Dynamic Bayesian models for projecting cancer incidence in Puerto Rico

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Abstract

- We estimate the present (2010) and predict the future (2014) of incidence for the top cancer tumor types in Puerto Rico (PR), by gender, age group and primary cancer site, to design public policy. Incidence data from Puerto Rico Central Cancer Registry were obtained for the years 1985 to 2004. The dynamic autoregressive models used in modern epidemiology are function of age-period-cohort (APC).
- We introduce a novel robust and stable prior the autoregressive variance, the scaled beta prior of the second kind (Beta2 prior).
- We found that this leads to a stable convergence of the model at the Markov Chain Monte Carlo (MCMC) implementation.
- We also produce statistical tools to check the goodness of fit and model selection.

This is an introduction to AGE-PERIOD-COHORT A-P-C Modeling and Prediction under a Bayesian Approach.

This is one of the most widely used tools in Predictive epidemiology modeling.

The data is either Incidence or Mortality, in this case of Cancer grouped and by tumor.

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Introduction

APC: Age-Period-Cohort model: three different factors, three different time frames:

1. **Age**: age at diagnosis.
2. **Period**: date of diagnosis. Factor that affects all in a given period: like Technological Advances.
3. **Cohort**: Date of Birth. The Generation Effect: like Smoking or Diet Habits etc.

As an hypothetical situation: If person has diagnosis age at 65 years old in the running period $(2010 - 2014)$ then his cohort is from $1945 - 1949$.

Aggregated Data Provided by Cancer Registry CCCUPR

We have twenty single years of Incidence data and Twenty one years of mortality. There are two long term five years prediction points 2009 to 2014 (10 years of prediction).

	Incidence	Mortality
Years	1985 – 2004	1986-2006
Types	All cases $\star$ including Lung, Colon, Breast and Breast Malignant etc.	All cases $\star$ including Lung, Colon, Breast.

$\star$

Cancer cases excluding basal and squamous cell skin cancers and in situ carcinomas except urinary bladder.
Mortality data are waiting for validation. Mortality data are from July 06, 2010

Methods The Basic Hierarchical Model

The Age, Period and Cohort model(APC) is a particular type of panel data that is applied to Tumor Incidence Counts (Death Counts).Lets denote the incidence (death) counts as y_{at} by age groups or bands $(a = 1, \ldots, A)$ and periods $(t = 1, \ldots, T)$. There is a natural implicit cohort dimension related to each age band and period,[Breslow and Clayton(1993)]. The APC model introduce three factors multiplicative model, separated effects due to age, period and cohort of incidence in a particular decease [WC and RS.(1996)] Lee (1996).

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Formally the model is of the form:

$$y_{a,t} \sim Pois(\mu_{a,t})$$

$$log(\mu_{a,t}) = \lambda_0 + \varphi_a + \theta_t + \alpha_c \qquad \begin{array}{l} a = 1, \ldots, A \\ t = 1, \ldots, T \\ c = A + T - a \end{array} \tag{1}$$

Where $\mu_{a,t}$ are the unknown true expected counts with the age, period and cohort effects. The usual constrain is that $\sum_a \varphi = \sum_t \theta = \sum_c \alpha = 0$. see for example Bray (2002), *Applied Statistics*,**51**, 151-164.

The use of model 1 to estimate the rate per 100,000, $\lambda_{a,t}$ can be found just evaluating $\mu_{a,t}$ as follows

$$\mu_{a,t} = e^{\lambda_0+\varphi_a+\theta_t+\alpha_c}$$

Then using the population estimator or the historical value $P_{a,t}$ (Population at period t and age band a) we get the cases per 100,000

$$\lambda_{a,t} = \mu_{a,t} * \frac{100,000}{P_{a,t}}.$$

This population estimates are given in the "Junta de Planificación" (1985-2015).

Hierarchical APC model implementation

The model can be stated as Poisson likelihood :

$$y_{a,t} \sim Pois(\mu_{a,t})$$

$$log\,\mu_{a,t} = \lambda_0 + \varphi_a + \theta_t + \alpha_c$$

where $y_{a,t}$ is the occurrence in each age band (a) and period (t). Here we use autoregressive priors on the parameters, as an example we present those for θ. As an example here are two versions:

RW1: **Constant Time Trend**:

$$p(\theta_1) \propto const., \;\; \theta_t|\theta_{t-1} \sim N(\theta_{t-1}, \tau)$$

RW2: **Linear Time Trend**: The one used in our calculations.

$$\theta_t|\theta_{t-1}, \theta_{t-2} \sim N(2\theta_{t-1} - \theta_{t-2}, \tau)$$

Note that τ is precision, reciprocal of Variance and that RW2 has a local time linear trend.

$$\theta_t - \theta_{t-1} = \theta_{t-1} - \theta_{t-2} + \epsilon$$

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Structure of Age effect

The age structure follows a normal autoregressive prior of order two(RW2). This is that for $a = 3 \ldots A$ we have

$$\varphi_a \sim N(\mu_\varphi, \tau_1)$$

where setting μ_φ with the property that

$$\mu_\varphi - \varphi_{a-1} = \varphi_{a-1} - \varphi_{a-2}$$

defining $\varphi_1 = 0$ and $\varphi_2 \sim N(0, 0.001)$.

Structure of Period effect

The period structure as the age component follows a normal autoregressive prior of order two(RW2). This is that for $t = 3 \ldots T + 2$ we have

$$\theta_t \sim N(\mu_\theta, \tau_2)$$

where setting μ_θ with the property that

$$\mu_\theta - \theta_{t-1} = \theta_{t-1} - \theta_{t-2}$$

defining $\theta_1 = 0$ and $\theta_2 \sim N(0, 0.001)$.

Structure of Cohort effect

The Cohort structure as the age component follows a normal autoregressive prior of order two(RW2). The cohorts index are defined as is that for $c = 3 \ldots C = A - 1 + T$. Note that the cohort parameters do not represent distinct birth cohorts, each parameter α_c correspond to a birth cohort of the length of two years, and the birth cohort defined by two consecutive cohort parameters overlap by one year

$$\alpha_a \sim N(\mu_\alpha, \tau_3)$$

where setting μ_θ with the property that

$$\mu_\alpha - \alpha_{c-1} = \alpha_{c-1} - \alpha_{c-2}$$

defining $\alpha_1 = \alpha_2 = 0$.

Priors on Precisions Priors τ

Usually in literature, priors on precisions $\tau_i = \frac{1}{\sigma^2}$ for $i = 1 \ldots 3$ are worked from the fact that

$$\nu \frac{\sigma_0^2}{\sigma^2} \sim \chi_\nu^2$$

where σ_0 is a guess at σ and ν is the prior degrees of freedom. The problem of this approach is that there is a lack of robustness and wide probability intervals.

In order to be more robust we improve this model using the following novel assumption:

$$\frac{\sigma_0^2}{\sigma^2} \sim \beta_2(p, q, \sigma_0)$$

where $\beta_2(p, q, \sigma_0)$ is the scale Beta probability distribution of the second kind.

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Taking $\frac{\sigma^2}{\sigma_0^2} = \gamma^2$ in other term $\sigma^2 = \gamma^2\sigma_0^2$then $d\gamma^2 = \frac{1}{\sigma_0^2}d\sigma^2$.

$$
\begin{aligned}
p(\gamma^2|p,q,\sigma_0) &= \frac{\Gamma(p+q)}{\Gamma(p)\Gamma(q)} \frac{(\gamma^2\sigma_0^2)^{p-1}}{(\frac{\sigma_0^2}{\sigma_0^2})^{p+q}(1+\gamma^2\sigma_0^2)^{p+q}}\sigma_0^2 \\
&= \frac{\Gamma(p+q)}{\Gamma(p)\Gamma(q)(\sigma_0^2)^q} \frac{(\gamma^2)^{p-1}}{(\frac{1}{\sigma_0^2}+\gamma^2)^{p+q}} \\
E(\gamma^2) &= \frac{E(\sigma^2)}{\sigma_0^2} = \frac{p}{\sigma_0^2(q-1)} \\
Var(\gamma^2) &= \frac{p(p+q-1)}{\sigma_0^4(q-1)(q-2)^2}
\end{aligned}
$$

In practice this was more stable and accelerated in convergence of the Gibbs sampler
(WinBUGS[Spiegelhalter et al.(1998)Spiegelhalter, Thomas, and Best]).

Age-standardized incidence and mortality.

A "natural" age standardized measure is suggested by Wong (2007), the weighted arithmetic mean across the age bands. We will call the new parameter $\hat{\lambda}_t$ defined as

$$\hat{\lambda}_t = E_t(\lambda_{a,t}) = \sum_{i=1}^{A} \lambda_{i,t}\left(\frac{P_{i,t}}{\sum_{t=1}^{A} P_{i,t}}\right)$$

NOTE:However there may be wild variations with age! This is just a weighed mean useful for comparisons.

Model checking via cross validation of a model.

Since the APC model is used here as a predictor tool a fair cross validation is needed in order to have some sense in the models predicted ability.
There are several ways to implement a cross validation.
Cross-validation method for evaluating a model

- (1) remove part of the data,
- (2) fit the model the smaller dataset excluding the removed part,
- (3) use the fitted model to predict the removed part,
- (4) summarizing the prediction error by comparing to the actual left-out data.

Leave the last one out. **Not using the data twice.**

We removed the data of the period $2000 - 2004$ from the data and fitted the model to compare how close the estimator is to the historical value. The calculation using the full APC model using the **All cancer type** dataset is presented here.

We got an estimated **age standardized expectation rate** of 538.47 with probability intervals given in the following table.

Historic	0%	25%	50%	75%	100%
538.47	185.50	**468.45**	537.10	**626.20**	2620.00

The median value is really close to the historical value. Doing the same process with al the specific age values provide us with a fair prediction assessment on each of the bands age as presented in the next table.

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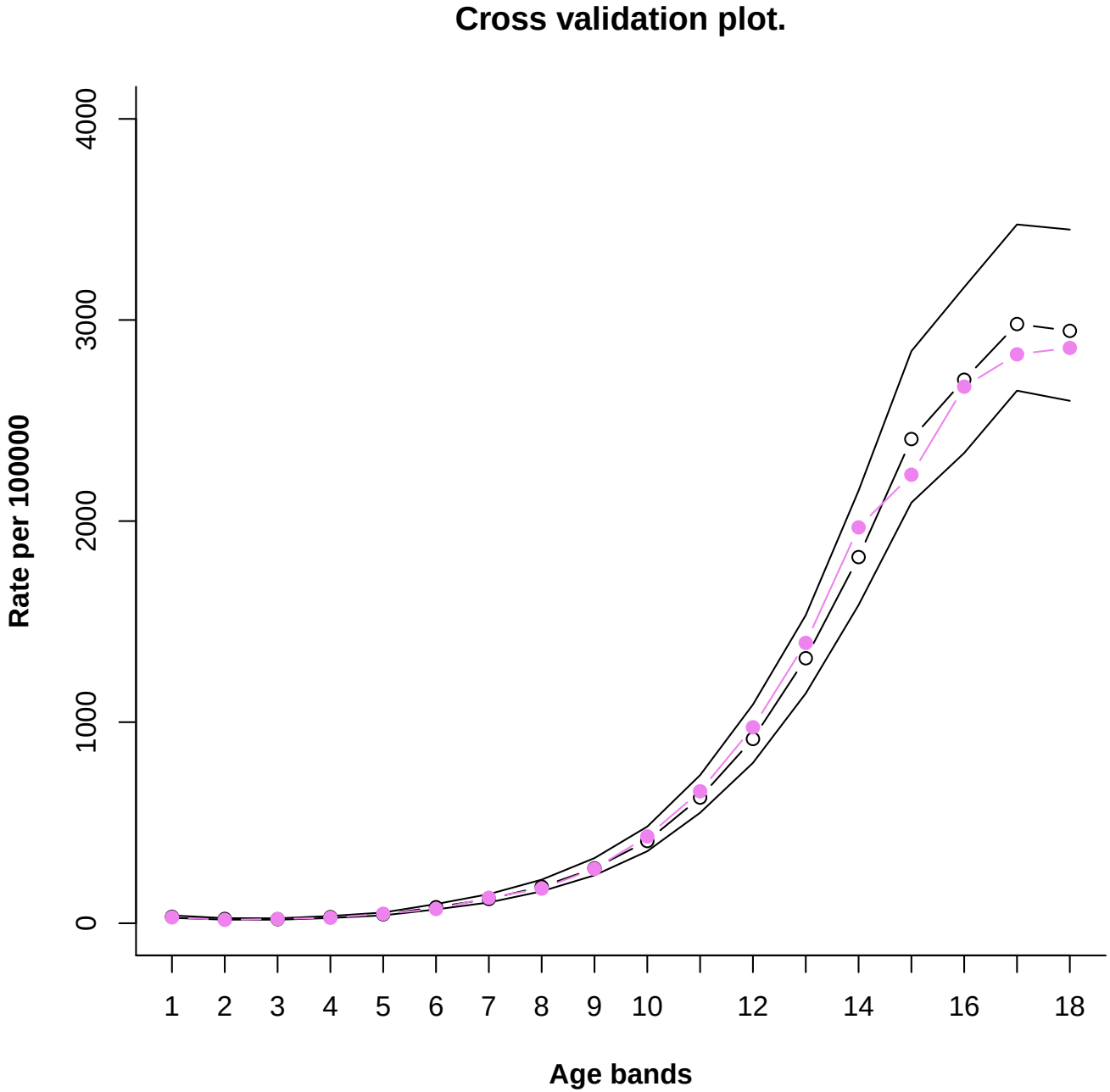
Cross validation plot.
Rate per 100000
0
1000
2000
3000
4000
1
2
3
4
5
6
7
8
9
10
12
14
16
18
Age bands

Age bands	Historic	0%	25%	50%	75%	100%
0	29.52	11.87	26.7	32.27	38.86	160.9
5	17.18	7.36	17.93	21.54	25.36	108.4
10	21.02	7.63	17.54	20.22	24.5	102.7
15	27.62	10.89	26.1	30.54	35.79	138.2
20	47.16	14.25	39.23	44.49	53.22	219.8
25	70.91	25.43	68.86	79.95	95.49	366.4
30	126.79	37.76	103.3	120.8	144.65	562.7
35	172.28	55.66	158.8	181.7	216.75	845.3
40	270.92	93.16	238.35	273.4	323.9	1371
45	431.69	143	358.15	409	480.75	1979
50	656.32	211.7	549.4	625.1	736.55	2989
55	974.73	309	797.4	916.6	1087.5	4372
60	1394.48	449.5	1143	1318	1532	6468
65	1968.65	638.6	1582.5	1821	2151	9041
70	2230.64	837.4	2091.5	2408	2845	11910
75	2668.51	937	2338.5	2703	3163	13110
80	2829.22	1104	2648.5	2980	3475	14590
85	2861.31	1007	2598	2946	3449.5	14940

Model Selection Using Deviance Information Criteria

Spiegelhalter et al (2002) proposed a Bayesian model comparison criterion based on this principle:

- Deviance Information Criterion, DIC = goodness of fit + complexity.
- The complexity estimate the number of parameters.
- The measure of the fit it is via the Deviance.
- Models with smaller DIC tend to be better predictions.
- DIC can be monitored in WinBUGS from Inference/DIC menu or direct calculates using R.

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Type of models used.

- The general model. Age, Period and Cohort.
- Age and Period model.
- Age and Cohort model.
- Period and Cohort model.

We use the DIC to compare different types of incidence data sets in Puerto Rico.

All of the calculations are in an interface between WinBUGS and MATLAB or WinBUGS and R (Sturtz,Ligges,Gelman(2005)). Since there a a hierarchical Bayesian structure it is convenient to use of the Gibbs Sampler algorithm to do the calculations.

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Model Selection Table for Liver Cancer

Type	Sex	pD	DIC
Liver APC Model	Both	20.57	430.832
Liver AC Model	Both	21.333	444.898
Liver AP Model	Both	14.406	436.897
Liver PC Model	Both	14.138	560.504
Liver APC Model	Male	20.089	394.243
Liver AC Model	Male	19.741	408.759
Liver AP Model	Male	13.893	408.047
Liver PC Model	Male	13.59	502.512
Liver APC Model	Female	16.118	328.688
Liver AC Model	Female	15.039	330.904
Liver AP Model	Female	10.424	327.888
Liver PC Model	Female	11.026	342.197

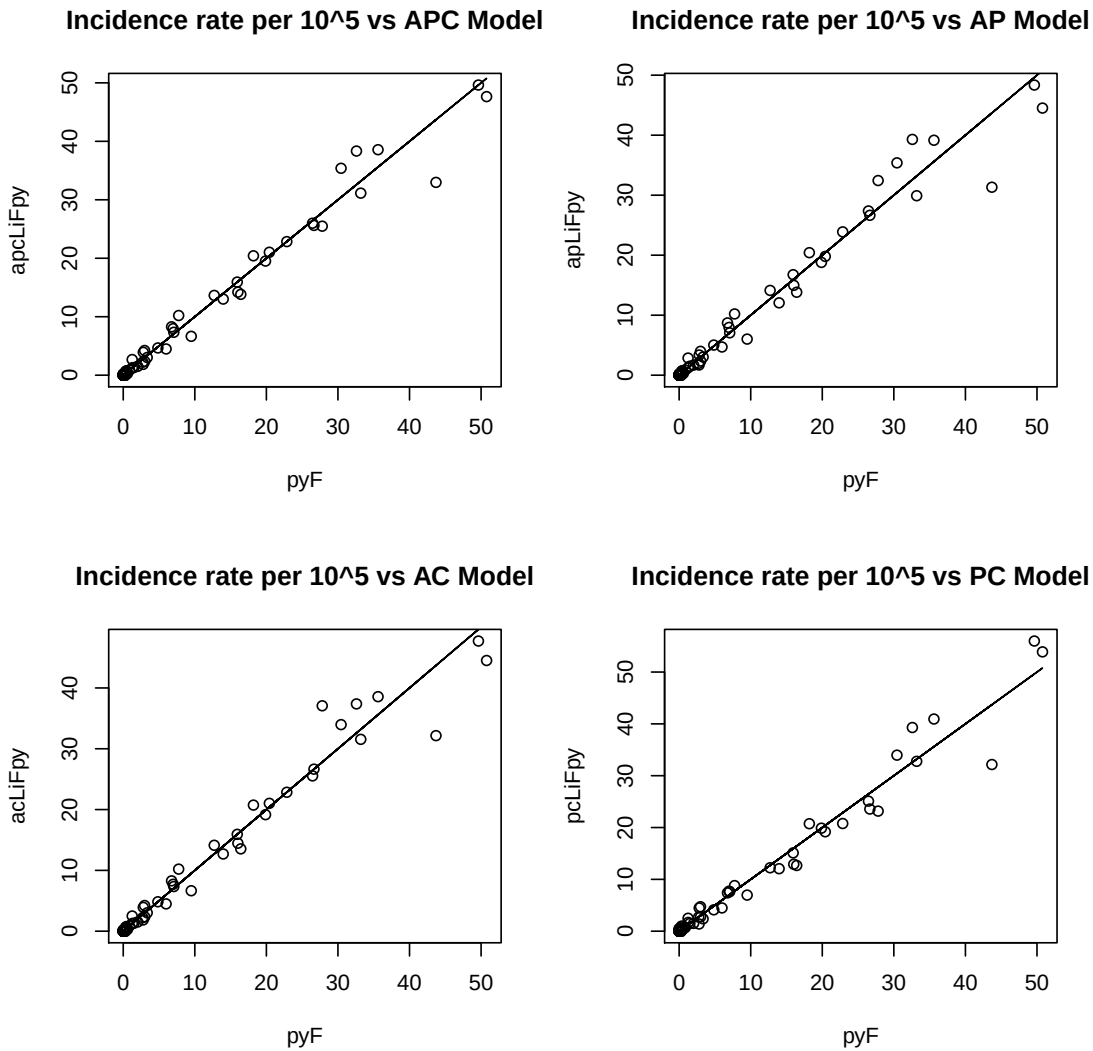

Figure: Goodness of fit for female Liver cancer data.

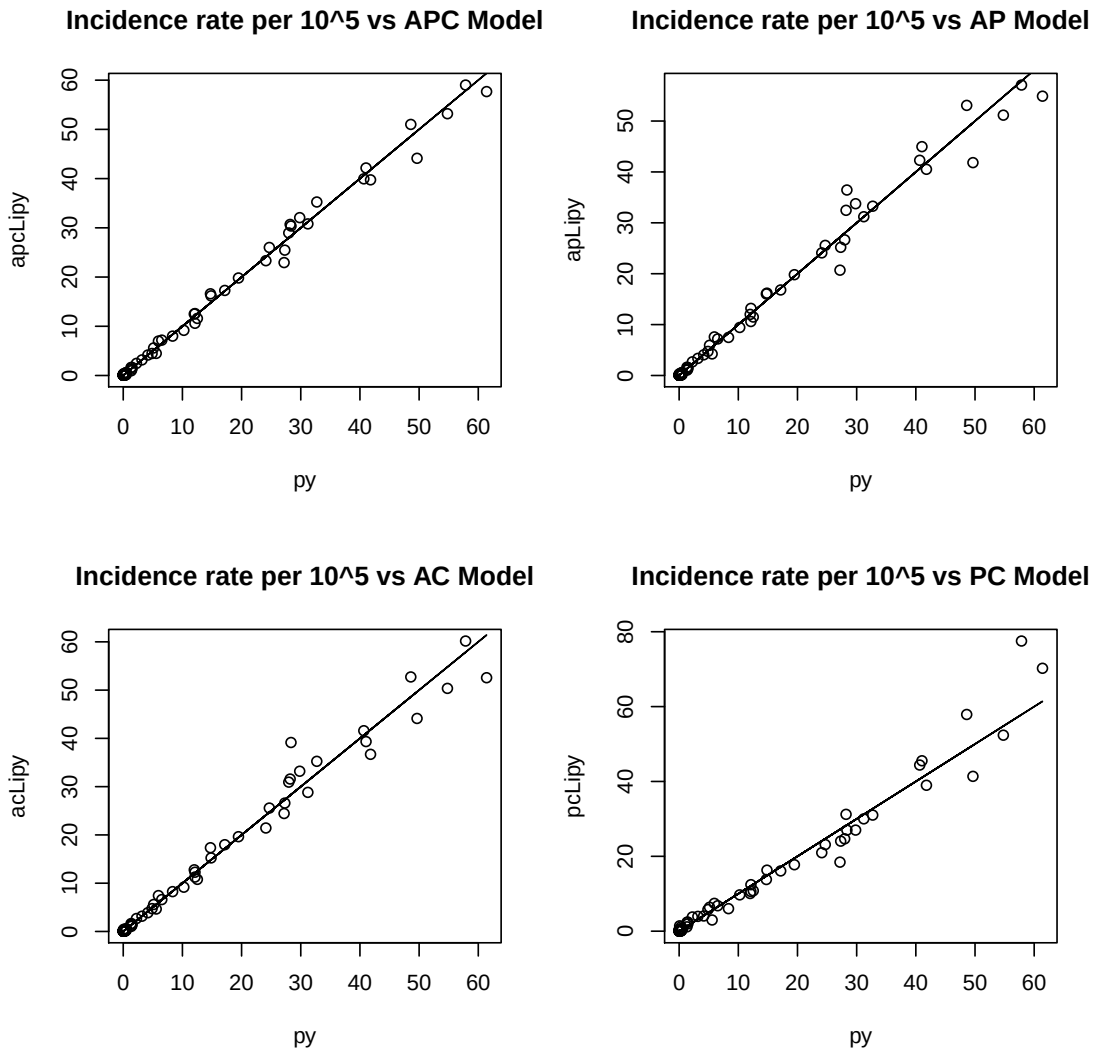

Figure: Goodness of fit for male Liver cancer data.

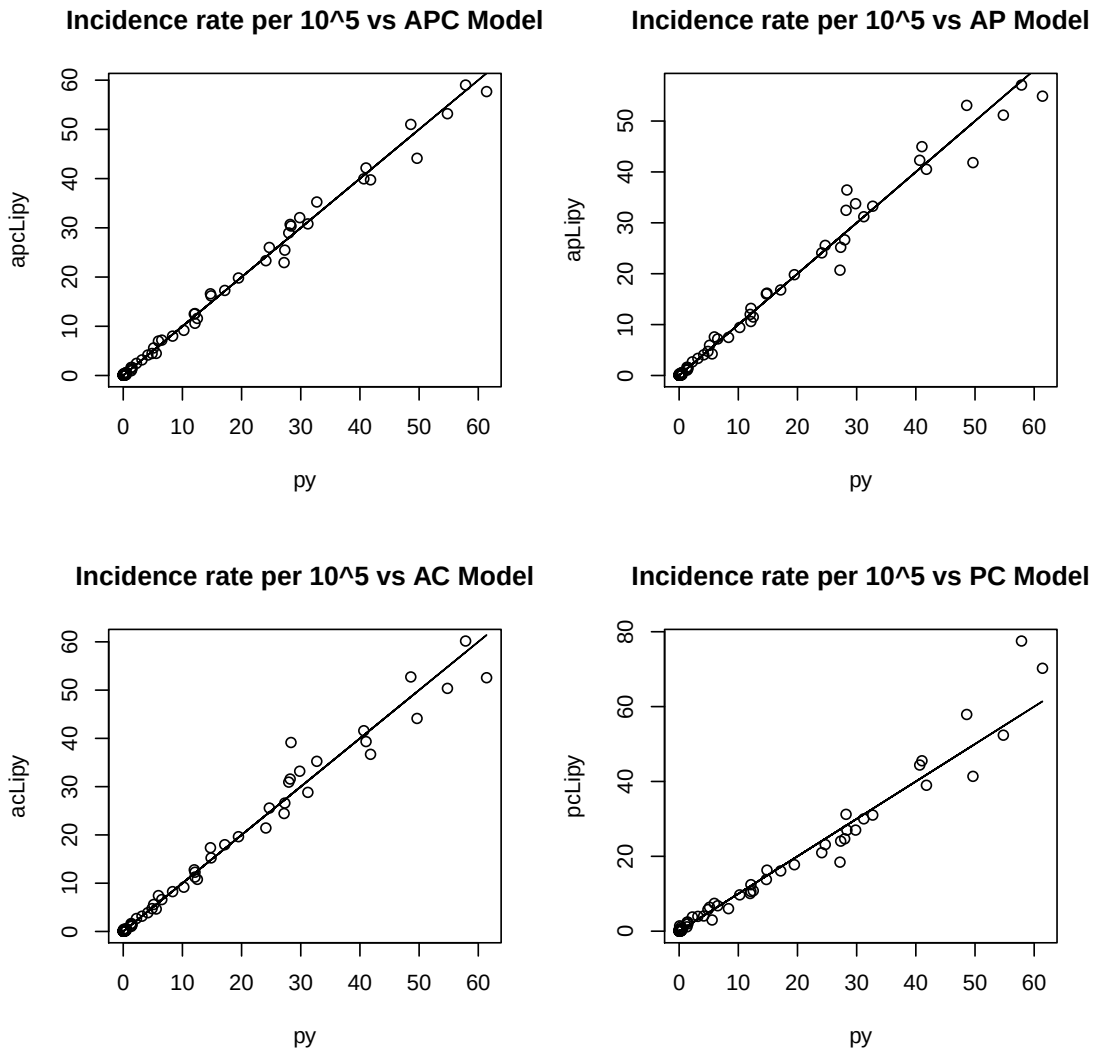

Figure: Goodness of fit for male and female Liver cancer data.

Results

The following figures presents incidence cancer historical values $1985-1989$, $1990-1994$, $1995-1999$ and $2000-2004$ and posterior median estimators for $2005-2009$ and $2010-2014$ with probability intervals provided by the CCRPR.For this, population estimators of Puerto Rico from 1985 to 2014 were used. Each one of the graphs presents the historical data and the estimated quinquennial periods starting in 2005 and 2010 respectively.

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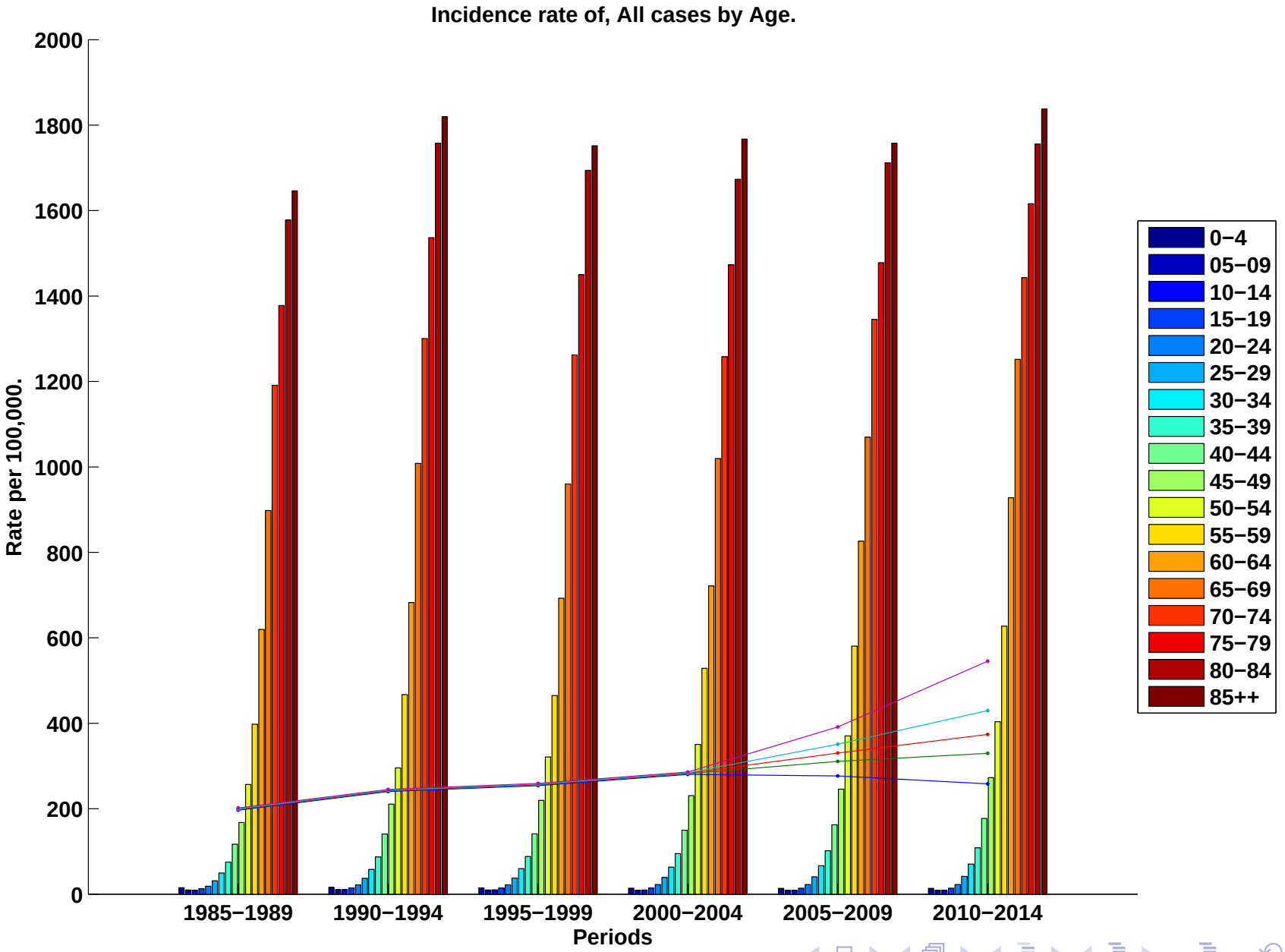
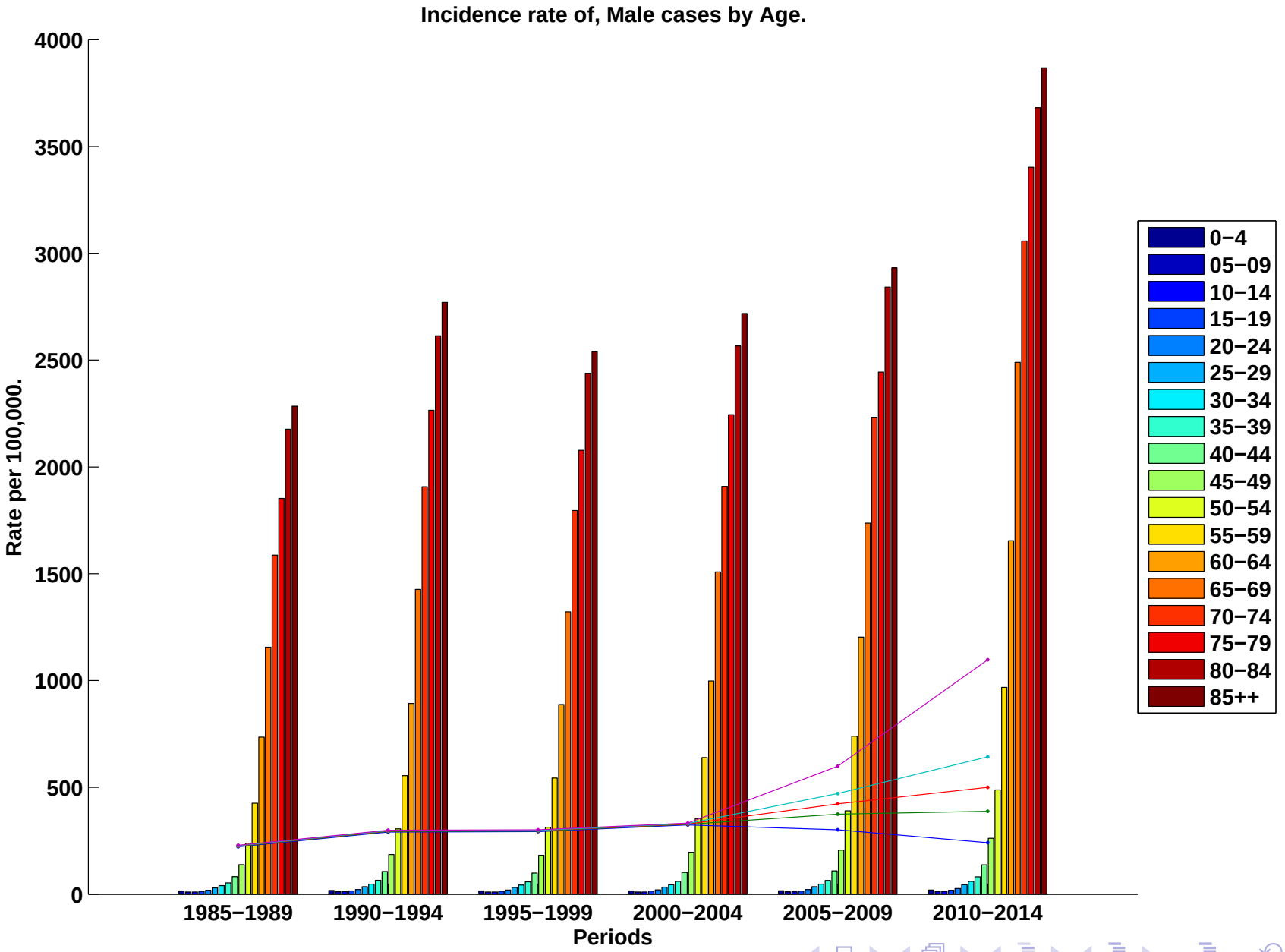
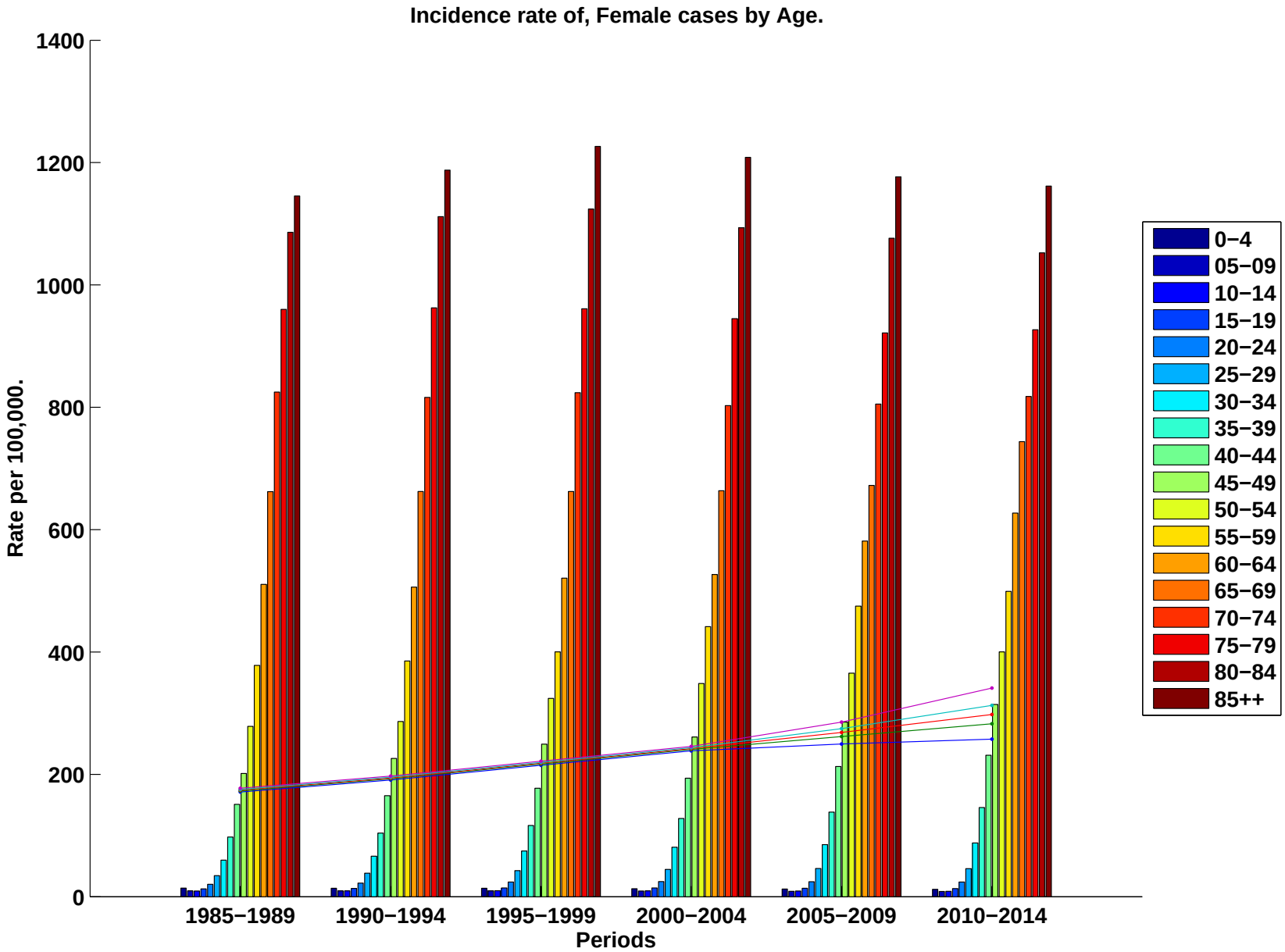

Incidence rate of, All cases by Age.
Rate per 100,000.
2000
1800
1600
1400
1200
1000
800
600
400
200
0
1985−1989
1990−1994
1995−1999
2000−2004
2005−2009
2010−2014
Periods
0−4
05−09
10−14
15−19
20−24
25−29
30−34
35−39
40−44
45−49
50−54
55−59
60−64
65−69
70−74
75−79
80−84
85++


Incidence rate of, Male cases by Age.
Rate per 100,000.
4000
3500
3000
2500
2000
1500
1000
500
0
1985−1989
1990−1994
1995−1999
2000−2004
2005−2009
2010−2014
Periods
0−4
05−09
10−14
15−19
20−24
25−29
30−34
35−39
40−44
45−49
50−54
55−59
60−64
65−69
70−74
75−79
80−84
85++


Incidence rate of, Female cases by Age.
Rate per 100,000.
1400
1200
1000
800
600
400
200
0
1985−1989
1990−1994
1995−1999
2000−2004
2005−2009
2010−2014
Periods
0−4
05−09
10−14
15−19
20−24
25−29
30−34
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45−49
50−54
55−59
60−64
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85++

Observations and Conclusions.

- The Bayesian Approach to Statistics is flexible and based on evidence, the natural choice for Epidemiological Predictive Models, like Age-Period-Cohort models, and also for Clinical Trials.
- Age-Period-Cohort can be used besides Cancer, to several other Health Problems like Tuberculosis, Cardiovascular Disease etc. It serves to chronic diseases in epidemiology or of social events in social studies or demography.
- A-P-C permits both long term prediction and short term prediction.
- A-P-C models allows to "predict the present time" and/or the near future.
- A-P-C allows comparison of the importance of the effect by Age, effect by Period and by Cohort.
- The A-P-C models can incorporate Geographical Sites inside the general Hierarchical model, if the geographical data is available.

Bibliography I


N. E. Breslow and D. G. Clayton.
Approximate inference in generalized linear mixed models.
Journal of the American Statistical Association, 1993.


D. Spiegelhalter, A. Thomas, and N. Best.
WinBUGS - Bayesian inference using Gibbs sampling for Windows: Version 1.1.1.
MRC Biostatistics Unit, Cambrigde, 1998.


Lee WC and Lin RS.
Autoregressive age-period-cohort models.
Statistics in Medicine, 1996.