ONLINE BAYESIAN APNEA-BRADYCARDIA DETECTION USING AUTO-REGRESSIVE MODELS

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ABSTRACT

This paper proposes an online Bayesian method to detect change points in auto-regressive (AR) processes with unknown model orders. The AR model is frequently used in the spectral analysis of RR series extracted from electrocardiographic signals (ECG) [1, 2]. By relaxing the model order constraint, we aim to detect apnea-bradycardia (AB) episodes from abrupt changes in the model space. An efficient recursive algorithm inspired from the work of Godsil *et al.* [3, 4] is proposed to update with fixed complexity the joint posterior distribution of the AR coefficients and model orders. Simulation results show fast convergence of the estimated distribution, thus making it an efficient tool to detect underlying AR model changes in time series. For AB detections with annotated ECG data, the detection sensitivity (TP/(TP + FN)) reaches 98% over a total of 50 episodes with 92% specificity (TN/(TN + FP)). We also discovered an interesting property in terms of detection delay ($-3.64s \pm 4.34$), compared with the experts' off-line annotations. The negative mean in detection delay suggests that AR model changes might occur before the onset of AB episodes while from the clinical point of view, it is essential to achieve reliable early stage detection of AB episodes to enable the initiation of quick nursing actions [5].

1. INTRODUCTION

AB episodes are defined as a respiratory pause, accompanied with a fall in heart rate. These episodes are common in preterm infants and may seriously compromise oxygenation and tissue perfusion and lead to neurological morbidity or even infant death [6, 7]. In the domain of biomedical signal analysis and in particular for the ECG signal, the AR model is traditionally used to compute the power spectrum density for RR interval time-series. Broadman *et al.* studied the impact of using different criteria (Akaike, Parzen, Rissanen) in determining the model order and proposed a fixed optimal order for the spectral analysis of RR series [2]. Unlike the previous studies based on the power spectrum analysis of RR series (first proposed by [1]), we adopt here a Bayesian approach by considering the model order as a random variable and the goal is to detect AB episodes by abrupt changes in the AR model space.

The idea is to fully exploit the recurrence relations of the RR series using AR models with unknown coefficients and orders. Indeed, the short-time stationary nature in the RR signal (as an indicator of the heart rate variability) is ideally modeled by the slowly-changing AR coefficients and model orders [1] while the non-stationary event that corresponds to apnea-bradycardia episodes results in abrupt changes in both the AR coefficients and model orders. It is then possible to detect AB events by investigating the evolution of these parameters.

Inspired from the previous works of J. Godsill *et al.* in the off-line AR model selection and parameter estimation problem [3, 4], we propose to update online and recursively the joint posterior distribution of the AR coefficients and orders while the marginal distribution of model orders is achieved by integrating out the normally distributed AR coefficients. A sufficient number of model orders are included for the posterior distribution evaluation to cover a large scale of physiological heart rate variability origins [8]. We also optimize the computational complexity and robustness of the algorithm by keeping track the Cholesky factor of the covariance inverse of the AR coefficients' estimation, since it is always well-defined, monotonously increasing by construction and better conditioned than the covariance matrix and its inverse. It is shown that the update cost is $\mathcal{O}(k^2)$ for AR(k) and does not increase over time, thus allowing an efficient clinical real-time implementation. Compared with previous works on the detection of AB events by using the Hidden Semi-Markov models (HSMM) [9], the proposed method does not use model parameters trained from a heterogeneous database since the estimation of the joint distribution and detection of distribution shifts are performed simultaneously upon each single patient and consequently there is no inter-patient variabilities issue to be dealt with. Higher sensitivity rate and earlier detections are also important improvements in performance of the proposed method.

The paper is organized as follows. Section 2 details the signal model and the on-line recursive update algorithm. Simulation results are given to illustrate the fast convergence property of the joint distribution estimation. Based on the

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convergence property, the AR innovation noise level is defined to detect AB events in real clinical database. Section 3 illustrates results on the annotated database of ECG signal acquired from the target population of preterm infants suffering from AB episodes. Finally, in section 4 we discuss possible extensions of our work.

2. METHOD

2.1. Signal Model

A time serie $\{\boldsymbol{y}_n\}_{1,\dots,N}$ modeled by an AR process obeys :

$$\boldsymbol{y}_n = \sum_{i=1}^{k} \alpha_i^{(k)} \boldsymbol{y}_{n-i} + \epsilon_n, \tag{1}$$

for which $k \in \mathbb{N}$ denotes the model order and ϵ_n the innovation process. The latter is supposed to follow an *i.i.d.* Gaussian distribution $\mathcal{N}(0, \sigma_\epsilon^2)$ for its well-behaved mathematical properties even though other marginal distributions such as Laplace process [10], generalized Laplacian [11] and geometric α-Laplace distributions [12] are also extensively studied as data models.

The matrix form of the AR process writes also :

$$\boldsymbol{y}_{k+1:n} = \mathbf{Y}_{(k:n-1)} \bar{\alpha}^{(k)} + \epsilon \tag{2}$$

where $\boldsymbol{y}_{k+1:n} = [\boldsymbol{y}_{k+1}, \dots, \boldsymbol{y}_n]^{\mathrm{t}}$ represents the observation data of increasing size, $\bar{\alpha}^{(k)} = [\alpha_1^{(k)}, \dots, \alpha_k^{(k)}]^{\mathrm{t}}$ the AR coefficient vector and $\mathbf{Y}_{(k:n-1)}$ the $(n-k) \times k$ Toeplitz matrix whose first line is $\boldsymbol{y}_{k:1}^{\mathrm{t}}$ and the first column is $\boldsymbol{y}_{k:n-1}$.

The model order selection problem is addressed by J. Godsill *et al.* [3, 4] within a Bayesian framework, in which reversible jump Markov chain Monte Carlo (MCMC) algorithms [13] are developed to perform the required integration by stochastic simulation. They found that the marginalization technique in the sampling of model orders (by integrating out AR coefficients) is more efficient and robust numerically. Similar results in partially collapsed MCMC samplers are also discussed in the blind deconvolution problem [14, 15]. In the current study, we adopt the Gaussian assumption concerning the AR coefficients $\bar{\alpha}^{(k)} \sim \mathcal{N}(\mathbf{0}, \sigma_\alpha^2 \mathbf{I}_k)$ to allow its integration and the marginal posterior law of the model order writes according to [3] :

$$p(k|\boldsymbol{y}_{1:n}, \sigma_\alpha^2, \sigma_\epsilon^2) \propto \frac{p(k)\sqrt{|\mathbf{C}_{k,n}|}}{\sigma_\alpha^k} \exp\left(\frac{\mu_{k,n}^{\mathrm{t}} \mathbf{C}_{k,n}^{-1} \mu_{k,n}}{2}\right) \tag{3}$$

where $p(k)$ denotes the prior distribution and

$$\mathbf{C}_{k,n}^{-1} = \sigma_\epsilon^{-2} \mathbf{Y}_{(k:n-1)}^{\mathrm{t}} \mathbf{Y}_{(k:n-1)} + \sigma_\alpha^{-2} \mathbf{I}_k, \tag{4}$$

$$\mu_{k,n} = \sigma_\epsilon^{-2} \mathbf{C}_{k,n} \mathbf{Y}_{(k:n-1)}^{\mathrm{t}} \boldsymbol{y}_{k+1:n}. \tag{5}$$

A normalization is imposed for a given order range :

$$\sum_{k=k_{\min}}^{k_{\max}} p(k|\boldsymbol{y}_{1:n}, \sigma_\alpha^2, \sigma_\epsilon^2) = 1. \tag{6}$$

To access the joint AR model order and coefficients distribution, we use the following conditional distribution of $\bar{\alpha}^{(k)}$ given AR(k) [3]:

$$\bar{\alpha}^{(k)}|k, \boldsymbol{y}_{1:n}, \sigma_\alpha^2, \sigma_\epsilon^2 \sim \mathcal{N}(\mu_{k,n}, \mathbf{C}_{k,n}).$$

It is essential then that the update cost of Eq. (3) does *not* increase with time even though $\mathbf{C}_{k,n}$ and $\mu_{k,n}$ involve matrices whose dimensions increase with n, such as $\mathbf{Y}_{(k:n-1)}$ (cf Eqs.(4) (5)). In other words, an efficient recursive scheme is required to update $\{|\mathbf{C}_{k,n}|, \mu_{k,n}^{\mathrm{t}} \mathbf{C}_{k,n}^{-1} \mu_{k,n}\}$ with fixed complexity in regard to n. We note that unlike the MCMC framework [3, 4] that solves the model selection and parameter estimation problem off-line, the objective of this paper is to detect as early as possible abrupt changes of both AR coefficients and model orders based on online non-stationary observations.

2.2. Recursive update

We propose the recursive updates of Eq. (3) using the rank-1 Cholesky factor update of $\mathbf{C}_{k,n}^{-1}$. This is not only possible but also numerically stable because the covariance inverse is a positive-definite matrix with increasing eigenvalues by definition (cf Eq. (4)). Its Cholesky factor is also better-conditioned than the covariance and the inverse itself. The rank-1 update is based on the following relation from Eq. (4) :

$$\mathbf{C}_{k,n}^{-1} = \mathbf{C}_{k,n-1}^{-1} + \sigma_\epsilon^{-2} \boldsymbol{y}_{n-1:n-k} \boldsymbol{y}_{n-1:n-k}^{\mathrm{t}}. \tag{7}$$

Notice that $\mathbf{C}_{k,n}^{-1}$ is always a $k \times k$ matrix.We apply the rank-1 Cholesky factor update procedure (see details in [16]):

$$\mathbf{F}_{k,n} = \texttt{cholupdate}(\mathbf{F}_{k,n-1}, \sigma_\epsilon^{-1} \boldsymbol{y}_{n-1:n-k}), \tag{8}$$

with $\mathbf{F}_{k,n}$ (and $\mathbf{F}_{k,n-1}$) the upper-triangular matrix such that $\mathbf{F}_{k,n}^{\mathrm{t}} \mathbf{F}_{k,n} = \mathbf{C}_{k,n}^{-1}$ (and $\mathbf{F}_{k,n-1}^{\mathrm{t}} \mathbf{F}_{k,n-1} = \mathbf{C}_{k,n-1}^{-1}$ *resp.*). The rank-1 Cholesky factor update operation costs $\mathcal{O}(k^2)$ and also simplifies the term $|\mathbf{C}_{k,n}|$ since :

$$\sqrt{|\mathbf{C}_{k,n}|} = \left(\prod \texttt{diag}(\mathbf{F}_{\texttt{k,n}})\right)^{-1}, \tag{9}$$

where `diag` extracts the diagonal part of a square matrix and $\prod$ calculates the product of all components.

From Eq. (5) we can rewrite :

$$\begin{aligned} \mu_{k,n}^{\mathrm{t}} \mathbf{C}_{k,n}^{-1} \mu_{k,n} &= \sigma_\epsilon^{-4} \boldsymbol{y}_{k+1:n}^{\mathrm{t}} \mathbf{Y}_{(k:n-1)} \mathbf{C}_{k,n} \mathbf{Y}_{(k:n-1)}^{\mathrm{t}} \boldsymbol{y}_{k+1:n} \\ &= \sigma_\epsilon^{-4} \boldsymbol{y}_{k+1:n}^{\mathrm{t}} \mathbf{Y}_{(k:n-1)} (\mathbf{F}_{k,n}^{-1} \mathbf{F}_{k,n}^{-\mathrm{t}}) \mathbf{Y}_{(k:n-1)}^{\mathrm{t}} \boldsymbol{y}_{k+1:n} \\ &= \left| \sigma_\epsilon^{-2} \mathbf{F}_{k,n}^{-\mathrm{t}} \boldsymbol{R}_{k,n} \right|^2, \end{aligned} \tag{10}$$

where $\boldsymbol{R}_{k,n} = \mathbf{Y}_{(k:n-1)}^{\mathrm{t}} \boldsymbol{y}_{k+1:n}$ can be updated by :

$$\boldsymbol{R}_{k,n} = \boldsymbol{R}_{k,n-1} + \boldsymbol{y}_n \cdot \boldsymbol{y}_{n-1:n-k} \tag{11}$$

Note that the left division of a lower-triangular matrix in Eq. (10) costs $\mathcal{O}(k^2)$.

To recapitulate, the pseudo-code of the recursive update algorithm is given in Tab. 1. It costs $\mathcal{O}(k^2)$ in complexity and requires the storage of an upper-triangular matrix $\mathbf{F}_{k,n}$ ($k \times k$

in dimension) and a column vector $\boldsymbol{R}_{k,n}$ of $k \times 1$, both fixed with respect to n and the observation dimensions.

Algorithm 1 Recursive update of AR order probability

for $k \in \{k_{\min}, \ldots, k_{\max}\}$ **do** ▷ Initialization
  $\mathbf{F}_{k,k_{\max}} = \frac{1}{\sigma_\alpha}\mathbf{I}_k$
  $\boldsymbol{R}_{k,k_{\max}} = [\underbrace{0, \ldots, 0}_{k}]^{\mathrm{t}}$
end for
for $n = k_{\max} + 1, \ldots$ **do** ▷ main loop
  for each model $k \in \{k_{\min}, \ldots, k_{\max}\}$ **do**
    Update $\mathbf{F}_{k,n}$ using Eq. (8);
    Update $\boldsymbol{R}_{k,n}$ using Eq. (11);
    Evaluate Eq. (3) using Eqs. (9)(10);
  end for
  Normalize $p(k|\boldsymbol{y}_{1:n}, \sigma_\alpha^2, \sigma_\epsilon^2)$ using Eq. (6).
end for

2.3. Simulation results

The simulation tests on stationary AR processes is designed to validate the on-line model selection algorithm. A total of 100 time series are generated using AR model with orders ranging from 3 to 11 for 1000 samples. The AR model coefficients are generated using random poles within the unit circle to ensure the process stability whereas $\sigma_\alpha^2 = 1$ is arbitrarily fixed in the algorithm. The AR process noise variance $\sigma_\epsilon^2 = 0.2$ is supposed to be known. Prior distribution $p(k)$ is supposed to be uniform from $k_{\min}$ to $k_{\max}$ since we privilege here that the data speak for themselves.

Typical results of the marginal posterior probability of model orders are illustrated in Fig. 1(a) and the covariance norms' decay are shown in Fig. 1(b) for all models AR(k) in the same example : both the AR coefficients in each model AR(k) and the marginal model order distribution $p(k|\boldsymbol{y}_{1:n}, \sigma_\alpha^2, \sigma_\epsilon^2)$ converges rapidly. It is also observed (but not illustrated due to space limit) that the Euclidian distances between the estimated $\bar{\alpha}^{(k)}$ and the *true* AR coefficients converge in a similar manner.

2.4. AR Model shift detection

In a perfectly stationary case, the AR(k) coefficients' estimate covariance $\mathbf{C}_{k,n}$ is decreasing as n augments by construction (cf Eq. (4)). It is confirmed in simulation results and the evolution of $|\mathbf{C}_{k,n}|$ in Fig. 1(b) also shows the convergence speed. Therefore, the joint posterior probabilities $p(\bar{\alpha}^{(k)}, k|\boldsymbol{y}_{1:n}, \sigma_\alpha^2, \sigma_\epsilon^2)$ converge to a series of Dirac functions, each having a weight factor equal to $p(k|\boldsymbol{y}_{1:n}, \sigma_\alpha^2, \sigma_\epsilon^2)$. This interesting property is the key to the non-stationarity detection from two distinct AR models.

The model shift detector on the other hand, is supposed to work on non-stationary time series for which change points delimits the short-time stationary periods. We define the AR process noise level by integrating out both the AR coefficients and the model order :

$$\widehat{\varepsilon_n^2} = \frac{1}{L}\sum_{k=k_{\min}}^{k_{\max}} \left|\boldsymbol{y}_{n-L+1:n} - \mathbf{Y}_{(n-L:n-1)}\mu_{k,n}\right|^2 p(k|\boldsymbol{y}_{1:n}, \sigma_\alpha^2, \sigma_\epsilon^2), \quad (12)$$

for which a moving window of length $L \geq 1$ is applied. It is a reasonable approximation of

$$\frac{1}{L}\sum_{k=k_{\min}}^{k_{\max}} \int \left|\boldsymbol{y}_{n-L+1:n} - \mathbf{Y}_{(n-L:n-1)}\bar{\alpha}^{(k)}\right|^2 p(k, \bar{\alpha}^{(k)}|\boldsymbol{y}_{1:n}, \sigma_\alpha^2, \sigma_\epsilon^2)\mathrm{d}\bar{\alpha}^{(k)}$$

by taking $p(\bar{\alpha}^{(k)}|k, \boldsymbol{y}_{1:n}, \sigma_\alpha^2, \sigma_\epsilon^2) = \delta(\bar{\alpha}^{(k)} - \mu_{k,n})$ due to the fast convergence property. The measured noise level $\widehat{\varepsilon_n^2}$ shown in the upper panel of Fig. 2(b) corresponds to a simulated AR model change (lower panel of Fig. 2). It is evident that the shift in AR model space is associated with the noise level increase.

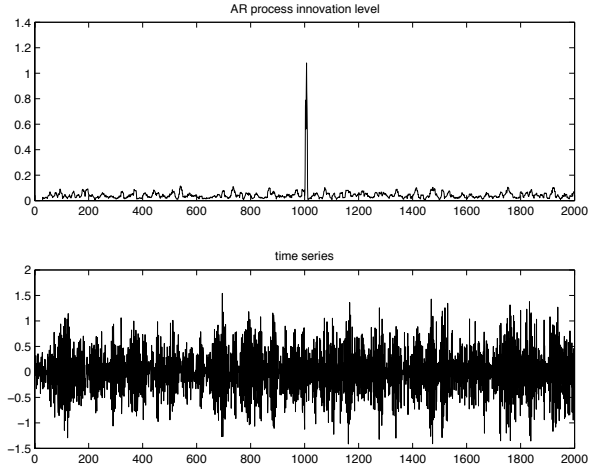

Fig. 2. Detection of AR process model change. The simulated change point occurred at the 1000-th sample (lower panel). The AR process noise level surges in the upper panel from the 1002-th sample till the 1011-th sample and is followed by stabilization.

In the following test, a simple relative thresholding on the $\widehat{\varepsilon_n^2}$ is used to detect change point of AR models and re-initiates the recursive algorithm in Tab. 1, from which $\{p(k|\boldsymbol{y}_{1:n}, \sigma_\alpha^2, \sigma_\epsilon^2), \mu_{k,n}\}$ are used to update $\widehat{\varepsilon_n^2}$ with Eq. (12).

3. EXPERIMENTS ON AB DETECTION

For the detection of AB events in real ECG signals, we used a database with manual annotations on the 50 RR series from 32 preterm infants. The proposed algorithm is applied on the RR series extracted from raw ECG signals (cf [17] for details) in

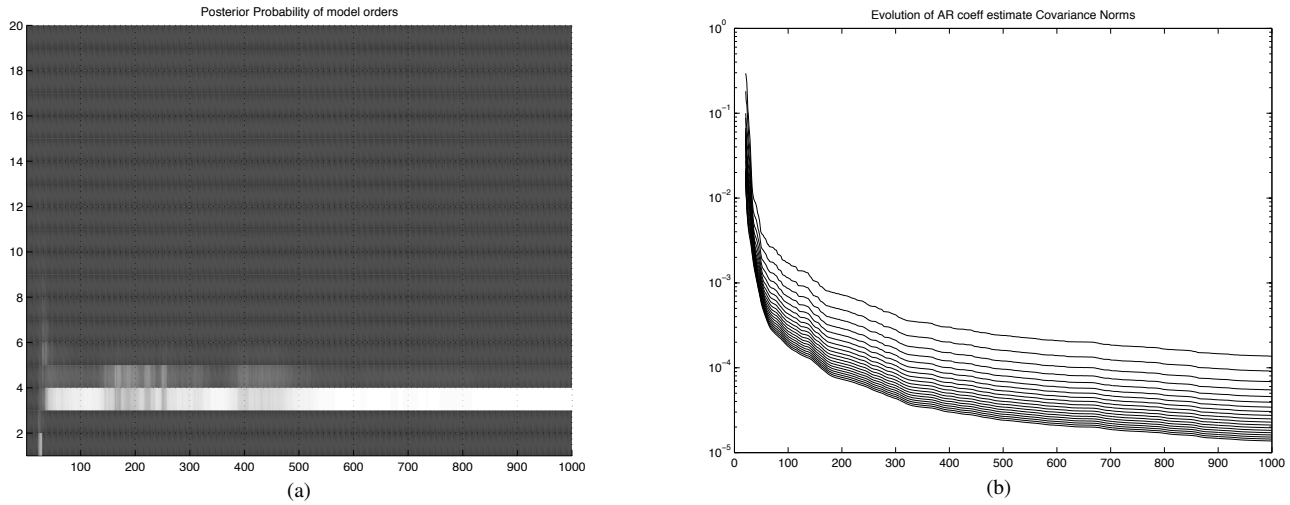

Fig. 1. Typical simulation results using an AR(4) of 1000 points (see x-axis in both (a) and (b)). The marginal posterior distribution of the model order (ranging from 2 to 20 of y-axis) is presented in (a) with grayscale proportional to the probability value, while in (b) are illustrated the norms of $\bar{\alpha}^{(k)}$ estimation covariance $|\mathbf{C}_{k,n}|$ for all k : quick convergence relative to the initial values is observed and final decays range from 10^{-3} to 10^{-4}.

the database. It is a real challenge due to the *off-line* diagnosis procedure of experts.

The maximum AR model order $Q_{\max}$ is set to 20 to cover a large scale of physiological heart rate variability origins [8] for real ECG experiments. The same $\{\sigma_\alpha^2, \sigma_\epsilon^2\}$ are used as in the simulation tests and the window length $L = 10$ is set for the update of $\widehat{\varepsilon_n^2}$ in Eq. (12). An AB event is detected when the $\widehat{\varepsilon_n^2}$ surpasses a thresholding level (10 times the mean level of the previous minute).

We compared the overall performances relative to the HSMM method proposed in [9] for which the same ECG database is used. True positives (TP), true negatives (TN), false positives (FP) and false negatives (FN) were determined for each sample by comparing the obtained detections with the available annotations. TP occur when a detection falls within a 20 s window, centered at the annotation. The window is chosen to be large enough to evaluate the detection delay. All other detections are noted as FP while annotations without corresponding detections are considered as FN. Since each entry in the dataset contains an annotated AB event, the number of TN is calculated by $\lfloor \text{length of entry}(s)/20 \rfloor - \text{FP} - 1$. Figures of merit (sensitivity and specificity functions) are then evaluated and reported in Tab. 1. One remarkable advantage of our method is the ability to capture AR model changes that take place priorly to the onset of AB events and thus yield an enormous gain in the detection delay, though this is done at the cost of a minor increase in the number of FP detections (lower SPC level).

Table 1. Comparison of sensitivity, specificity and detection delay results

Method	SEN (%)	SPC (%)	Delay (sec)
HSMM [9]	90.38	92.23	0.92 ± 3.56
AR Shift	98.00	91.17	-3.67 ± 4.34

4. CONCLUSION AND PERSPECTIVES

A novel online detection algorithm of autoregressive model change is presented in the present study with applications in the automatic surveillance of the apnea-bradycardia events in preterm infants, a difficult problem in the modeling and exploiting of the dynamics in biomedical time series. Model simplicity associated with optimized computing efficiency are the key issues in real time implementation of the proposed algorithm. Results obtained from simulated AR signals demonstrate the interest of the proposed method : 1) the joint posterior distributions of the AR model order and coefficients can be estimated on line recursively with fixed computation complexity, 2) they converge rapidly and can be used as a reliable marker of model shift. The AR process noise level is designed to integrate in a Bayesian manner the model choice and parameter estimation and to characterize the rapid shift in the AR model space. Experiments' results on real ECG data with experts' annotations confirm the feasibility of the proposed method.

In the future, we aim at extending the current algorithm framework to include several interesting aspects : 1) testing different prior distributions of model orders $p(k)$ in the context of preterm infants suffering from AB episodes with clinically plausible prior knowledge, 2) relaxing the $k_{\max}$ constraint and track the AR order distribution in a particle filter manner. We are also encouraged to enrich the experimental validation by comparing with other online segmentation algorithms, in particular the MCMC-based batch segmentation procedure by Punskaya *et al.* [18].

5. REFERENCES

[1] S. Akselrod, D. Gordon, F. A. Ubel, S. C. Shanon, A. C. Barger, and R. J. Cohen, "Power spectrum analysis of heart rate fluctuation: A quantitative probe of beat-to-beat cardiovascular control," *Science*, vol. 213, pp. 220–222, 1981.

[2] A. Boardman, F. Schlindwein, A. Rocha, and A. Leite, "A study on the optimum order of autoregressive models for heart rate variability," *Physiol. Meas.*, vol. 23, pp. 325–336, 2002.

[3] Paul Troughton and Simon J. Godsill, "A reversible jump sampler for autoregressive time series, employing full conditionals to achieve efficient model space moves," Tech. Rep., Cambridge, UK, 1998.

[4] J. Vermaak, C. Andrieu, A. Doucet, and S. J. Godsill, "Bayesian model selection of autoregressive processes," *J. TIME SERIES ANALYSIS*, 2000.

[5] R. Pichardo, J. Adam, E. Rosow, J. Bronzino, and L. Eisenfeld, "Vibrotactile stimulation system to treat apnea of prematurity," *Biomed Instrum Technol.*, vol. 37, no. 1, pp. 34–40, 2003.

[6] A. Janvier, M. Khairy, A. Kokkotis, C. Cormier, D. Messmer, and K.J. Barrington, "Apnea is associated with neurodevelopmental impairment in very low birth weight infants," *J Perinatol.*, vol. 24, no. 12, pp. 763–8, 2004.

[7] F. Pillekamp, C. Hermann, T. Keller, A. von Gontard, A. Kribs, and B. Roth, "Factors influencing apnea and bradycardia of prematurity-implications for neurodevelopment," *Neonatology*, vol. 91, no. 3, pp. 155–61, 2007.

[8] M. Malik, "Heart rate variability: standards of measurement, physiological interpretation and clinical use. task force of the european society of cardiology and the north american society of pacing and electrophysiology," *Circulation*, vol. 93, no. 5, pp. 1043–65, 1996.

[9] M. Altuve, G. Carrault, A. Beuchée, P. Pladys, and A. I. Hernández, "On-line apnea-bradycardia detection using hidden semi-markov models," in *IEEE Eng Med Biol Soc.*, Aug. 2011, pp. 4374–77.

[10] L. S. Dewald and P. A. Lewis, "A new Laplace Second-order autoregressive time-series model - NLAR(2)," *IEEE Transactions on Information theory*, vol. IT-31, no. 5, pp. 645–51, 1985.

[11] V. S. Lekshmi, J. Joy, and K. K. Jose, "Generalized laplacian and geometric α-laplace distributions with applications in time series modeling," *Statist. Methods*, vol. 5, no. 2, pp. 140–155, 2003.

[12] K. Jayakumar, K. Kalyanaraman, and R.N. Pillai, "α-laplace processes," *Math. Comput. Modeling*, vol. 22, pp. 109–116, 1995.

[13] P. J. Green, "Reversible jump markov chain monte carlo computation and bayesian model determination," *Biometrika*, vol. 82, no. 4, pp. 711–732, 1995.

[14] D. Ge, Jérôme Idier, and E. Le Carpentier, "Enhanced sampling schemes for mcmc based blind bernoulli-gaussian deconvolution," *Signal Processing*, pp. 759–772, 2011.

[15] G. Kail, J-Y. Tourneret, F. Hlawatsch, and N. Dobigeon, "Blind deconvolution of sparse pulse sequences under a minimum distance constraint: A partially collapsed gibbs sampler method," *IEEE Trans. Signal Process.*, pp. 2727–43, 2012.

[16] J.J. Dongarra, J.R. Bunch, C.B. Moler, and G.W. Stewart, *LINPACK Users' Guide*, SIAM, Philadelphia, 1979.

[17] J. Dumont, A.I. Hernández, , and G. Carrault, "Improving ecg beats delineation with an evolutionary optimization process," *IEEE Trans. Biomed. Eng.*, vol. 57, no. 3, pp. 607–15, 2010.

[18] E. Punskaya, C. Andrieu, A. Doucet, and W. Fitzgerald, "Bayesian curve fitting using mcmc with applications to signal segmentation," *IEEE Trans. Signal Processing*, vol. 50, no. 3, pp. 747–58, 2002.