Bayesian Age-Period-Cohort Modeling and Prediction – BAMP

Volker J. Schmid
Imperial College London

Leonhard Held
Universität Zürich

Abstract

The software package BAMP provides a method of analyzing incidence or mortality data on the Lexis diagram, using a Bayesian version of an age-period-cohort model. A hierarchical model is assumed with a binomial model in the first-stage. As smoothing priors for the age, period and cohort parameters random walks of first and second order, with and without an additional unstructured component are available. Unstructured heterogeneity can also be included in the model.

In order to evaluate the model fit, posterior deviance, DIC and predictive deviances are computed. By projecting the random walk prior into the future, future death rates can be predicted.

Keywords: Bayesian hierarchical models, age-period-cohort models, prediction.

1. Introduction

In epidemiology, incidence and mortality counts are usually stratified by incidence (or mortality) year and age groups. Figure 1 shows an example dataset for the 5-year-periods 1965–69 to 1995–99 with data for the age groups 30–34 up to 70–74 depicted in a Lexis diagram (Lexis 1875). Often the covariates which cause these incidences cannot be observed directly. A commonly used approach in such a situation is the age-period-cohort (APC) model. Here the incidence rates are analyzed with regard to three different time scales, age (time between birth and death), period (time of death) and cohort (time of birth). This three time scales are surrogate measures, which can give an indication to the underlying causes of a disease Holford (1998): Age is often the main factor in such an analysis as it accounts for consistent extrinsic factors. The effect of the period accounts for all factors, which affect every person at a time period in history such as pollution or medical advances. The cohort effect accounts for events, which affect generations, e.g., malnutrition of children during or after wars or changing habits...
like the increasing number of young female smokers (Knorr-Held and Rainer 2001).

In this paper we present the software BAMP (Bayesian Age-Period-Cohort Modeling and Prediction), which allows to analyze incidence count data with a Bayesian age-period-cohort model. BAMP analyzes incidence or mortality count data with a Bayesian age-period-cohort model and allows to include several features:

- The input data do not have to be on the same time scale, for example period can be in one year intervals and age grouped in five year intervals; however, time scales have to be equidistant,
- BAMP allows for prediction of the future number of cases,
- BAMP allows retrospective predictions for existing data for model checking purposes,
- BAMP can analyze different APC models, i.e., with and without additional global and local heterogeneity, with RW priors of first or second order, and AP and AC models (Clayton and Schifflers 1987).

BAMP is available for free download at http://www.volkerschmid.de/bamp.html.

There are some graphical routines available in order to

- plot estimated age, period and cohort effects (only for RW1 model)
- compare observed with fitted and predicted rates
- graphically assess the "significance" of the unstructured parameters. This helps to identify unstructured variation in the data which cannot be described by the age, period and cohort parameters alone.

Section 2 describes the theory of Bayesian age-period-cohort models and modifications to the basic model -

and to add additional heterogeneity parameters. An important feature of Bayesian APC models is the possibility of projecting future incidence rates; this is also described in Section 2. Section 3 describes how BAMP is used and how different models can be compared. Section 4 describes additional scripts for visualizing results.

## 2. Bayesian APC models

In the following let $i = i, \ldots, I$ denote the index of the age group, $j = 1, \ldots, J$ the index of the period and $k = 1, \ldots, K$ the index of the birth cohort. The cohort index can explicitly be computed from age group and period index of an incidence, see also Figure 1; if age and period are on the same time scale, the cohort index is

$$ k = k(i, j) = (I - i) + j. \quad (1) $$

If age and period are measured on different scales Equation 1 has to be changed accordingly (Holford 1983); as example, if data are give per year, but the age groups cover five years, the cohort index is

$$ k = k(i, j) = 5 \cdot (I - i) + j. \quad (2) $$
In classical APC literature (for an overview see Heuer 1994) the APC model is often regarded as a log-linear Poisson model. As an alternative a binomial logit model can be formulated (both models are approximately identical): The counts of incidences $y_{ij}$ in age group $i$ in period $j$ follow a binomial distribution with parameters $p_{ij}$ and $n_{ij}$. Here $n_{ij}$ is the known population size of age group $i$ at period $j$ and $p_{ij}$ is the unknown incidence probability. The logit of the incidence probability is decomposed in an intercept $\mu$, age effect $\theta_i$, period effect $\phi_j$ and cohort effect $\psi_k$,

$$y_{ij} \sim B(n_{ij}, p_{ij}),$$

$$\eta_{ij} = \log \left( \frac{p_{ij}}{1 - p_{ij}} \right) = \mu + \theta_i + \phi_j + \psi_k.$$ 

2.1. Non-identifiability

To make the intercept $\mu$ identifiable, the following restrictions have to be imposed

$$\sum_i \theta_i = \sum_j \phi_j = \sum_k \psi_k = 0.$$ 

However, the APC parameters in this model are still not identifiable. It can be seen from (1) that for every transformation

$$\mu \rightarrow \mu - c \cdot I; \quad \theta_i \rightarrow \theta_i + c \cdot i; \quad \phi_j \rightarrow \phi_j - c \cdot j; \quad \psi_k \rightarrow \psi_k + c \cdot k$$
for all $i, j$ and $k$ with any $c \in \mathbb{IR}$ the linear predictor $\eta_{ij}$ is not changed. Therefore the linear predictor can always be identified and interpreted, but age, period and cohort effects cannot.

Figure 2 shows the problem of non-identifiability. The figure shows two possible parameter sets for the example dataset in Figure 1. Depending on the transformation, the period effect is decreasing and the cohort effect is increasing or *vice versa*. However, the change in trend at cohort $k = 8$ remains unchanged. This is, because the non-identifiability only affects linear trends; change points and other non-linear trends can be identified (up to the linear trend) – like the non-linear effect of age in the example. Therefore the interpretation of the estimated APC effects has to be restricted to non-linear trends. BAMP provides second differences for this purpose.

### 2.2. Bayesian hierarchical model

BAMP uses a Bayesian hierarchical approach for the APC model. Following Berzuini and Clayton (1994) random walk (RW) priors of different orders are used for the APC parameters $\theta$, $\phi$ and $\psi$. The RW1 prior assumes a constant trend over the time scale, whereas the RW2 prior assumes a linear time trend. Therefore the order of the random walk should be chosen depending on whether a constant or a linear time trend can be assumed. However, in the APC model the RW prior also acts as a stochastic restriction: With a RW1 the first-order differences of an effects are stochastically restricted to zero; this makes the APC effects
identifiable. With a RW 2 the second-order differences are stochastically restricted to zero; this restriction however is too weak to assure identifiability.

In the following we describe random walk priors for the period effect \( \phi \) – the age and the cohort effects \( \theta \) and \( \psi \) can be treated analogously. For random walks of first order (RW 1) we assume

\[
p(\phi_1) \propto \text{const.}
\]

\[
\phi_j|\phi_{j-1} \sim N(\phi_{j-1}, \kappa^{-1}), \text{ for } j = 2, \ldots, J
\]  

(7)

with \( \kappa^{-1} \) a precision parameter; for random walks of second order (RW 2) we assume

\[
p(\phi_1) = p(\phi_2) \propto \text{const.}
\]

\[
\phi_j|\phi_{j-1}, \phi_{j-2} \sim N(2\phi_{j-1} - \phi_{j-2}, \kappa^{-1}) \text{ for } j = 3, \ldots, J.
\]  

(8)

The joint distribution of \( \Phi = (\phi_1, \ldots, \phi_J) \) is

\[
p(\Phi) \propto \lambda^{rg(R)/2} \exp \left( -\frac{\lambda}{2} \Phi'R\Phi \right),
\]

with \( R \) the precision matrix of RW 1 (Clayton 1996) or RW 2 (Berzuini, Clayton, and Bernardinelli 1993).

The precision parameter \( \kappa \) is a smoothing parameter and will be estimated simultaneously in the model. The higher the precision, the smoother the estimated parameter vector. A Gamma distribution \( \text{Ga}(a,b) \) is used for the precision parameters. Often \( a = 1 \) and \( b = 0.001 \) or \( a = b = 0.001 \) is chosen. When using a RW 2 prior it is often advisable to use a smaller value for \( b \) in order to get smooth estimates (e.g., \( b = 10^{-5} \)).

For the intercept \( \mu \) \textbf{BAMP} uses a flat prior

\[
p(\mu) \propto \text{const.}
\]

Identifiability of the intercept is guaranteed with the restrictions stated in (5).

In the Bayesian setting a random walk of first order imposes a stochastic constraint: the RW 1 model will prefer the one transformation Equation 6, where the quadratic first differences are minimal - i.e., the APC effects are kept as constant as possible. Therefore the APC effects can be identified by the software with this model, nevertheless the restriction in interpretation of the resulting estimations still apply.

2.3. Projection

Whereas RW 1 implies a constant time trend, RW 2 implies a linear time trend. In both cases the priors can be used to gain projections for future time points. The projected effects can be computed by

\[
\phi_{J+1} \sim N(\phi_J, \kappa^{-1}) \text{ for RW 1,}
\]

\[
\phi_{J+1} \sim N(2\phi_J - \phi_{J-1}, \kappa^{-1}) \text{ for RW 2.}
\]  

(9)

The Bayesian APC model allows to extrapolate period and cohort effects. The age effect can also be extrapolated, however this is usually not necessary, as data cover all age groups of interest.
In order to get the projection of a future rate \( p_{i,J+1} \) the projected period and cohort effects from Equation 9 are applied to Equation 4:

\[
\eta_{i,J+1} = \mu + \theta_i + \phi_{J+1} + \psi_{k(i,J+1)}
\]

and

\[
p_{i,J+1} = \frac{\exp(\eta_{i,J+1})}{1 + \exp(\eta_{i,J+1})}.
\]

The projection of future cases can then be computed using the binomial distribution Equation 3; however the population size \( n_{i,J+1} \) must be known or projected by an adequate method to estimate the number of cases. Further future rates \( p_{i,J+2}, p_{i,J+3}, \ldots \) can be derived analogously.

### 2.4. Inference

The full conditional of the APC parameter vectors are non-standard distributions. Therefore BAMP uses a Metropolis-Hastings (MH) algorithm to sample from the posterior. Useful Gaussian proposals for the MH algorithm can be derived using Taylor approximation of second degree (Gamerman 1997; Schmid 2004). BAMP uses an algorithm proposed by Rue (2001) for effective sampling from multivariate normal distributions.

The full conditional of the hyper parameter \( \kappa \) is a Gamma distribution with parameters \( a + \text{rg}(R)/2 \) and \( b + \frac{1}{2} \Phi'R\Phi \). Also, the full conditionals of \( \tau \) and \( \nu \) are Gamma distributions; therefore the precisions can be sampled using Gibbs steps.

### 2.5. Additional global heterogeneity

Knorr-Held and Rainer (2001) propose an additional parameter \( z_{ij} \) for the APC model. This parameter accounts for heterogeneity which can not be explained by the APC effects, like overdispersion. The model has the following form:

\[
\eta_{ij} = \mu + \theta_i + \phi_j + \psi_k + z_{ij}.
\]  

(10)

A Gaussian distribution

\[
z_{ij} \sim \mathcal{N}(0, \delta^{-1})
\]

is used as prior for the additional heterogeneity with a \( \text{Ga}(a_\delta, b_\delta) \) prior for the precision parameter \( \delta \).

This model has an interesting technical advantage. Using a reparametrization as proposed by Besag, Green, Higdon, and Mengersen (1995), the full conditionals of the APC effects are Gaussian distributions, such that Gibbs step can be applied (Knorr-Held and Rainer 2001).

### 2.6. Additional heterogeneity on a time scale

In some analyzes using APC models, the estimated effects are too rough because of additional heterogeneity in the effects or outliers in the data. Therefore not only the variance of these effects is overestimated, but also the credibility intervals of the projection will be too broad.

A solution for this can be to introduce additional parameters for heterogeneity on one or more time scales. Even in the model with additional global heterogeneity parameter \( z_{ij} \) (Section 2.5) an additional heterogeneity parameter may be useful, in order to keep the variance of \( z_{ij} \) small.
Let us assume that the period effect a priori follows
\[
\phi_j \sim N(\phi_j^*, \lambda_1) \text{ for } j = 1, \ldots, J,
\]
with a random walk prior with precision \(\lambda_2\) for \(\Phi^* = (\phi_1^*, \ldots, \phi_J^*)'\). Let \(\tilde{\Phi} = (\tilde{\phi}_1, \ldots, \tilde{\phi}_{(2J)})'\) be the joint vector of \(\Phi\) and \(\Phi^*\) with
\[
\begin{align*}
\tilde{\phi}_{(2j)−1} &= \phi_j \\
\tilde{\phi}_{(2j)} &= \phi_j^*
\end{align*}
\]
for \(j = 1, \ldots, J\). Then the joint prior distribution of \(\phi\) and \(\phi^*\) can be formulated as prior distribution of \(\tilde{\phi}\):
\[
p(\tilde{\phi}) \propto \exp \left[ -\frac{1}{2} \tilde{\Phi}'(\lambda_1 I \otimes A + \lambda_2 R \otimes B)\tilde{\Phi} \right]
\]
with
\[
A = \begin{pmatrix} 1 & -1 \\ -1 & 1 \end{pmatrix} \quad \text{and} \quad B = \begin{pmatrix} 0 & 0 \\ 0 & 1 \end{pmatrix}
\]
and \(\otimes\) the Kronecker matrix product.

An analogous modification of the prior can be formulated for cohort and age, however, in practice there is rarely a need for additional heterogeneity for age. Models with additional heterogeneity on more than one time scale are possible, but in these models the stochastic restriction, which comes with the use of RW1 priors, does not longer apply.

3. Using BAMP

BAMP is a stand alone software. All necessary settings are loaded from a .ini file, by default called bamp.ini. Before executing BAMP, edit the bamp.ini file or write your own .ini file (see Section 3.1.1). Execute the software by typing

```
bamp your-ini-file.ini
```

in the command line. On window-based operating systems, BAMP can be executed with a double click on the BAMP icon. BAMP will then use the bamp.ini file by default. On Microsoft Windows systems the file cygwin1.dll has to be in the same folder as bamp.exe.

3.1. Input files

*.ini file

All parameters and input files are specified in a .ini file, by default called bamp.ini. Tables 1 to 2 show the variables which can be defined in the .ini file. The last column of the tables show the default values. Lines signed with †are mandatory, lines with ‡are mandatory if applicable (eg. parameter for the gamma priors must be given, unless the corresponding effect is discarded from the model). Each row in the *.ini file consist of the name of the variable and the value, separated by a “:”. The order of the lines is arbitrary.
Table 1: Variables in the .ini file – part 1.

**Data files**

Two files containing data are necessary: the *cases file* contains the number of disease cases, the *population file* the number of persons under risk. Both files must be in the form of a matrix with $T$ rows and $J$ columns. If dataorder:1, the data files will be transposed (i.e. the files are matrices with $J$ rows and $T$ columns). To predict rates for existing data (predictions:2) for $S$ periods both files must have $T + S$ rows ($T + S$ columns for dataorder:1). For given population data (predictions:3), the *population file* must have $T + S$ rows ($T + S$ columns for dataorder:1). In all cases redundant rows will be ignored.

**Priors for APC effects**

For the age, period and cohort effects the following priors are available, set age block, period block and cohort block accordingly.

0: Discard effect from the model (for AP and AC model)
The MCMC algorithm produces samples from the posterior distribution of all unknown parameters. These samples are written to the **temp folder**. After finishing the MCMC run, the software calculates quantiles of the samples from the posterior distribution. These quantiles

### 3.2. Output files

The MCMC algorithm produces samples from the posterior distribution of all unknown parameters. These samples are written to the **temp folder**. After finishing the MCMC run, the software calculates quantiles of the samples from the posterior distribution. These quantiles

### Table 2: Variables in the `.ini` file – part 2.

| Variable          | Description                                                                 | Value |
|-------------------|-----------------------------------------------------------------------------|-------|
| age block         | prior of age effect, see Paragraph *Priors for APC effects*                 | 0     |
| age hyperpar. a   | parameters \( a \) and \( b \) of the gamma prior of the precision of the age effect | \( a \) |
| age hyperpar. b   | of the age effect                                                          | \( b \) |
| age hyperpar.2 a  | parameters \( a \) and \( b \) of the gamma prior of the precision of the unstructured age effect | \( a \) |
| age hyperpar.2 b  | of the unstructured age effect                                              | \( b \) |
| period block      | prior of period effect, see Paragraph *Priors for APC effects*              | 0     |
| period hyperpar. a| parameters \( a \) and \( b \) of the gamma prior of the precision of the period effect | \( a \) |
| period hyperpar. b| of the period effect                                                        | \( b \) |
| period hyperpar.2 a| parameters \( a \) and \( b \) of the gamma prior of the precision of the unstructured period effect | \( a \) |
| period hyperpar.2 b| of the unstructured period effect                                           | \( b \) |
| cohort block      | prior of the cohort effect, see Paragraph *Priors for APC effects*          | 0     |
| cohort hyperpar. a| parameters \( a \) and \( b \) of the gamma prior of the precision of the cohort effect | \( a \) |
| cohort hyperpar. b| of the cohort effect                                                        | \( b \) |
| cohort hyperpar.2 a| parameters \( a \) and \( b \) of the gamma prior of the precision of the unstructured cohort effect | \( a \) |
| cohort hyperpar.2 b| of the unstructured cohort effect                                           | \( b \) |
| z mode            | 0: with, 1: without pixel-wise heterogeneity parameter                      | 1     |
| z hyperpar. a     | parameters \( a \) and \( b \) of the gamma prior of the precision of the pixel-wise heterogeneity parameter | \( a \) |
| z hyperpar. b     | of the pixel-wise heterogeneity parameter                                   | \( b \) |
| quantile 1        | quantiles of the posterior for output                                       | -1    |
| quantile 2        | (-1: none)                                                                  | -1    |
| quantile 3        |                                                                               | -1    |
| quantile 4        |                                                                               | -1    |
| quantile 5        |                                                                               | -1    |
| period covariate  | path and name of the covariable data file for period                       | \( \) |
| period start      | first time point to use from covariables data set                          | \( \) |
| cohort covariate  | path and name of the covariable data file for cohort                        | \( \) |
| cohort start      | first time point to use from covariables data set                          | \( \) |

1: RW 1 prior

2: RW 2 prior

3: RW 1 prior with additional unstructured heterogeneity (see Section 2.6)

4: RW 2 prior with additional unstructured heterogeneity (see Section 2.6)

8: RW 1 prior with use of covariates (see Section 3.4)

9: RW 2 prior with use of covariates (see Section 3.4)
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will be written in the output folder. The variables quantile 1 to quantile 5 specify the quantiles, which will be calculated. Variables set to -1 will be omitted.

The output consists of the following files:

- **theta.txt, phi.txt, psi.txt**: Quantiles of the age, period, cohort effect; each quantile is a row (these will only be produced for RW 1 priors)
- **theta2.txt, phi2.txt, psi2.txt**: Quantiles of second differences of the age, period, cohort effects (these can always be identified and interpreted)
- **hyper.txt**: Quantiles of the precision parameters of age, period and cohort effects followed by the precision of the unstructured “random effects”, name of parameter and quantiles in each row
- **z.txt**: Quantiles of pixel-wise heterogeneity parameter, each block is one quantile of $T$ rows with $J$ columns
- **my.txt**: Quantiles of the intercept parameter $\mu$
- **devianz.txt** (if deviance $> 0$): Quantiles of the deviance of the model
- **devianz_prog.txt** (if prediction:2 and deviance:2): Quantiles of the deviance for the predicted periods (each row one period)
- **dic.txt**: deviance, effective number of parameters and DIC, see Spiegelhalter, Best, Carlin, and van der Linde (2002)
- **pr.txt**: Quantiles of predicted rates
- **y_pred.txt, ysum_pred.txt** (if prognosis:2,3, see Section 3.3): Quantiles of predicted cases per age groups and summed up
- **beta_phi.txt, beta_psi.txt**: period and cohort effect if covariates are used

### 3.3. Model fit, predictions

In order to evaluate the goodness of the model fit, BAMP calculates the posterior deviance. The deviance is defined as:

$$D = 2 \cdot \sum_{j,t} [l(\hat{y}_{jt}) - l(y_{jt})]$$

with $l(\hat{y}_{jt})$ the individual log-likelihood of the model and $l(y_{jt})$ the maximum individual log-likelihood achievable. The smaller the deviance, the better the fit of the model. However, the model fit will typically be good for any model as long the unstructured parameters are included. To compare the performance of different models, BAMP also provides the deviance information criterion DIC (Spiegelhalter et al. 2002) and the predictive deviance, see below.

To make predictions of further death rates, set predictions:1. Set number of predictions to the number of periods for which you want the projection. If you have population data for these periods, set predictions:3, the software will then provide predicted cases. In order to test the model you can also make prediction for existing data. Then the input files must
include this data, the matrices have to be of dimension $J$ times $(T + S)$ (see Section 3.1). Set deviance:2 and BAMP will calculate the predictive deviance for every projected period. The predictive deviance at time $t$ is defined as

$$D_t = 2 \cdot \sum_j \left[ l(\hat{y}_{jt}) - l(y_{jt}) \right]$$

with $\hat{y}_{jt}$ the predicted number of cases in age group $j$ at period $t$. The predictive deviance is a monotonic transformation of the logarithmic scoring rule as suggested initially by Good (1952), see also Gneiting and Raftery (2006), to quantify the quality of probabilistic forecasts.

### 3.4. Using covariates

By including a time-variable covariate effect, the Bayesian APC model might be improved:

$$\eta_{ij} = \mu + \theta_i + \beta_j x_{j-L} + \psi_k + z_{ij}$$

with a random walk prior for the regression parameter $\beta = (\beta_1, \ldots, \beta_J)$. The covariate $x = (x_{1-L}, \ldots, x_{J-L})$ enters with a time lag $L$.

The model is based on the idea, that one of the main effects can be explained by a covariate measure. In an analysis of lung cancer mortality data in West Germany Knorr-Held and Rainer (2001) present a model, where the period effect for females is explained by smoking habits, with a lag of 20–25 years. In a way, the substitution of one main effect with a covariate can be seen as a different type of restriction, where the model is restricted, so that one effect is linear dependent on the covariate.

However, it is not clear, if and how the covariates have to be standardized. If the covariate is near to zero, the credibility intervals get very broad, as Figure 3 shows for a lung disease dataset with the estimated amount of consumed tobacco as covariate, here the values are near to zero in the first years. If the covariate is exactly zero at one time point, the adjoined parameter indeed can not be estimated.

BAMP allows to include covariates in the age-period-cohort model. Covariate effects can either replace period or cohort effects. Let’s assume we have covariates $x_t$ for periods $t = 1 \ldots T$. We can introduce this covariate by replacing the period effect $\phi$ with $c_\phi \cdot x_t \beta^{(\phi)}$ with $c_\phi = \frac{1}{\sum_t x_t}$. For $\beta^{(\phi)}$, a random walk of first or second order can be chosen. In order to include covariates, period block has to been set to 8 (RW1) or 9 (RW2). The variable period
covariate gives the file name of the covariate data. The data have to be separated by space, tabulator or newline. The variable period start specifies, which line of the covariate file matches the first period of the cases/population data. Covariates for cohorts can equivalently be included; also both period and cohort effect can be replaced by covariates.

4. S-PLUS and R code for graphical output

The graphical routines for S-PLUS (Insightful Corp. 2003) and R (R Development Core Team 2007)

- plot estimated age, period and cohort effects (for RW1 priors only!)
- compare observed and fitted rates
- plot projected rates
- assess the "significance" of the unstructured parameters

Download the code from the BAMP homepage and edit the first lines as appropriate:

- startingage: the first age of the first age group of the data
- startingperiod: the first period of the data
- yearsperperiod: how many years are one period
- inifile: name of the .ini file

To start, copy the code to the directory where the .ini file is located, change to this directory and type

    Splus < bamp.splus  resp.  R --nosave < bamp.R

or start in S-PLUS or R via

    source(path/bamp.S)  resp.  source(path/bamp.R)

The resulting graphic file is named bamp.ps in the output directory.

5. Summary

Bayesian age-period-cohort models are a useful tool to analyze mortality and incidence rates stratified by age and period. A RW1 prior for all APC effects implies a stochastic restriction, solving the identifiability problem. However, with RW2 priors the main effects can not be identified. Whatever RW model is used, the linear trends can not be interpreted without considering the stochastic restrictions implied by the model, however, break points and other non-linear changes can be interpreted. Therefore APC models can be a first step for further analysis of the causes of incidence.
Several recent papers, including the work of exploit the use of Bayesian inference in APC modeling. A Bayesian APC models with RW 2 priors are used in Bray, Brennan, and Boffetta (2000) and Baker and Bray (2005) for projections of cancer mortality, Knorr-Held and Rainer (2001) present a model with overdispersion in a lung cancer study and exploit the use of covariates in a APC model, and Hansell, Held, Best, Schmid, and Aylin (2003) and Lopez, Shibuya, Rao, Mathers, Hansell, Held, Schmid, and Buist (2006) analyze COPD mortality trends with Bayesian APC model. These papers not only show the methodology of Bayesian APC models, but also the interpretation of results and of different possible models.

Predictions in the Bayesian APC model can easily be made by carrying forward the autoregressive priors. The prior has to be chosen carefully: predictions with RW 1 models may have a bias, if the assumption of constant time trends does not apply; models with RW 2 priors tend to have broader credibility intervals, see also the results of Knorr-Held and Rainer (2001) and Schmid and Held (2004).

**BAMP** provides a variety of different APC models. Global heterogeneity can be in- or excluded, additional heterogeneity on time scales is possible; one or even two of the APC effects can be discarded from the model. The different models can be compared via deviance, DIC and predictive qualities. **BAMP** is available for free download at [http://www.volkerschmid.de/bamp.html](http://www.volkerschmid.de/bamp.html).

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Affiliation:
Volker J. Schmid
Institute of Biomedical Engineering
Imperial College London
London SW7 2AZ, United Kingdom
E-mail: stats@volkerschmid.de
URL: http://www.volkerschmid.de/