A respiratory latent variable model for mechanically measured heartbeats

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Abstract. The effect of respiration on heartbeats in a mechanically measured cardiac signal was noticed already in the first respiratory *ballistocardiography* studies in the 1920s. The effect was described as a modulation of the heartbeat amplitude, and that view has persisted. Although a reasonable approximation, amplitude modulation is not an accurate description of the respiratory effect. In this paper, the respiratory variation is described with a linear latent variable model, where the direction of variation can be distinct from the direction of amplitude. The model was evaluated with seven ballistocardiograms from three healthy test subjects. Based on a *Bayesian information criterion* analysis, it was found to describe the variation accurately in all the cases. As the modelling of the heartbeat shape is improved, existing heartbeat detection methods can be made more accurate by applying the proposed model.

Keywords: ballistocardiography, respiration, Bayesian information criterion, probabilistic latent variable model, heart rate, heartbeat

1. Introduction

The measurement of the mechanical vibrations of the heart makes it possible to monitor the heart rate with minimal burden to the patient, as no electrodes need to be attached to the body. Since any sensor measuring mechanical vibrations also registers movements unrelated to the heart, detecting the heart rate is not possible when the patient is not still. Vibration-based cardiac monitoring is therefore excluded from situations where the heart rate data has to be available without interruptions. However, the mechanical approach is well suited for applications such as long-term sleep monitoring, where convenience is more important than the maximal availability of the heart rate data.

Ballistocardiography (BCG) was the first method for unobtrusively measuring the mechanical activity of the heart. It is based on measuring the minute movements

of the body caused by the heart, from the platform supporting the body. The earliest experiments date back to the 19th century (Gordon, 1877), but it was not until the work of Isaac Starr from the 1930s that the method became prominent. Ballistocardiography was to become a clinically significant tool, but the development of *electrocardiography* and the failure of BCG to meet high expectations led to a drastic diminution of BCG research activities from late 1950s. (Smith, 1974, ch. 2)

One of the reasons for the decline of BCG was that the recording apparatus was expensive and cumbersome. However, that is not the case any more. Recently, convenient and inexpensive force sensors have been developed for various setups such as chairs (Ritola, 2002; Koivistoinen et al., 2004), beds (Jacobs et al., 2004; Chee et al., 2005), pillows (Cha et al., 2008) and weighing scales (Inan, Etemadi, Wiard, Giovangrandi and Kovacs, 2009). In addition, methods that do not measure mechanical forces directly, but do it at a distance, have emerged. *Laser vibrocardiography* (Scalise et al., 2005) measures the movements of the body with a beam of laser pointed at the patient, whereas *radar mechanography* (Michahelles et al., 2004; Mohammad-Zadeh et al., 2007) is based on a Doppler radar.

The heart rate can be calculated from mechanical cardiac signals in two ways: by finding a peak corresponding to the heart rate from the frequency transform of the signal, or by finding the onsets of individual heartbeats and calculating the heart rate from inter-beat intervals. The latter method is preferable, as it better tolerates the variability of the heart rate caused by arrhythmias and respiration.

Various methods have been proposed for finding heartbeat onsets from mechanical cardiac signals. One approach is to locate the I and J complexes, which correspond to the major negative and positive deflections, of each heartbeat (Smrcka et al., 2006; Akhbardeh et al., 2007). The approach is based on rather strict assumptions about heartbeat shape, which do not hold in all situations. Another approach is to use a combination of wavelet filtering and peak detection (e.g. Zhu et al., 2006; Postolache et al., 2007), but also that suffers from specific assumptions. Some heartbeat detection methods model the heartbeat shape more flexibly, by calculating the similarity of a heartbeat template with consecutive signal segments, and detecting heartbeats where the similarity is high (Jansen et al., 1991; Shin et al., 2008). These methods are not tied to the heartbeat shape assumptions of a specific measurement setup and can be used in applications where signals measured in various situations need to be analysed. One such application is an unobtrusive sleep monitoring system that monitors the heart rate from the vibrations of a bedpost (e.g. Brink et al., 2006). As different beds and mattresses produce different heartbeat shapes, flexibility in detecting heartbeats is required.

Flexible heartbeat detection methods, such as the ones proposed by Jansen et al. and Shin et al., are based on quantifying the difference between consecutive signal segments and a heartbeat model. The quantification is more precise if the physiological variation in the heartbeat shape can be distinguished from other factors. That way the decision threshold for segment similarity can be set within physiological variation, which can be described, for example, with a *probabilistic latent variable model* (e.g. Bishop, 1999). The model should, in practice, concentrate on modelling the effect of respiration, as the physiological variation between temporally near heartbeats has been found to be caused mostly by respiration (Starr and Noordergraaf, 1967, p. 191).

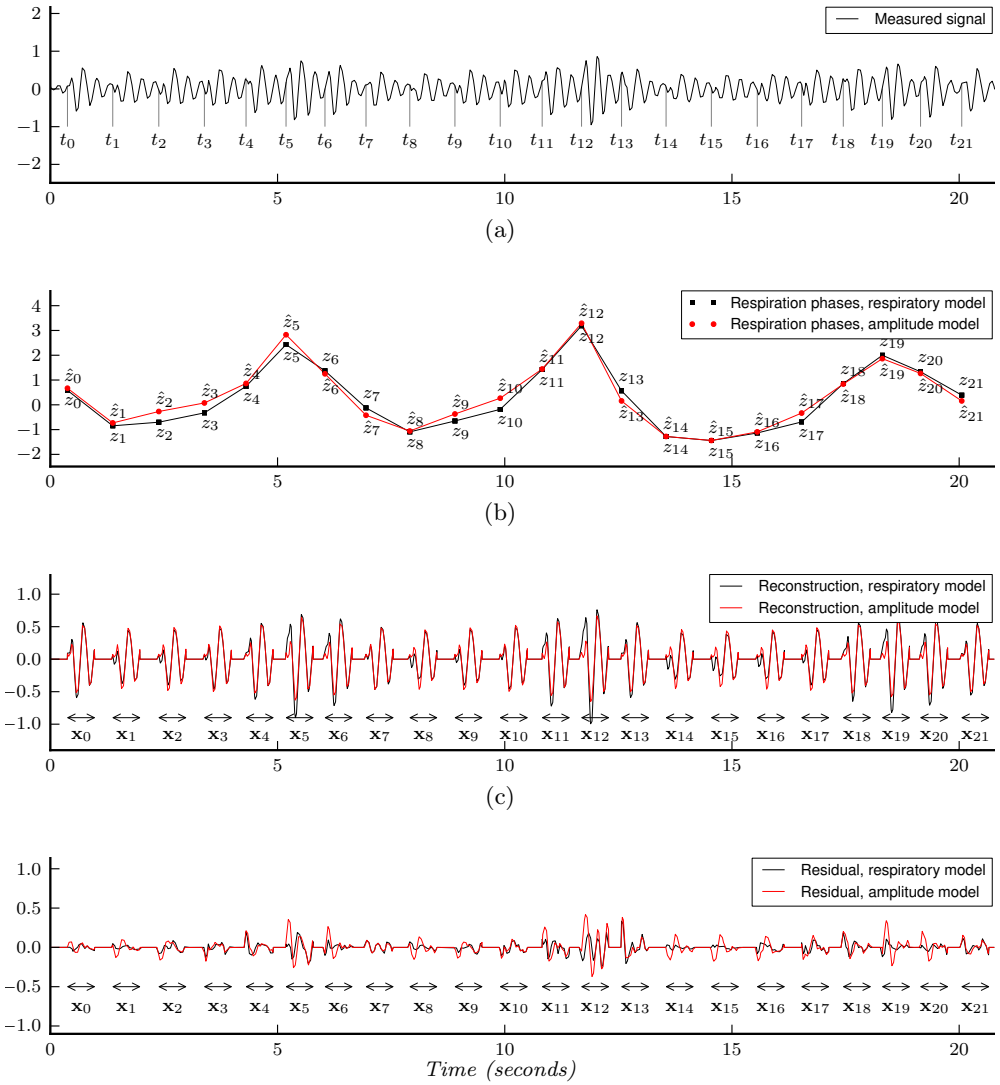

Figure 1. A BCG signal segment containing three respiration cycles is shown in (a). Each t_i denotes the onset of the ith heartbeat (x-axis, time in seconds). The respiratory latent variables z_i for the signal are shown in (b) for the respiratory model and amplitude model. The value of z_i corresponds to the amount of respiratory variation of heartbeat i (y-axis, arbitrary units). In (c), reconstructions of the signal with the two models are shown and (d) contains the residuals for the models. Only the signal sections corresponding to reconstructed heartbeats $\mathbf{x}_i$ are shown in the residual, which means that the residual is not about reconstructing the whole signal, but just heartbeats. The standard deviation of the respiration model residual is 37% lower than that of the amplitude model.

See figure 1 for an example of the respiratory effect.

In the first BCG studies, the patient was asked to hold his or her breath. When breathing during measurement became possible, it was noticed that the heartbeat

amplitude modulates by the phase of respiration (Heald and Tucker, 1922; Starr and Noordergraaf, 1967, p. 191). The view that the respiratory variation can be explained as a modulation of the amplitude is seen also in recent research. The heartbeat detection methods proposed by Paalasmaa and Ranta (2008) as well as Shin et al. (2008) are based on locating heartbeats with an amplitude-invariant similarity measure, which implies that the heartbeat shape is considered to only vary in amplitude. In addition to heartbeat morphology, also the inter-beat-interval varies by respiration phase (Yasuma and Hayano, 2004). Variation of the interval does affect the heartbeat shape, as it changes how adjacent heartbeats overlap.

With some measurement setups, the respiratory variation of the heartbeat shape cannot be described with a simple model. Tavakolian et al. (2008) found that the respiratory variation of the seismocardiogram is so significant that heartbeats corresponding to inspiration and expiration have to be treated separately when heartbeat shape averaging is performed for diagnostic purposes. The finding is consistent with the heartbeat model presented here, where respiratory variation is more complex than just amplitude modulation.

In this paper, a probabilistic latent variable model for the heartbeat shape, which concentrates on describing the respiratory variation, is presented. Applying the model to model-based heartbeat detection methods should make them more precise, as physiological variation can be better distinguished from other factors.

Section 2 describes the new latent variable model and in section 3 an evaluation of the model is presented. Section 4 describes the material of the study, results are presented in section 5 and concluding remarks are made in section 6.

2. Latent variable modelling of heartbeats

2.1. Latent variable modelling

Latent variable modelling (e.g. Bishop, 1999) is a technique where observed *data variables* are supplemented with unobserved *latent variables* that describe the underlying structure of the observed data. A data variable vector $\mathbf{a}$ is therefore considered to have been "generated" by a *latent variable model* f that is driven by the latent variable vector $\mathbf{b}$:

$$\mathbf{a} = f(\mathbf{b}) + \epsilon \tag{1}$$

$$\mathbf{a} = [a_1, a_2, \ldots, a_N]^T \qquad \mathbf{b} = [b_1, b_2, \ldots, b_M]^T \tag{2}$$

Generally, the model cannot, given the latent variables, describe the data variables exactly, so a noise term ϵ, which describes the error, is included.

There are usually fewer latent variables than data variables ($M < N$ in (2)), so latent variable modelling reduces the dimensionality of the observed data and thus provides a more compact representation. A physiological example of such model is the relationship between arterial blood pressure and the pulse transit time (PTT) to limbs (e.g. Lane et al., 1983). The model $f(p)$ describes the relationship as

$$\mathbf{t} = f(p) + \epsilon \tag{3}$$

$$f(p) = [f_h(p), f_h(p), f_f(p), f_f(p)]^T \tag{4}$$

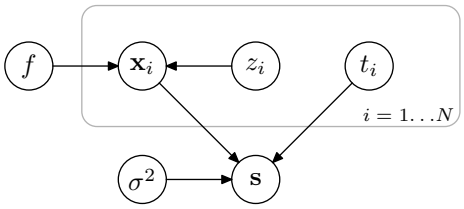

Figure 2. A graphical representation of equation (5). The values of the signal $\mathbf{s}$ are generated based on the shape $\mathbf{x}_i$ and location t_i of each of the N heartbeat waveforms, and noise with variance σ^2. The heartbeat shape $\mathbf{x}_i$ is generated with the model f based on the respiratory latent variable z_i.

where the vector $\mathbf{t} = [t_1, t_2, t_3, t_4]^T$ denotes the PTT to the four limbs and functions $f_h(p)$ and $f_f(p)$ determine the pulse transit times to hands and feet, respectively, given blood pressure p (the PTT to the right and left limb are assumed to be equal). An optimal form of $f(p)$ can be learnt from simultaneous measurements of PTT and blood pressure. The noise term ϵ contains the combined effect of all the other factors than blood pressure affecting the PTT.

With respiratory latent variable modelling of a heartbeat sequence, a signal $\mathbf{s}$ that contains heartbeats is considered to have been generated based on the latent variables that define the respiration phase z_i and onset time t_i of each heartbeat $\mathbf{x}_i$. Let $\mathbf{s}$ be a signal vector containing N heartbeat waveforms whose onsets are at $t_1, t_2, \ldots, t_N$, the length of each heartbeat vector $\mathbf{x}_i$ be D and the shape of each heartbeat be defined by function f. The function is a latent variable model of the shape of the heartbeat as it defines the shape of $\mathbf{x}_i$ based on a latent variable z_i. The values of the vector $\mathbf{s}$ are thus defined as

$$s_j = \left(\sum_{i=1}^{N} \mathbf{x}_i[j - t_i] \right) + \epsilon \tag{5}$$

where ϵ is a noise term corresponding to modelling error, $\mathbf{x}_i[j]$ denotes the jth item of vector $\mathbf{x}_i$ and $\mathbf{x}_i = f(z_i)$. The variance of noise is defined by parameter σ^2. A graphical description of the model is given in figure 2.

In practice, the model f has a known parametric form (such as the one proposed in this paper), so the heartbeat detection task consists of finding the parameters of the function f as well as the location t_i and latent variable z_i of each heartbeat so that ϵ in (5) is minimised. Minimising ϵ corresponds to finding the actual heartbeat locations, because if a set of heartbeat locations $t_1, t_2, \ldots, t_N$ results in a low modelling error, it is likely that the modelled heartbeats correspond to actual heartbeat events.

2.2. A new heartbeat model

A linear latent variable model, referred to as the *respiratory model*, is presented. The model describes the shape $\mathbf{x}_i$ of a heartbeat as a weighted sum of a mean heartbeat vector $\boldsymbol{\mu}$ and a respiratory component vector $\mathbf{w}$, both of which consist of D items:

$$\boldsymbol{\mu} = [\mu_1, \mu_2, \ldots, \mu_D]^T \qquad \mathbf{w} = [w_1, w_2, \ldots, w_D]^T \tag{6}$$

Vector $\mathbf{w}$ represents the direction of the respiratory variation and is weighted by a respiration phase variable z_i, which describes the magnitude of the respiratory effect

and normally follows the phase of respiration (Starr and Friedland, 1946). The formal description of the model is

$$\mathbf{x}_i = \mathbf{w}z_i + \boldsymbol{\mu} + \epsilon \tag{7}$$

where ϵ is a noise term. The intrinsic dimensionality of the model is 1, since the variation is due to the one-dimensional latent variable z_i.

Equation (7) does define a function of the latent variable z_i (the parameters of the function are $\mathbf{w}$ and $\boldsymbol{\mu}$), but the function notation $\mathbf{x}_i = f(z_i|\mathbf{w}, \boldsymbol{\mu}) + \epsilon$ is not used to keep presentation clearer.

3. Model evaluation

3.1. Compared models

The respiratory model is evaluated by comparing it to the *amplitude model*, which is another latent variable model for modelling the effect of respiration.

The amplitude model corresponds to the view that the amplitude of the heartbeat shape modulates by respiration, and its formal definition is

$$\mathbf{x}_i = (z_i + 1)\boldsymbol{\mu} + \epsilon \tag{8}$$

where the heartbeat shape $\mathbf{x}_i$ is the sum of the mean heartbeat vector $\boldsymbol{\mu}$ scaled by a factor of $z_i + 1$, and noise ϵ. The amplitude model is less complex than the respiratory model, as the shape of a heartbeat is determined by one vector $\boldsymbol{\mu}$ instead of two in the respiratory model ($\boldsymbol{\mu}$ and $\mathbf{w}$). The model can be described in terms of (7) by setting $\mathbf{w} = \boldsymbol{\mu}$, which makes comparing them easier.

3.2. Determining model parameters

The signal vector $\mathbf{s}$ and heartbeat vectors $\mathbf{x}_1, \mathbf{x}_2, \ldots, \mathbf{x}_N$ can be observed from a recorded BCG signal, by manually locating the heartbeats. The two models can then be compared by calculating which model gets a smaller value for modelling error variance σ^2, given the observed variables. The error variance is calculated as mean-square value of ϵ, which, for a set of N heartbeats, is given by

$$\sigma^2 = \frac{1}{N}\sum_{i=1}^{N} \|\mathbf{x}_i - (\mathbf{w}z_i + \boldsymbol{\mu})\|^2 \tag{9}$$

To calculate the variance, values for $\boldsymbol{\mu}$, $z_1, z_2, \ldots, z_N$ and $\mathbf{w}$ that result in a minimal σ^2 need to be determined. Vector $\mathbf{w}$ needs to be optimised, but the rest of the parameters have simple closed-form solutions.

The solution for $\boldsymbol{\mu}$ is, by definition, the mean of the N heartbeat vectors:

$$\boldsymbol{\mu} = \frac{1}{N}\sum_{i=1}^{N} \mathbf{x}_i \tag{10}$$

The mean heartbeat vector is also used as the respiratory component vector in the case of the amplitude model, as $\mathbf{w} = \boldsymbol{\mu}$ comes from the definition of the model.

For the respiratory model, $\mathbf{w}$ is determined based on a minimum-error formulation of *principal component analysis* (Pearson, 1901; Bishop, 2006, p. 563), which minimises σ^2. The formulation is based on the observation that σ^2 in (9) consists

of the variation in the heartbeat vectors that is orthogonal to $\mathbf{w}$. As a complete orthonormal base consists of D vectors $\mathbf{u}_1, \mathbf{u}_2, \ldots, \mathbf{u}_D$, vector $\mathbf{w}$ can be defined to be the first of them, in which case vectors $\mathbf{u}_2, \mathbf{u}_3, \ldots, \mathbf{u}_D$ are, by definition, orthogonal to $\mathbf{w}$. Thus, the modelling error $\mathbf{x}_i - (\mathbf{w}z_i + \boldsymbol{\mu})$ of each heartbeat in (9) can be represented as a weighted sum

$$\mathbf{x}_i - (\mathbf{w}z_i + \boldsymbol{\mu}) = \sum_{j=2}^{D} [(\mathbf{x}_i - \boldsymbol{\mu})^{\mathrm{T}} \mathbf{u}_j] \mathbf{u}_j \tag{11}$$

of the vectors $\mathbf{u}_2, \mathbf{u}_3, \ldots, \mathbf{u}_D$ where $(\mathbf{x}_i - \boldsymbol{\mu})^{\mathrm{T}} \mathbf{u}_j$ is the magnitude of the variation of $\mathbf{x}_i$ in the direction of $\mathbf{u}_j$. Substituting (11) to (9) , the variance can be formulated as

$$\sigma^2 = \frac{1}{N} \sum_{i=1}^{N} \sum_{j=2}^{D} [(\mathbf{x}_i - \boldsymbol{\mu})^{\mathrm{T}} \mathbf{u}_j]^2 = \sum_{j=2}^{D} \mathbf{u}_j^{\mathrm{T}} \mathbf{S} \mathbf{u}_j \tag{12}$$

where $\mathbf{S}$ is the data covariance matrix of the heartbeat vectors:

$$\mathbf{S} = \frac{1}{N} \sum_{i=1}^{N} (\mathbf{x}_i - \boldsymbol{\mu})(\mathbf{x}_i - \boldsymbol{\mu})^{\mathrm{T}} \tag{13}$$

Equation (12) is then minimised with respect to $\mathbf{u}_2, \mathbf{u}_3, \ldots, \mathbf{u}_D$ so that the orthonormality constraints $\mathbf{u}_j^{\mathrm{T}} \mathbf{u}_j = 1$, $j = 2 \ldots D$ are enforced with Lagrange multipliers. The resulting Lagrangian function

$$J = \sum_{j=2}^{D} [\mathbf{u}_j^{\mathrm{T}} \mathbf{S} \mathbf{u}_j + \lambda_j (1 - \mathbf{u}_j^{\mathrm{T}} \mathbf{u}_j)] \tag{14}$$

has stationary points given by the eigenvalue equation

$$\mathbf{S}\mathbf{u}_i = \lambda_i \mathbf{u}_i, \quad i = 1 \ldots D \tag{15}$$

and the minimum value for σ^2 is found at one of those points. Variance σ^2 corresponding to each stationary point is equal to the sum of the eigenvalues $2 \ldots D$ of the eigenvalue equation,

$$\sigma^2 = \sum_{j=2}^{D} \lambda_i \tag{16}$$

which means that the minimum value for (16) is attained if λ_1 is chosen to be the largest eigenvalue. Thus, the optimal $\mathbf{w}$ is the eigenvector corresponding to the largest eigenvalue of the covariance matrix $\mathbf{S}$:

$$\mathbf{w} = \mathbf{u}_1 \tag{17}$$

Finally, $\mathbf{w}$ is scaled to have identical variance with $\boldsymbol{\mu}$ so that it has the same magnitude as the $\mathbf{w}$ of the amplitude model.

After $\mathbf{w}$ has been determined, each z_i is calculated. In (7) the error ϵ is, by definition, orthogonal to $\mathbf{w}z_i$. Thus, in the subspace spanned by $\mathbf{w}$, $\mathbf{w}z_i$ is the nearest point to $\mathbf{x}_i - \boldsymbol{\mu}$, which results in z_i being the projection of $\mathbf{x}_i - \boldsymbol{\mu}$ onto the subspace:

$$z_i = \frac{(\mathbf{x}_i - \boldsymbol{\mu})^{\mathrm{T}} \mathbf{w}}{\|\mathbf{w}\|^2} \tag{18}$$

The value of each z_i should generally reflect the actual phase of respiration at time instant t_i. However, one notices that respiration phases can be derived from

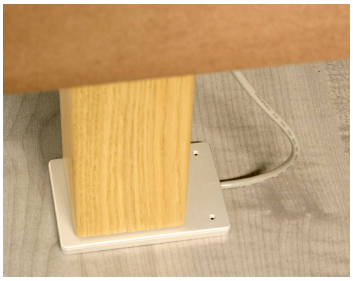

Figure 3. The bedpost sensor used in the measurements.

any heartbeat sequence even if the subject is holding breath. In those cases the value of z_i does not correspond to the phase of respiration but to the phase of the most systematic variation of the heartbeat waveform.

3.3. Bayesian information criterion

Evaluating the two models based on σ^2 alone has the drawback of favouring the more complex model. It is obvious that the respiratory model gets a smaller modelling error, because it is more complex and can thus model the variation in the test set $\mathbf{x}_1, \mathbf{x}_2, \ldots, \mathbf{x}_N$ more flexibly. It is therefore important to evaluate whether the modelling accuracy increases enough to justify a more complex model.

Bayesian information criterion (BIC) is a measure that takes model complexity into account and can be used in evaluating whether the increased complexity of the respiratory model, compared to the amplitude model, is justified.

The definition of the score for model $\mathcal{M}_i$ with parameters θ_i is

$$BIC_i = -2 \cdot \ln(L_i) + k_i \ln(N) \tag{19}$$

where L_i is the likelihood of data given the parameters, k_i is the dimensionality of θ_i and N denotes how many data points $\mathcal{D}$ contains (Schwarz, 1978; Kass and Raftery, 1995). BIC is formulated so that it asymptotically ($N \to \infty$) approaches model evidence $p(\mathcal{M}_i|\mathcal{D})$ scaled by -2. Thus, the model with the smallest BIC value is the

Table 1. The test cases with their evaluation. N is the number of heartbeats, BIC is a *Bayesian information criterion* score and σ is the standard deviation of ϵ. Subscript $_1$ corresponds to the respiratory model and $_2$ to the amplitude model, respectively.

Case	Test subject, description	Length (min.)	N	σ_1	σ_2	BIC_1	BIC_2
1	Subject 1, lateral	4.1	256	0.049	0.058	-144351.6	-129105.1
2	Subject 1, prone	4.8	296	0.059	0.063	-146205.0	-140251.5
3	Subject 1, supine	5.0	309	0.065	0.082	-141747.6	-117113.7
4	Subject 2, chair	2.4	177	0.068	0.081	-78119.3	-67771.6
5	Subject 3, lateral	5.4	347	0.088	0.105	-121860.8	-101094.6
6	Subject 3, prone	4.6	301	0.099	0.106	-92901.1	-86261.7
7	Subject 3, supine	5.5	353	0.080	0.101	-137155.2	-108248.8

most appropriate. The normal definition of model evidence, which is

$$p(\mathcal{M}_i|\mathcal{D}) = \frac{p(\mathcal{D}|\mathcal{M}_i)p(\mathcal{M}_i)}{p(\mathcal{D})} \tag{20}$$

cannot be used, because it involves calculating data likelihood as the integral

$$p(\mathcal{D}|\mathcal{M}_i) = \int p(\mathcal{D}|\mathcal{M}_i, \theta_i)p(\theta_i|\mathcal{M}_i)d\theta_i \tag{21}$$

where $\theta_i = \{\boldsymbol{\mu}, \mathbf{w}, z_1, z_2, \ldots, z_N, \sigma^2\}$. Integration is not possible, because it is difficult to define a justified prior distribution $p(\theta_i)$ for the parameters‡.

In order to calculate the likelihood L of each model, the two models are formulated as generative functions. The noise ϵ is assumed to be independent and normally distributed, so the likelihood of a heartbeat is given by

$$p(\mathbf{x}_i|z_i, \boldsymbol{\mu}, \mathbf{w}, \sigma^2) = \text{Normal}\left(\mathbf{x}_i|\mathbf{w}z_i + \boldsymbol{\mu}, \mathbf{C}\right) \tag{22}$$

where $\mathbf{C}$ is a $D \times D$ diagonal covariance matrix whose every value on the diagonal is σ^2. The variance is specific to the experimental setup and is affected by factors such as measurement noise and the regularity of cardiac function. Individual heartbeats are assumed to be independent, which results in the following likelihood for the heartbeat sequence:

$$L = \prod_{i=1}^{N} p(\mathbf{x}_i|z_i, \boldsymbol{\mu}, \mathbf{w}, \sigma^2) \tag{23}$$

$$= \prod_{i=1}^{N}\prod_{j=1}^{D} \left(\sigma\sqrt{2\pi}\right)^{-1} \exp\left(-\frac{(\mathbf{x}_i[j] - w_j z_i - \mu_j)^2}{2\sigma^2}\right) \tag{24}$$

The independence assumptions of heartbeats and the items of a heartbeat vector are not realistic, especially since consecutive vector items have a high correlation. However, for the purpose of comparing the two models, the assumptions are fine, as both models are treated the same way.

A BIC score BIC_i is then calculated based on the optimised parameter values and k, which expresses how many parameters the model has. For the respiratory model, $k = D + D + N + 1$ (from $\boldsymbol{\mu}$, $\mathbf{w}$, $z_1, z_2, \ldots, z_N$ and σ^2) and for the amplitude model, $k = D + N + 1$ (from $\boldsymbol{\mu}$, $z_1, z_2, \ldots, z_N$ and σ^2).

4. Material

4.1. Recordings

Single-channel ballistocardiograms were acquired in seven test cases from three healthy test subjects (table 1). The demographic data of the subjects are

- Subject 1: 25 year-old, male, height 175 cm, weight 70 kg
- Subject 2: 29, male, 185 cm, 80 kg
- Subject 3: 75, female, 160 cm, 53 kg.

‡ A somewhat reasonable prior distribution for z could be defined as follows. As respiration is a sinusoidal phenomenon, the theoretical likelihood of respiration phase is $p(r) \propto \arcsin'(r) = (1 - r^2)^{-1/2}$. If the respiration phase parameter is considered to also consist of Gaussian noise with variance σ^2, the likelihood of the respiration phase becomes $p(z) \propto \int \mathcal{N}(t|0, \sigma^2)(1 - (z + t)^2)^{-1/2}\mathrm{d}t$.

The ethicality of the data acquisition was ensured with the following principles

- Participation to the study was voluntary
- Test subjects gave their written informed consent
- Data acquisition did not cause any discomfort or risks
- Acquired data is stored in an anonymised form.

The BCG signals were measured in laboratory conditions with a piezo-electric bedpost vibration sensor (figure 3) and with a special ballistocardiography chair. A 300 Hz sampling rate was used. The bedpost sensor was installed to an Unikulma UnikMatic bed, which has a wooden frame, flexible wooden ribs and a 5 cm thick mattress supported by the ribs (Unikulma Ltd, Vantaa, Finland). A relatively thin mattress was used so that the signal quality would be maximal. The chair, which has been developed at Helsinki University of Technology, has a solid polystyrene foam construction, which reduces measurement resonances (Leppäkorpi and Koskinen, n.d.).

4.2. Extracting heartbeat vectors

The length of the heartbeat waveform was chosen to be 0.6 seconds ($D = 180$), which prevents the overlap of the previous and next heartbeat on a heartbeat vector $\mathbf{x}$. Truncation of the heartbeat vectors could be avoided if the signal (which consists of overlapping heartbeats) was decomposed into separate, non-overlapping, heartbeat waveforms using the method proposed by Inan, Etemadi, Wiard, Kovacs and Giovangrandi (2009). However, the aim of this paper is to show that the respiratory model is superior to the amplitude model, and for that the decomposition is not necessary.

The heartbeats in the signals were located manually in such a way that the first major negative deflection was positioned at 0.2 seconds in the heartbeat window. The test subjects made so few movements that only 3% of the respiration cycles contained a heartbeat that had to be discarded due to a movement artifact. The heartbeat locations were then fine-tuned with the following method. First, a heartbeat waveform ensemble average was calculated based on the manually detected heartbeat positions. Then, each heartbeat position was adjusted a few milliseconds backward or forward so that it would have a maximal correlation with the ensemble average. After the heartbeat positions had been determined, each signal was scaled so that the average heartbeat vector variance was unity in the signal.

5. Results

The material of this study is visualised in figures 4 and 5. In figure 4, the heartbeats of each case are plotted into the same frame so that the variation in the heartbeat shape is pronounced. Also the vectors $\mathbf{w}$ and $\boldsymbol{\mu}$ as well as the error terms ϵ for the respiratory and amplitude models are shown for each case.

Figure 5 shows the correspondence between the values z_i and a respiration reference signal. The reference signal is the low-frequency component of the measured BCG-signal, which is known to vary with the phase of respiration (Starr and Noordergraaf, 1967). The reference does not accurately quantify airflow to lungs, but does describe the approximate timing of respiration cycles. Cases 1 and 7 are

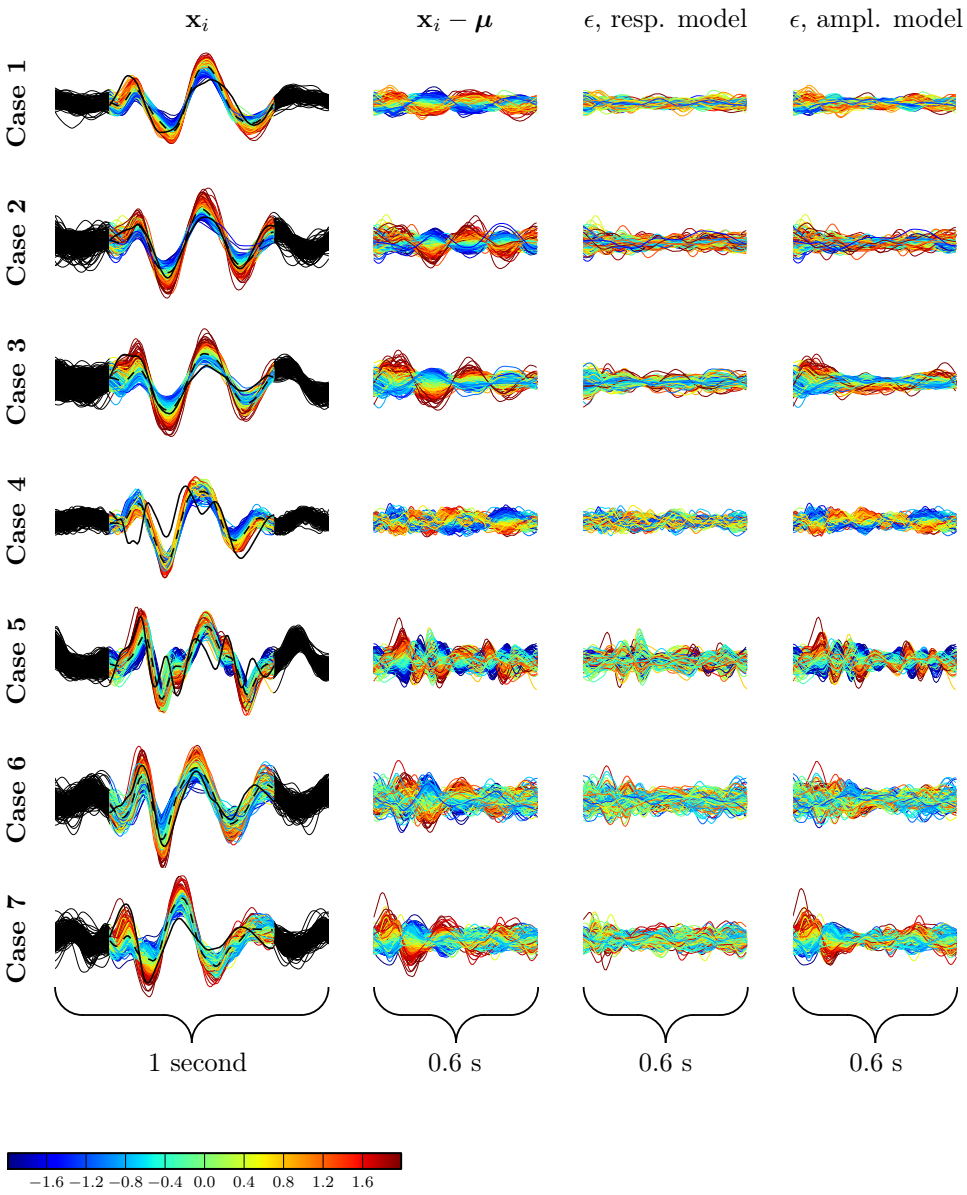

Figure 4. Heartbeat waveforms $(\mathbf{x}_1, \mathbf{x}_2, \ldots, \mathbf{x}_N)$ for each case are plotted in the first column, with the context before and after each $\mathbf{x}_i$ shown in black. The mean heartbeat $\boldsymbol{\mu}$ (- - -) and respiratory component $\mathbf{w}$ (——) are shown as black lines. The second column contains the heartbeat waveforms minus the mean heartbeat $(\mathbf{x}_1 - \boldsymbol{\mu}, \mathbf{x}_2 - \boldsymbol{\mu}, \ldots, \mathbf{x}_N - \boldsymbol{\mu})$. The error terms ϵ of the respiratory model and amplitude model are in the third and fourth columns, respectively. The colour (or shade) of each line shows the value of the respiratory latent variable z_i of the line, which can be looked up from the colorbar. The vertical dimension is in arbitrary units and is identical for all the plots in the figure. The horizontal dimension is time. The respiratory model explains the heartbeat shape variation $\mathbf{x}_i - \boldsymbol{\mu}$ better, because the error term ϵ of the respiratory model has less structure than that of the amplitude model.

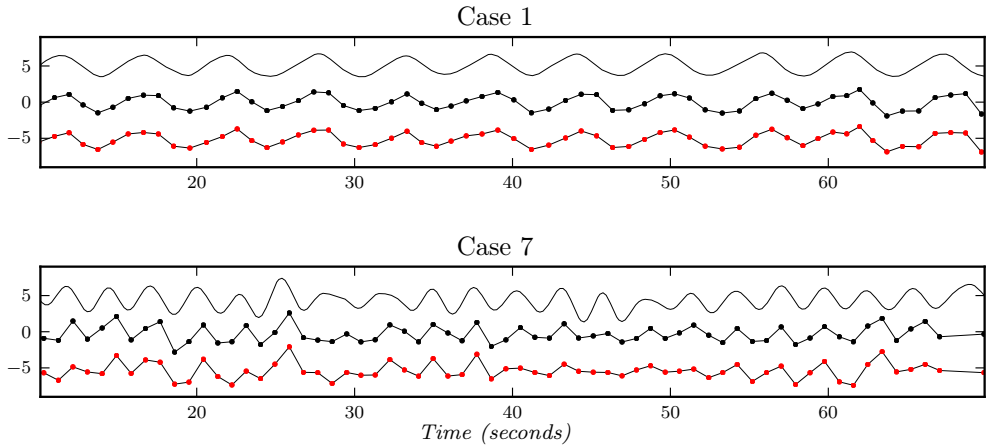

Figure 5. The correspondence between a respiration reference signal and the respiratory latent variables z_i of the respiratory model and amplitude model is shown for cases 1 and 7. The top curve is a respiration reference signal and the middle as well as bottom curves correspond to the z_i values of the respiratory and amplitude models, respectively. Top and bottom curves are offset by ± 5 y-units.

shown in the figure, because they are exemplars of a high and low correlation between the reference and the respiratory latent variables. That the variables would accurately track the respiration phase is not relevant, because the improvement of the model is in making heartbeat detection more accurate, not respiration rate detection.

The quantitative evaluation of the respiratory model is summarised in table 1. The evaluation is based on comparing the error terms and *Bayesian information criterion* (BIC) values of the respiratory and amplitude models. The error term tells how well a model fits the data, without taking into account the complexity of the model. Increasing the complexity results in a smaller error term, but is not always desirable, as the model eventually becomes more complex than the underlying process of the data (over-fitting). BIC values, on the other hand, include a penalty term for model complexity (k_i in (19)), so the model with the best BIC value can be considered the most suitable. The quantitative analysis shows that the respiratory model is more suitable for describing the respiratory variation of heartbeats as the error terms and BIC values are smaller in all cases.

6. Discussion and conclusions

A heartbeat model, which takes respiratory variation into account with a respiratory component vector $\mathbf{w}$ scaled with a latent variable z_i, was presented. The model was compared to a model representing the current view of the respiratory variation of heartbeats, the *amplitude model*. The comparison shows that the new model is more adequate in describing the variation in all seven tested cases.

The evaluation of the model is based on BCG signals acquired in only two different measurement setups from only three different test subjects. Moreover, the evaluation set does not contain signals with a high heart rate or arrhythmias. However, the goal of this paper is to show that a more complex model than the current amplitude model

is required when mechanically measured heartbeats are modelled. For that purpose, a relatively small evaluation set with ordinary signals is sufficient, because it is unlikely that the simpler amplitude model would perform better in more complex situations. Modelling signals with arrhythmias or a high heart rate should be done in such a way that the overlap of heartbeats is handled properly, such as using the method proposed by Inan, Etemadi, Wiard, Kovacs and Giovangrandi (2009).

As the presented model has a linear structure, it is fair to ask if a linear model provides just the right amount of complexity for describing respiratory variation. However, as the error terms of the proposed model seem to have no clear structure (figure 4), a more complex model that would also cover variation of the error terms does not seem realistic. Nevertheless, more complex models could be explored in situations where the effect of respiration is not moderate, but drastically changes the shape (Tavakolian et al., 2008).

The presented model can be applied, for example, to the heartbeat detection method proposed by Jansen et al. (1991), which is based on calculating the correlation between a heartbeat template $\boldsymbol{\mu}$ and consecutive signal segments $\mathbf{x}_i$. The application of the model involves performing the transformation

$$\mathbf{x}_i \longleftarrow \mathbf{x}_i - \frac{(\mathbf{x}_i - \boldsymbol{\mu})^{\mathrm{T}}\mathbf{w}}{\|\mathbf{w}\|^2}\mathbf{w} \tag{25}$$

before calculating the correlation, which corresponds to removing the effect of respiration. The transformation is based on $\mathbf{w}$, which needs to be determined. One way would be to first set $\mathbf{w} = \boldsymbol{\mu}$ and after, say, a hundred heartbeats have been detected, update $\mathbf{w}$ with (17). More precise estimates of $\mathbf{w}$ can be calculated as more and more heartbeats are accumulated.

The proposed model has practical utility as it can improve the precision of heartbeat detection methods. It is, however, not a complete model as it tells that the heartbeat shape does vary by respiration, but not *how* it varies. A more complete model would define a prior distribution $p(\boldsymbol{\mu}, \mathbf{w}, z_1, z_2, \ldots, z_N, t_1, t_2, \ldots, t_N)$ for the model parameters and would thus describe what kind of heartbeat shapes and their variations are physiologically possible. For example, the prior $p(t_1, t_2, \ldots, t_N)$ could be defined based on the heartbeat interval model proposed by Barbieri and Brown (2006).

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