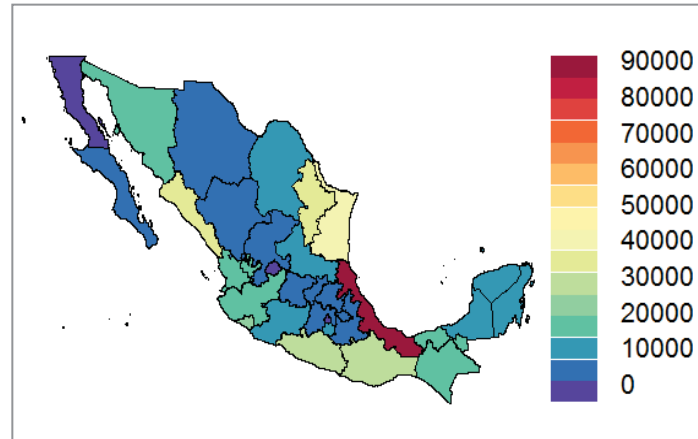
Model

- Poisson GAM:

$$g(\mu_{ti}) = \mathfrak{s}(t') + \sum_{j=1}^J \mathfrak{s}(X_{jti}) + \sum_{k=1}^K \beta_k(Z_{kti}) + \log(\xi_{ti}) + d_i + \alpha$$

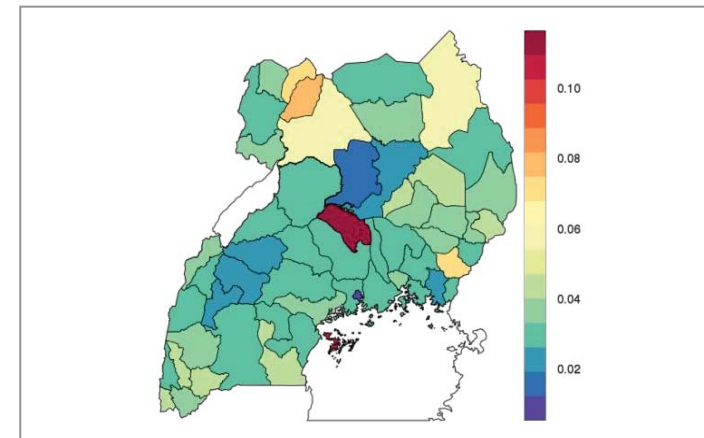
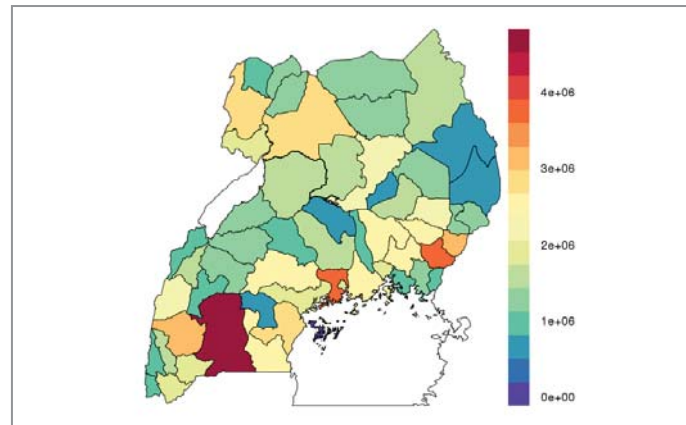
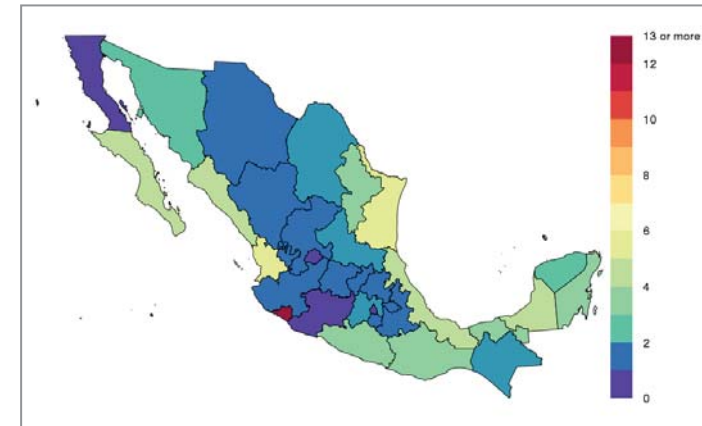
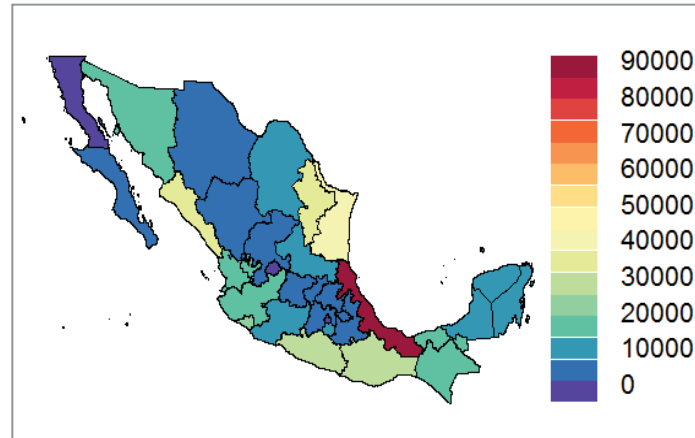
Log of the **population** (ξ) at time t and administrative unit i as an **offset**. No regression parameter estimated for it.

Why the offset?



You may see more cases in a region just because they have a larger population!

Why the offset?



Mean monthly disease occurrence per province (left panel)
vs. mean monthly incidence rate (right panel)

Model

- Poisson GAM:

$$g(\mu_{ti}) = \eta(t') + \sum_{j=1}^J \eta(X_{jti}) + \sum_{k=1}^K \beta_k(Z_{kti}) + \log(\xi_{ti}) + d_i + \alpha$$

Fixed-effects to control for possible omitted variable bias in each administrative unit

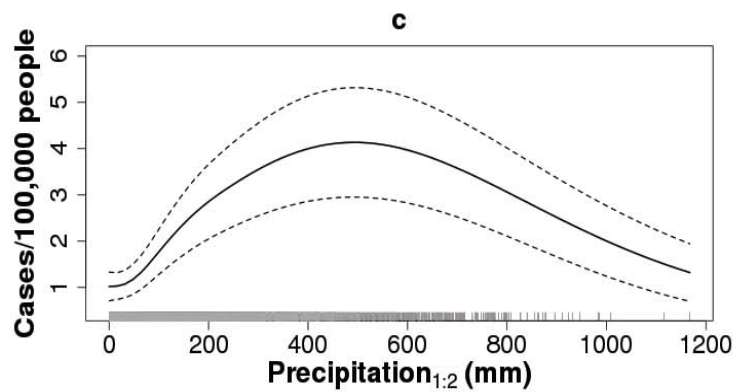
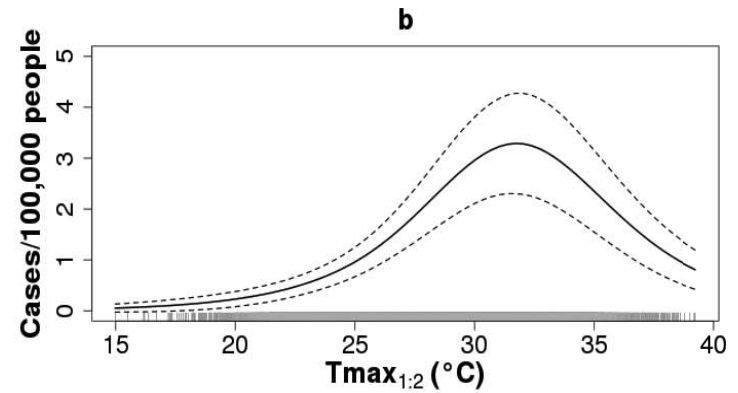
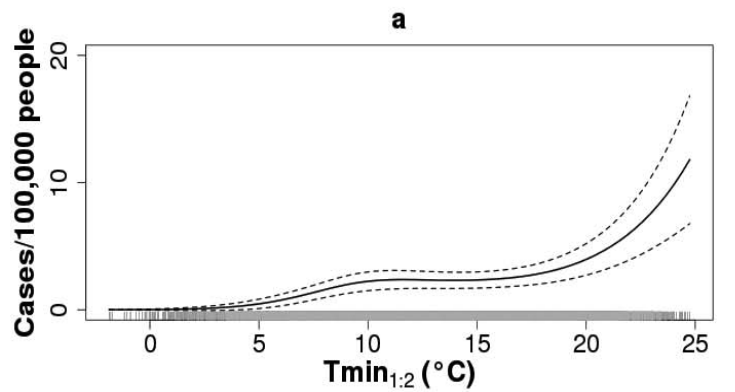
Model

- Poisson GAM:

$$g(\mu_{ti}) = \eta(t') + \sum_{j=1}^J \eta(X_{jti}) + \sum_{k=1}^K \beta_k(Z_{kti}) + \log(\xi_{ti}) + d_i + \alpha$$

Intercept (the log of the expected incidence rate when all variables in the model are evaluated at zero).

Dengue-weather

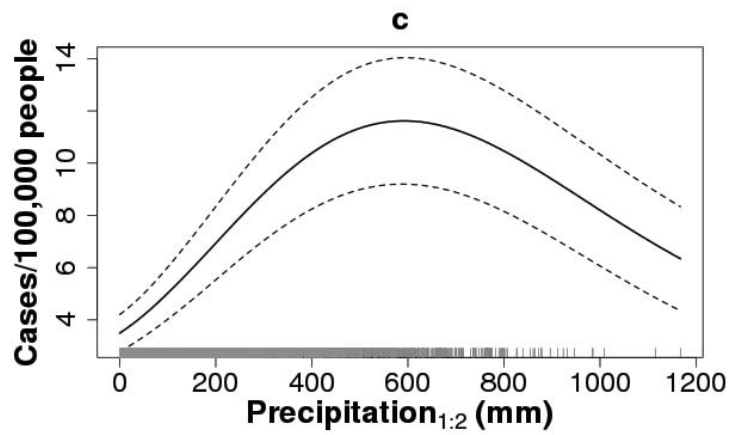
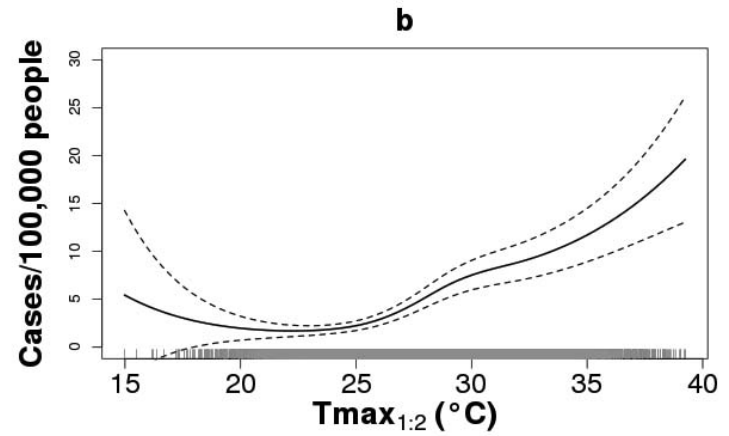
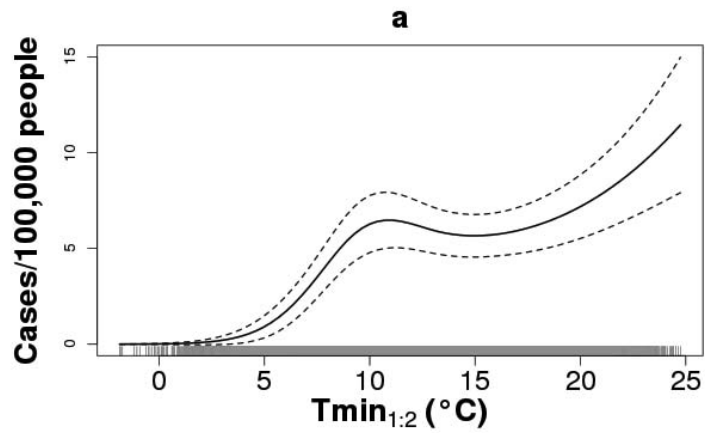




Autocorrelation?

- Dengue transmission implies one person leading to one or more secondary infections
 - Violation of independence
- Include log-transformed cases in the previous month (plus 1!)

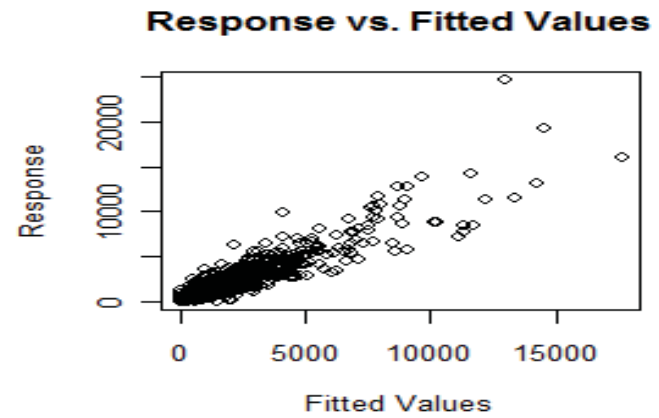
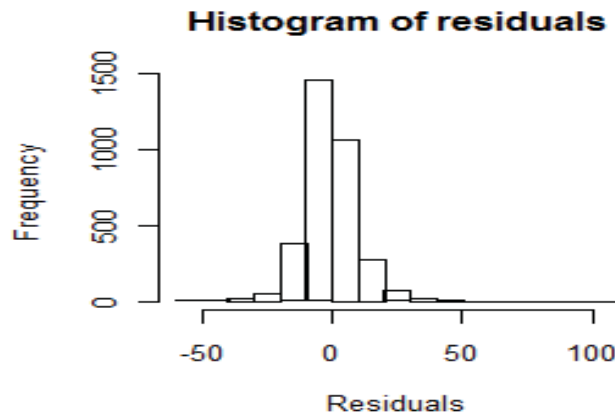
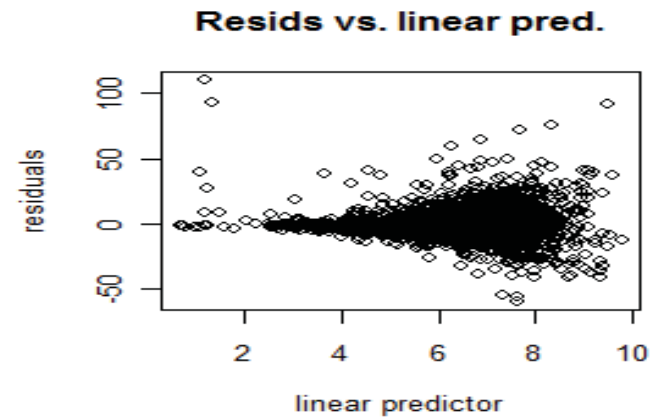
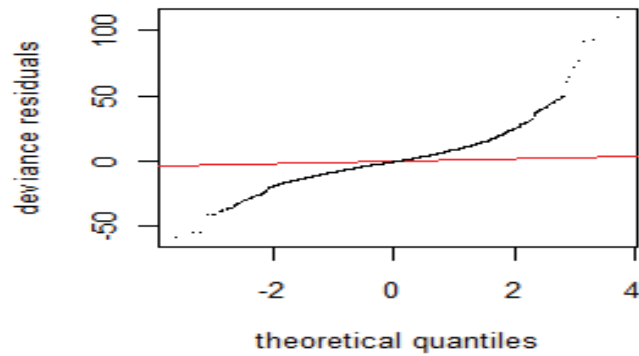
AR1 adjusted



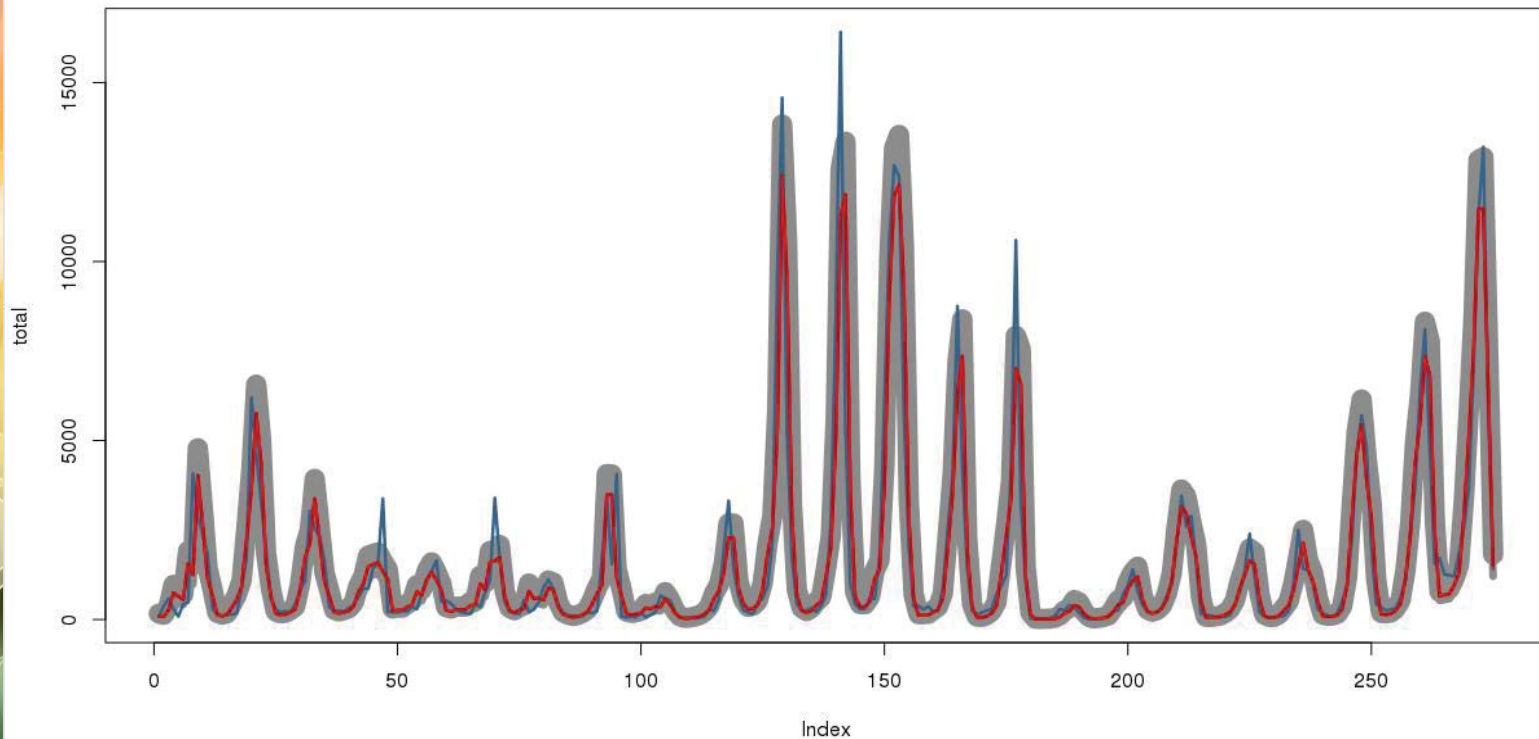
Model comparison

Model	AIC	GCV	PACF	Adj. R2	Deviance explained
Unadjusted	767573	88.1	0.63	0.38	62%
Autocorrelation adjusted	373465	41.8	0.06	0.68	82%

gam.check()

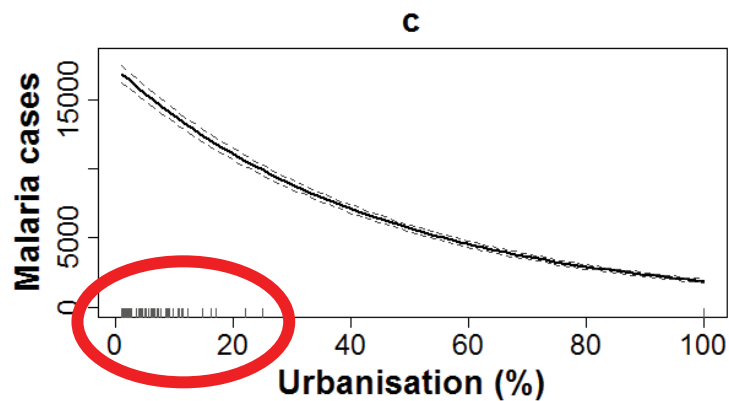
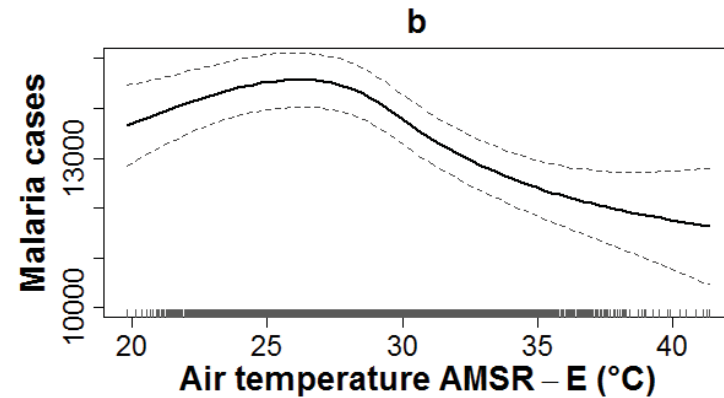
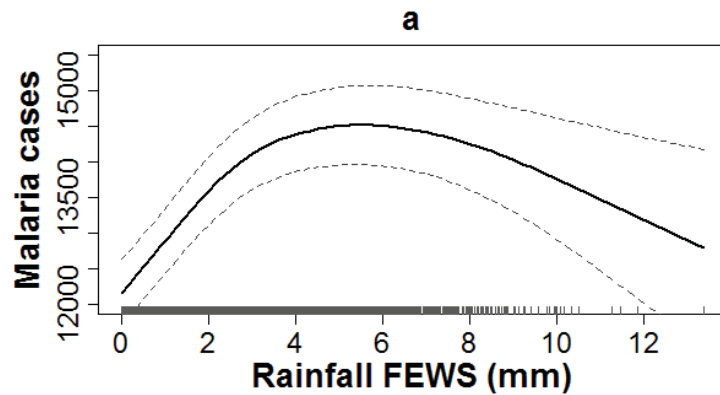


Fitted values



Total number of dengue cases in the country (blue line) and GAM-estimated number of cases (red line). The gray shadow indicates the 95% confidence interval.

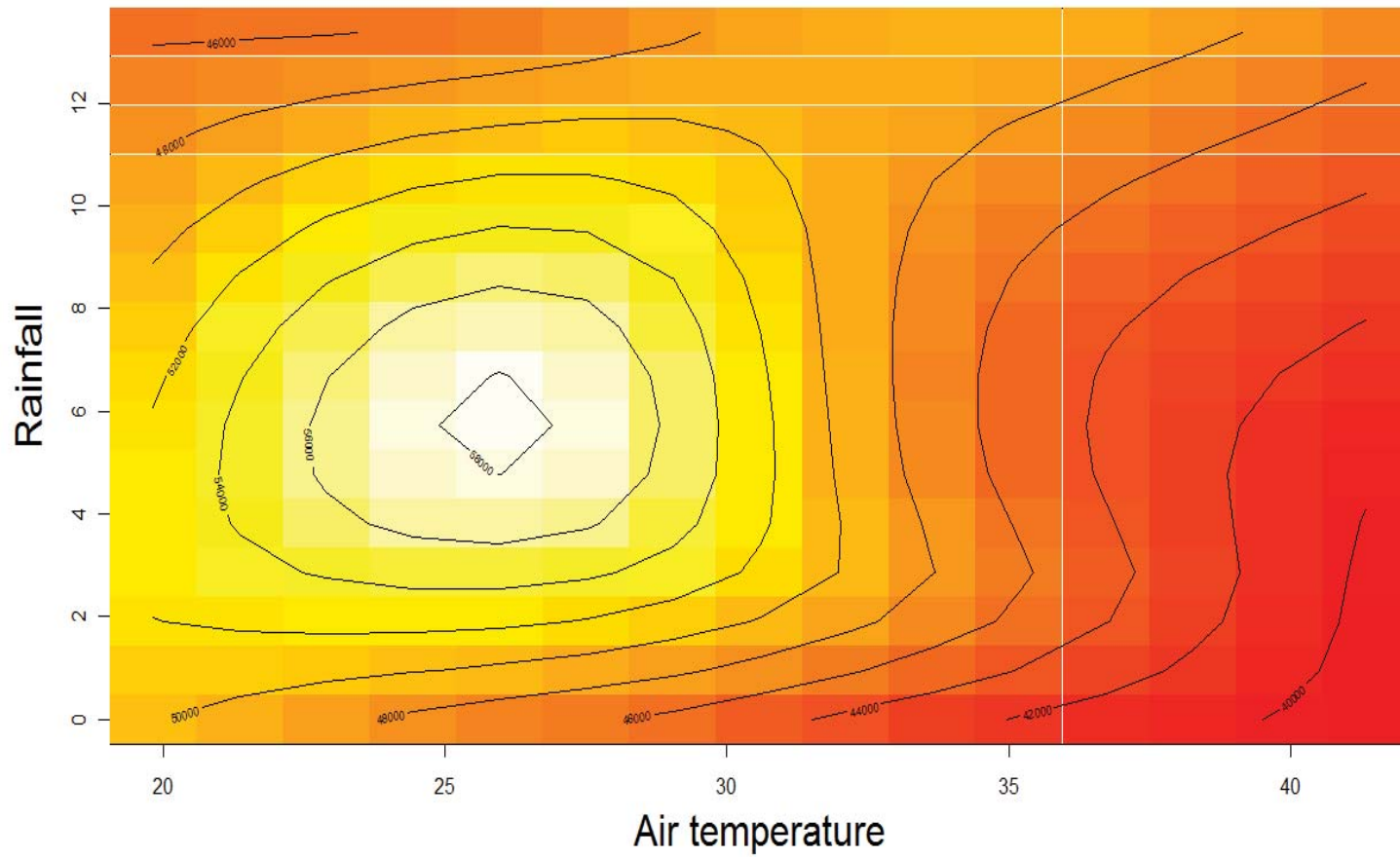
Malaria results



What about interactions?

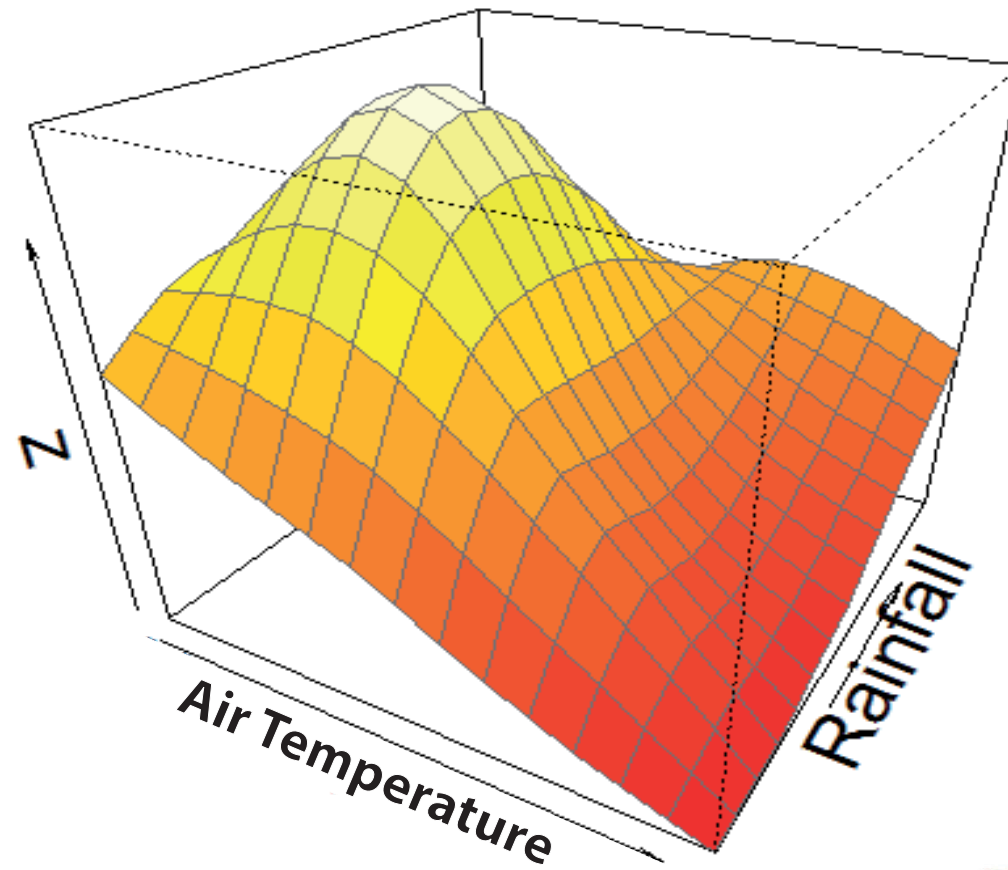
Interaction

AirTemp * Rain interaction



Interaction (perspective)

AirTemp * Precip interaction



Model comparison

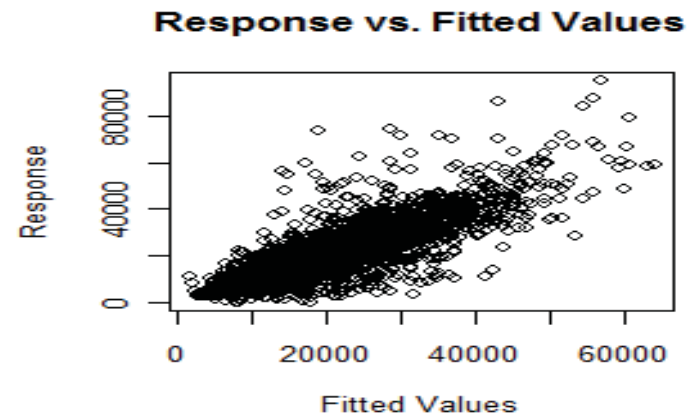
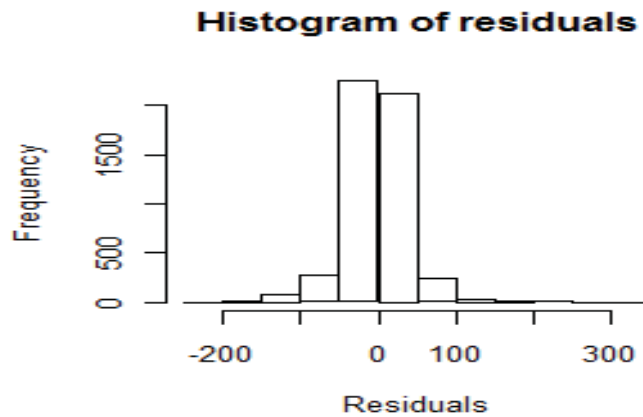
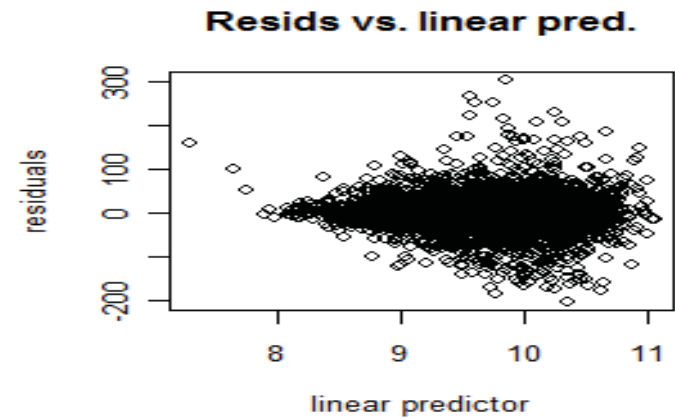
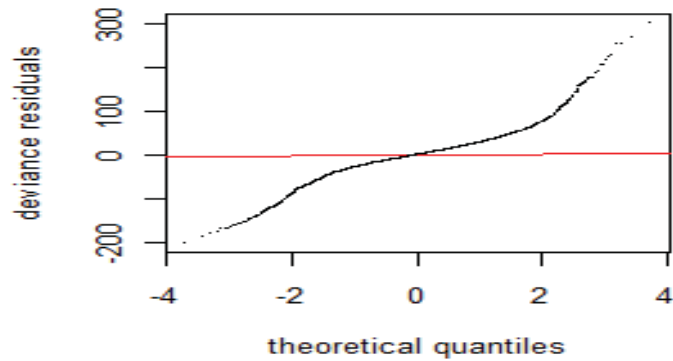
Model	AIC	GCV	PACF	Adj. R2	Deviance explained
No interaction	7632333	1592	-0.02	0.73	64%
With interaction	7621546	1592	-0.02	0.73	64%

```

Resid. Df Resid. Dev      Df Deviance      F    Pr(>F)
1      4932.6      7574649
2      4930.3      7563858  2.271    10792  3.0974  0.03882 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
' ' 1

```


gam.check()





Some limitations

- Underreporting
- Spatial autocorrelation
- Spatial aggregation
- Different seasonal trends between districts or regions
- Serotype fluctuations

Some coding tips!

```
# 1. Include a smooth for time with 2 df per year  
# when the number of years = 6  
# 2. Enter climate variables as smooth functions  
# 3. Add other predictors in a linear fashion  
# 4. Fit Poisson model with quasi-likelihood  
# 5. Offset by population
```

```
mymodel <- gam(Totalcases ~  
  + s(time, bs = 'cr', k = 12)  
  + s(temperature, bs = 'cr')  
  + s(rainfall, bs = 'cr')  
  + urbanisation  
  + offset(log(population))  
, # Do not delete this comma!  
  data = mydata,  
  family = poisson(link = 'log'),  
  scale = -1) # for quasi-likelihood
```

```
summary(mymodel)
```

```
pacf(mymodel)
```

```
gam.check(mymodel)
```

```
?gam.check # To look for help
```

How to add an autocorrelation term

```
# 6. Adjust by autocorrelation
```

```
mymodel2 <- gam(Totalcases ~  
  + s(time, bs = 'cr', k = 12)  
  + s(temperature, bs = 'cr')  
  + s(rainfall, bs = 'cr')  
  + urbanisation  
  + offset(log(population))  
  + log(LagTotalcases+1)  
  , # Do not delete this comma!  
  data = mydata,  
  family = poisson(link = 'log'),  
  scale = -1) # for quasi-likelihood  
  
summary(mymodel2)
```

```
# 7. compare the 2 models
```

```
anova(mymodel, mymodel2, test = 'F')  
pacf(mymodel2)  
gam.check(mymodel2)
```

Plotting a gam

```
# 8. plot your results
```

```
plot.gam(mymodel2,  
  all.terms = F,  
  scale = 0,  
  pages = 1,  
  rug = T,  
  shade = T,  
  se = T,  
  lwd = 1.75,  
  col = '#FF8000',  
  shade.col = "gray88",  
  trans = exp,  
  seWithMean = F,  
  main = "My model 2",  
  cex.main = 1.2,  
  cex.lab = 1.5)
```

Plotting a smooth interaction

```
# 9. Create a 3D plot for the interaction term
par(mar = c(5,5,3,3))
vis.gam(mymodel2, view = c('temperature', 'rainfall'),
        plot.type = 'persp', color = 'heat', n.grid = 15,
        border = 'gray45', type = 'response',
        main = 'Temperature * Rainfall interaction',
        phi = 30, theta = 30, cex.main = 1.5,
        cex.lab = 2, ylab = 'Rainfall',
        xlab = 'Temperature')
```

```
# 10. Plot a contour of the interaction
par(mar = c(5,5,3,3))
vis.gam(mymodel2, view = c('temperature', 'rainfall'),
        plot.type = 'contour', color = 'heat',
        n.grid = 15, contour.col = 'black',
        type = 'response',
        main = 'Temperature * Rainfall interaction',
        cex.main = 1.5, cex.lab = 2,
        ylab = 'Rainfall', xlab = 'Temperature')
```



Recommended reading

- Kirkwood, B & Sterne, J. *Essential medical statistics* (2008) Blackwell Publishing.
- Cohen, J. et al., *Applied Multiple Regression/Correlation Analysis for the Behavioral Sciences* (2003) Lawrence Erlbaum
- Keele, L. *Semiparametric regression for the social sciences* (2008). Blackwell
- Shumway, & Stoffer, D. *Time Series Analysis and Its Applications With R Examples* (2006) Springer
- Gelman, A & , J. *Data Analysis Using Regression and Multilevel/Hierarchical Models* (2007) Cambridge University Press



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