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Computerized Interpretation of Cardiovascular Physiological Signals[1]

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1. Introduction

The conventional mode of health delivery can be profiled as follows: a patient, if he does not feel good, will visit his physician and report his symptoms (e.g., headache, bellyache, and nausea, etc); the physician strives to make a few empirical hypotheses based on the patient's complaints and medical history; in general, the physician has to further examine the patient's vital signs (e.g., body temperature, blood pressure, and pulse, etc.) so as to confirm or reject his initial hypotheses; if the physician is confident enough on his hypotheses, the final diagnosis decision can be made and the according treatments are hereby delivered; if not, the physician will resort to various medical instruments (e.g., electrocardiography, ultrasonography, and computed tomography, etc) and laboratory tests (e.g., blood test, urinalysis, and immunological analysis, etc); during this procedure, the initial hypotheses may be updated at any time; to those complicated diseases, the physicians will propose a few tentative treatments and modify them in accordance with clinical observations.

It is noteworthy that above procedure is triggered and driven by patients' symptoms. But most symptoms are subjective, and are late manifestations of a disease or a group of diseases. In other words, they often incur expensive and painful clinical treatments. Furthermore, once the patients perceive malign symptoms, they may have missed the best opportunity of medical treatments. Take cardiovascular diseases (CVDs) for an example. Nowadays it is possible to treat or relieve nearly all CVDs by medical interventions, such as controlling blood pressure and blood cholesterol. In the case of refractory or congenital CVDs, various sophisticated clinical instruments and operations, including pacemakers, prosthetic valves, coronary artery bypass and even whole heart transplantation, have been developed and practiced too. As a consequence, the World Health Organization (WHO) reports "… at least 80% of premature deaths from heart disease and stroke could be avoided

[1] Adapted from LI Bing Nan (2009) Wavelet Neural Networks: The Fusion of HC and SC for Computerized Physiological Signal Interpretation, PhD Dissertation, University of Macau, Taipa, Macau

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through effective reduction of risk factors." Unfortunately, it is still reported over 861,826 American deaths due to CVDs (35.2% of all deaths) in 2005 (Rosamond et al., 2008), and over 4.35 million European deaths (49% of all deaths) each year (Petersen et al., 2005). Such paradoxical results may be attributed to that various cardiovascular risks, such as arteriosclerosis and other peripheral arterial diseases, are asymptomatic whereas they have been able to cause a deadly stroke or heart attack (Cohn et al., 2003).

For better healthcare, the individuals are hereby being expected to assume more responsibility for their own health, for example, having their blood pressure checked regularly (WHO, 1998). It is now one of the hottest topics in science and engineering to make such self-examination easier. For instance, IBM has declared their understandings on the future healthcare: "…the ability to securely capture sensitive medical data has the potential to allow healthcare to move from the traditional doctor's office to wherever the patient happens to be… in the future, technology will enable: millions of people with chronic diseases will be able to have their conditions monitored as they go about their daily life through sensors at home… a pill dispenser will help patients track their drug regimen and automatically transmit such data to caregivers… virtual doctors can check blood pressure, pulse and others remotely, and follow up if necessary…" (http://www-07.ibm.com/innovation/in/ideas/five_in_five/). As a matter of fact, there have been a few cost-effective instrumentations recommended and practiced for self-serviced healthcare at home (Korhonen et al., 2003), (Scalvini et al., 2005). In contrast to those subjective symptoms, the measured vital signs or physiological signals are generally more sensitive to various pathophysiological alterations. Then home subjects can take care of their own health condition better. However, till now their prevalence is not as optimistic as expected yet. The reason is multifold. We argue that the competence of computerized interpretation of cardiovascular physiological signals, such as electrocardiograms (ECG) and arterial blood pressure (ABP) waveforms from self-serviced cardiovascular health monitoring, should be paid special attention.

1.1 Cardiovascular system and diseases

Various nutrients and oxygen necessary for life maintenance are transported by the blood circulation in cardiovascular system (CVS). Meanwhile, circulatory system is responsible to discharge various metabolic wastes away. Hosting blood circulation, CVS is thus of vital importance for body health. In a broad sense, CVS is comprised of the subsystems for a complete blood circulation, namely pulmonary circulation, cardiac circulation and systemic circulation (Fig. 1). The subsystems in red, originated from the pulmonary capillaries, to left heart, arterial system and systemic capillaries, are responsible to transporting the oxygenic blood to various body organs and tissues. In contrast, those subsystems in blue, including systemic capillaries, venous system, right heart and pulmonary arteries, are in charge of collecting deoxygenated blood back to pulmonary circulation. The capillary circulations connect the venous circulation and the arterial one. But the heart is at the center of circulatory system. It coordinates and drives the overall procedure of blood circulation.

The heart, the lung, the vasculature and the blood are vital components for cardiovascular circulation. Any adverse alteration in them will evoke a series of deadly threatens to body health. Therefore it is not surprising that CVDs have been one of leading causes of death for years. In general, CVDs may result in arrhythmia. It disturbs the essential procedure of

blood perfusion and nourishment. But the cardiovascular deterioration often commences with arteriosclerosis, a procedure of plaque deposit so that the vasculature turns to stiffened. The stiffened vasculature increases cardiac workload as well as blood pressure. High blood pressure not only impairs myocardium but also further exacerbates arteriosclerosis to stenosis. The late implications are often thrombosis and embolism, which may cause cerebral ischemia (stroke) or cardiac ischemia (heart attack). In a word, it is important to have cardiovascular rhythm and vascular elasticity checked frequently.

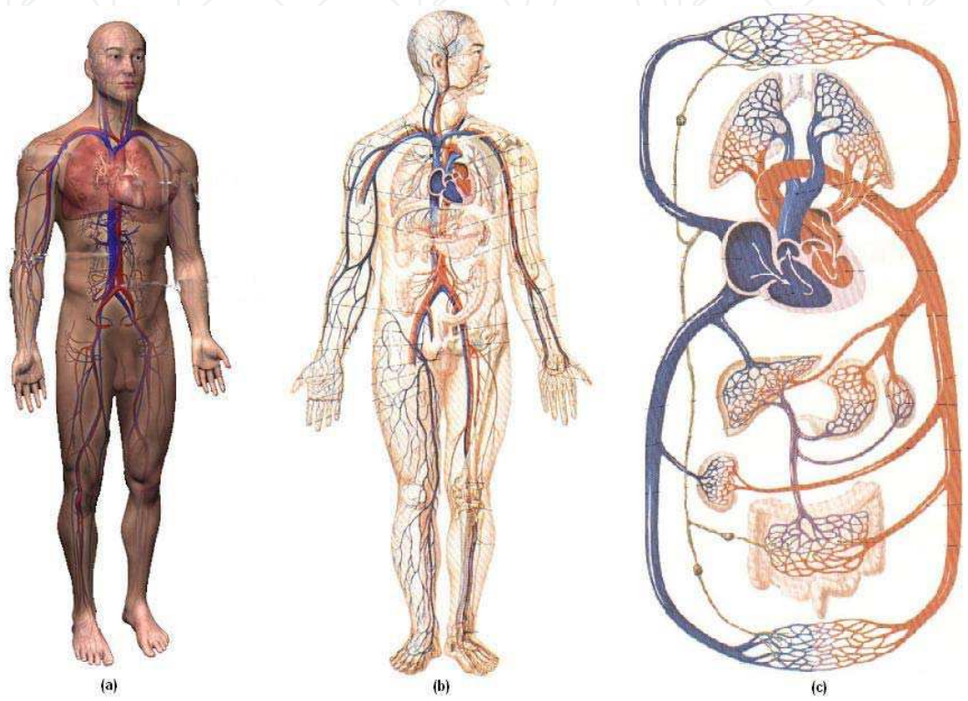

Fig. 1. The circulatory system
(a) Adapted from www.3dscience.com 2009; (b) and (c) Adapted from www.bbioo.com 2009

1.2 Non-invasive cardiovascular health monitoring

In respect to the importance of CVS on body health, the relevant investigations never cease in the past centuries; various methodological and technological breakthroughs keep advancing the development of cardiovascular health monitoring and treatments in clinical medicine (WHO and CDC 2004). Modern healthcare technologies make clinical physicians able to inspect CVS condition in depth. However, with respect to their complexity or costs, most of them are not suitable for routine cardiovascular health monitoring at home. Up to now, merely a few cost-effective technologies, such as electrocardiography and sphygmography, have been extensively investigated and practiced for that purpose (Welkowitz 1981).

1.2.1 Electrocardiography

Electrocardiography strives to manifest the cardiac electrical conduct system, which supervises the myocardial behaviours of systole and diastole. A normal cardiac rhythm commences with the electrical impulse by sinoatrial node (Fig. 2). It propagates to right and

left atria and makes their myocardium contract. Then, the stimulus travels to atrioventricular node. After a delay, it conducts throughout ventricular myocardium in the line of HIS bundle, Left and Right Bundle Branches, and a dense network of Purkinje Fibers (Klabunde 2004). Following that electrical stimulus, four cardiac chambers contract and pump blood step by step. In other words, for efficient blood circulation, the electrical conduct system is of vital importance as it controls and coordinates the overall procedure of myocardial systole and diastole.

In essence, electrocardiography takes advantage of human body's homogeneous conduction, which projects the variation of myocardial potentials over time to body surface. To measure myocardial behaviours from different perspectives, electrocardiography has been evolved to 12-lead ECGs (Fig. 3). Among them, one to three of bipolar leads (i.e., Lead I, II, and III) or unipolar leads (i.e., Lead *a*VR, *a*VL, and *a*VF) are friendly for user manipulation, and hereby receive more attention for home health monitoring.

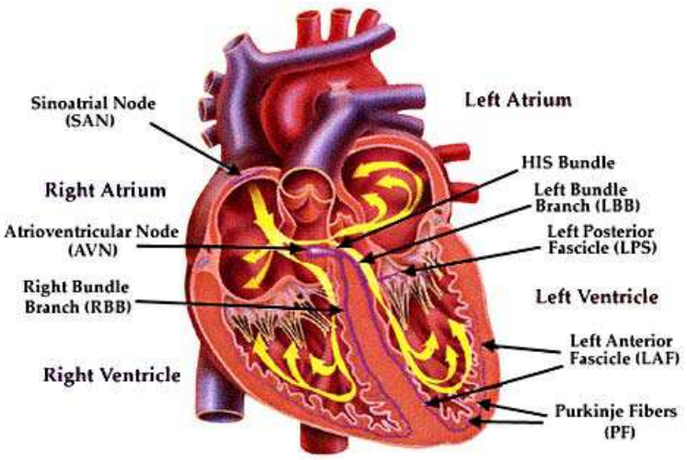

Fig. 2. Cardiac electrical conduction system (courtesy of Marquette Electronics 1996)

Electrocardiography is widely recommended in clinical medicine for the analysis of cardiac arrhythmia, conduction abnormality, electrolyte disturbances, and so on (Bacquer et al., 1998). But it is noteworthy that ECG is not able to reflect myocardial contractility directly, whereas they may give a rough indication of increased or decreased contractility. In contrast, arterial blood pressure and its waveforms have been long recommended as the quantitative indicators of myocardial contractility and the workloads (Rego and Souza 2002).

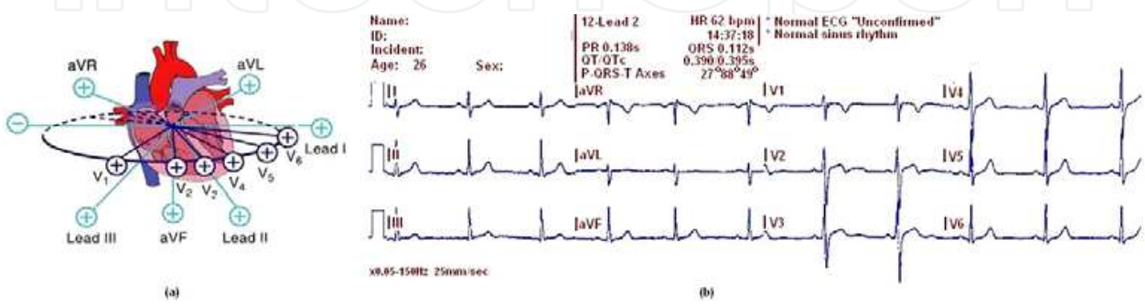

Fig. 3. 12-lead ECG monitoring (adapted from www.wikipedia.com 2009)
(a) Illustrative lead placement; (b) Exemplified ECG recordings

1.2.2 Sphygmography

The assessment of arterial blood pressure is an integral part of cardiovascular examination in clinical medicine. Various sphygmomanometers have been well developed for blood pressure measurement. But they merely report a few rough estimates of arterial blood pressure, including systolic pressure, diastolic pressure and mean pressure. They are obviously not enough to characterize the complicated procedure of blood circulation. Hence, other than blood pressure values, those experienced physicians are apt to master the variations of arterial blood pressure. In general, they palpate the variations by their fingers at accessible arteries and evaluate cardiovascular circulation comprehensively (Fig. 4a). Nowadays there have been many technologies developed for measuring sphygmograms, namely, recording the dynamical ABP waveforms precisely. It is definitely beneficial to the reproducible interpretation. As a matter of fact, the routine practice of non-invasive cardiovascular health monitoring prefers the techniques of applanation tonometry (Fig. 4b).

Fig. 4. Non-invasive monitoring of ABP waveforms (adapted from www.wikimedia.org 2009)

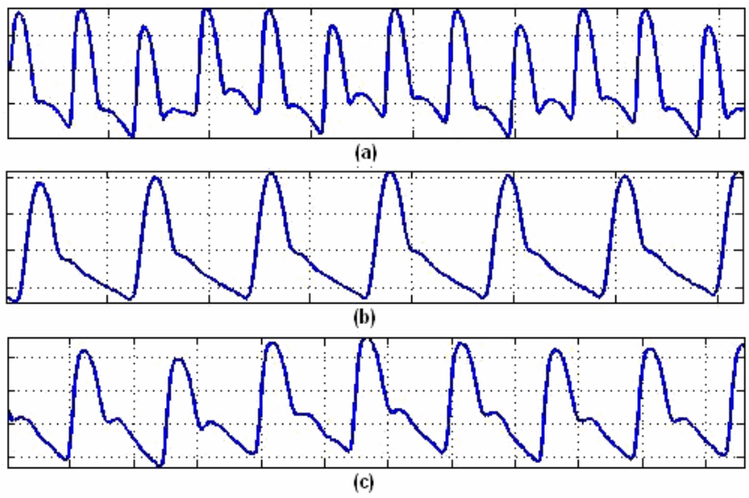

Fig. 5. Illustrative ABP waveforms
(a): Catheterization [MIMIC/03701: 0-5.8s];
(b): Photoplethysmography [FANTASIA/f2o01: 0-5.8s];
(c): Applanation tonometry [GXABP/05607080306: 0-5.8s]

In non-invasive applanation tonometry, a high-fidelity tonometer is placed on the accessible arteries with gentle pressure so as to occlude blood flow partially. It is hereby possible to capture the variation of arterial blood pressure through that site and convert it into other types of electrical signals (Fig. 5). It has been claimed by previous investigators that such non-invasive ABP waveforms are reliable and comparative to those obtained invasively by intra-arterial measurement (Sato et al., 1993).

2. Computerized physiological signal interpretation

Year	Regularization	Delineation	Quality Evaluation	Modeling	Recognition and Classification
1960	Spectral analyis				Spectral analysis
1961			Heuristic decision		Heuristic decision
1962	Linear regression	Derivative analysis			Adaptive filters
1968	Linear filters				Thresholding
1973					Template matching
1975		Syntactic method			
1978					Bayesian theory
1980					Decision table
1985	Filter banks				
1989					FL
1990				Spectrotemporal analysis	Hidden Markov models
1991					Multilayer perceptrons (MLP)
1995		GA		WT	ART
1996				HT	Fuzzy ARTMAP; WN
1997					Gaussian probability network
1998				PCA	RBF
1999					Complexity measurement
2000				Combined HT and SOM	
2001		Fuzzy NN			
2002	ICA				
2003					Inductive logic programming
2004					Competitive WN
2006					Data mining
2007					Geometric matching

Table 1. Advances of computerized ECG interpretation in chronicle

Disease diagnosis and health prognosis by arterial pulse waveforms came into being in the centuries B.C. in China, but till 1896 the Italian scientist Scipione Riva-Rocci invented the first quantitative sphygmomanometer to measure blood pressure (WHO and CDC 2004). The advances of applanation tonometers (Papaioannou et al., 2004) and photoplethysmographers (Allen 2007) make it possible to quantitatively observe the hemodynamical procedure of arterial blood pressure. The first contemporary electrocardiograph was invented by Willem Einthoven (Holland, 1860-1927) in 1901, and the first portable Holter Monitor was introduced in 1949 for obtaining ambulatory ECG. The introduction of computers into their interpretation can be gone back to 1960s (Warner 1965), but became commercially available in 1970s (Bailey et al., 1974). The readers may refer (Cox et al., 1972) and (Thomas et al., 1979) for a detailed review on the early-stage development of computerized physiological signal interpretation.

2.1 Overview

Year	Preprocessing and Modeling	Recognition and Classification	Cardiovascular System Modeling	
			Cardiac Function	Vascular Property
1967				LPM
1968	Thresholding			
1971	Polynomial			
1972	Heuristic decision			
1973			Diastolic waveform analysis	Linear LPM
1974		Linear curvature		
1976		Syntactic method		4-element LPM
1983			Spectral analysis	
1985	Filter banks			
1986				Area analysis
1988	PCA			
1992	NN			
1993			Transfer function	
1994			Template matching	
1995				Transit time
1997				Physical model
1998			8-element LPM	
1999				Windkessel model
2002	Refractory period		Linear regression	
2003				Systolic waveform analysis
2004	Fuzzy logics			
2005	WT	Adaptive filter banks		
2006			Modified Windkessel model	
2007				Support vector machine

Table 2. Advances of computerized ABP interpretation in chronicle

In general, a system oriented to ECG interpretation is comprised of the essential modules for (1) signal regularization to suppress various noises and artefacts; (2) adaptive delineation of critical points; (3) signal quality evaluation to find out those "dominant" and "ectopic" beats; (4) feature characterization for reliable and consistent classification; and (5) recognition and classification to assist medical diagnosis or health prognosis (Kligfield et al., 2007). Till now a plethora of computational methods and techniques have been proposed and validated for that purpose. A few representative ones were selected and listed in Table 1. Note that it is extremely difficult to figure out the progressive participation of different methods and techniques in computerized ECG interpretation. So Table 1 is absolutely not exhaustive. The situation is similar to Table 2, which illustrates the progressive development of computerized ABP interpretation. However, the major contributions of computers in this field are cardiovascular system modelling and risk factor derivation, but not pattern analysis and waveform classification.

2.2 Current state of the art

In essence, computerized interpretation is oriented to inferring the intrinsic health messages from non-invasive ECG and/or ABP. In the early stage of computerized ECG interpretation, the advances were mainly focused on modelling the practical expertise by heuristic decisions and syntactic methods. In addition, various well-developed methods, such as spectral analysis and linear regression, were programmed for automated signal processing and recognition. Later, to cope with ECG complexity as well as variability, more analytical methods, including Hilbert transform (HT), Hermite decomposition (HD), wavelet transform (WT), principal component analysis (PCA) and independent component analysis (ICA), were introduced step by step. It is deemed such alternative descriptions are more suitable for computerized interpretation.

To different signals and applications, above techniques keep invariant in terms of their analytical models and computing methods. It is totally different from the methods like neural networks (NN), fuzzy logics (FL), genetic algorithms (GA) and adaptive resonance theory (ART), whose models are dynamically adjustable in different cases. Consequently, they are particularly suitable for discovering the nonlinear relationships between physiological signals and health prognosis. Zadeh and other pioneer investigators defined the latter paradigms as soft computing (Zadeh 2007). In essence, soft computing is oriented to attacking the uncertainty and the imprecision in the real world by a consortium of NN, FL and other evolutionary computing techniques. As a comparison, it is appropriate to term the analytical methodologies like spectral analysis and WT as hard computing.

Since the models of hard computing have been formulated exactly, there are not so many stories reported on the integration of hard computing paradigms. On the contrary, soft computing is integrative in nature (Kecman 2001). As a consequence, many integrative paradigms, such as Fuzzy ARTMAP (Ham & Han 1996) and GreyART Network (Wen et al., 2007), were applied to computerized ECG interpretation soon after the introduction of soft computing. In addition, as stated in reference (Ovaska et al., 2002), (Tsoukalas & Uhrig 1997), (Thuillard 2001), (Iyengar 2002), the methodologies of hard computing and soft computing are not in a competitive position, but often complementarily implemented in various engineering applications. As to computerized ECG interpretation, the investigators are now more interested to fuse the paradigms of hard computing and soft computing for integrative advantages.

By observing the published investigations, the integration is generally achieved with two different kinds of paradigms. The first one is to extract patterns and features by hard computing but associate them to health prognosis adaptively by soft computing. This kind of paradigms is easily understandable, and not so challenging in terms of engineering implementation. Hence, a plethora of successful stories have been reported, including the combination of PCA and Multilayer Perceptrons (MLP) (Papaloukas et al., 2002), the combination of Hermite polynomials and neuro-fuzzy systems (Linh et al., 2003), and the combination of HD and Support Vector Machines (SVM) (Osowski et al., 2004). Another kind of paradigms is to fully integrate the analytical models and the computing methods of hard computing and soft computing. They are conceptually elegant but more challenging for engineering implementation. The pilot paradigms with applications in ECG interpretation include Wavelet Networks (Dickhaus & Heinrich 1996), Bayesian Probability Network (Long et al., 1997), and so forth.

Despite with a long history in clinical medicine, the advances of computerized ABP interpretation are not as optimistic as those of ECG interpretation (Table 2). It may be due to the intrinsically qualitative methodology in traditional Pulse Diagnostics (Fei 2003). On the contrary, the computers are good at digital and quantitative processing and analysis only. Thus it is necessary to introduce various quantitative indices for computerized ABP interpretation (Luo et al., 2005). The prevailing methods and techniques in this field are mainly focused on deriving quantitative risk factors, including cardiac output, arterial compliance and vascular resistance, by means of various analogous electrical models representing a CVS. Those models are possibly comprised of the capacitances analogous to arterial compliance, the resistances analogous to vascular resistance, the inductances analogous to blood inertia, and so on. However, no matter the low-order Windkessel models (Goldwyn & Watt 1967) or the high-order transmission line models (Heldt et al., 2002), their effectiveness and reliability are still arguing and pending for further investigation (Frank et al., 1973; Murray and Foster 1996).

Quite few paradigms were reported to recognize and classify non-invasive ABP waveforms by means of pattern recognition and computational intelligence, which on the contrary have been prevalent for computerized ECG interpretation. In this chapter, one of our ultimate goals is to investigate the applications of hard computing, soft computing and their fusion for computerized ABP interpretation. The attention will be particularly concentrated on the refractory variability of non-invasive physiological signals.

3. Physiological signal modelling

3.1 Conventional waveform analysis

In clinical medicine, the cardiologists are concerned with the rhythms, amplitudes and waveforms as a whole for physiological signal interpretation (Fei 2003; Yanowitz 2007). It is possible to formulate their expertise and experience into computer languages, and let the computers analyze those physiological signals automatically (Miyahara et al., 1968; Belforte et al., 1979; Degani & Bortolan 1989). The first step in advancing computerized physiological signal interpretation was to mimic the decision making procedure of clinical experts. In general, the clinical experts have been trained well to inspect various metrics of physiological signals, including their rhythms, amplitudes, waveforms and various derivative parameters (Fig. 6). From this point of view, the computers are even better to

measure those parameters (Caceres et al., 1962). Nevertheless, such kind of information is susceptible to various instrumental and manual artefacts. In terms of non-invasive physiological measurements, it is particularly difficult to guarantee the accuracy of amplitude information. That is why morphological analysis and rhythm information turn to more and more popular in computerized physiological signal interpretation.

As early as in 1960s (Okajima et al., 1963), a few pioneer investigators have noticed the uniqueness of computer ECG interpretation. In order to disregard the effects of insignificant factors, such as pulse rate and age, they proposed to extract and normalize the QRS complex for pattern recognition. This idea, namely morphological analysis instead of metric measurement, was revisited more than once in the following years (Bemmel et al., 1973; Maitra & Zucker 1975; Suppappola et al., 1997; Laguna et al., 1999). In those systems, the ECG waveforms or their components (e.g., QRS complex, ST-T segmentation, etc) were regularized and normalized beat by beat for morphological analysis. Thus the beat-to-beat amplitude variations were diminished in those paradigms. It was deemed that various insignificant constituents in ECGs may be suppressed effectively. As a consequence, although the amplitudes bring important pathophysiological clues (Petrutiu et al., 2006), morphological analysis becomes more and more popular in computerized ECG interpretation (Weiben et al., 1999; Lagerholm et al., 2000; Linh et al., 2003; Chazal et al., 2004; Osowski et al., 2004; Christov et al., 2005).

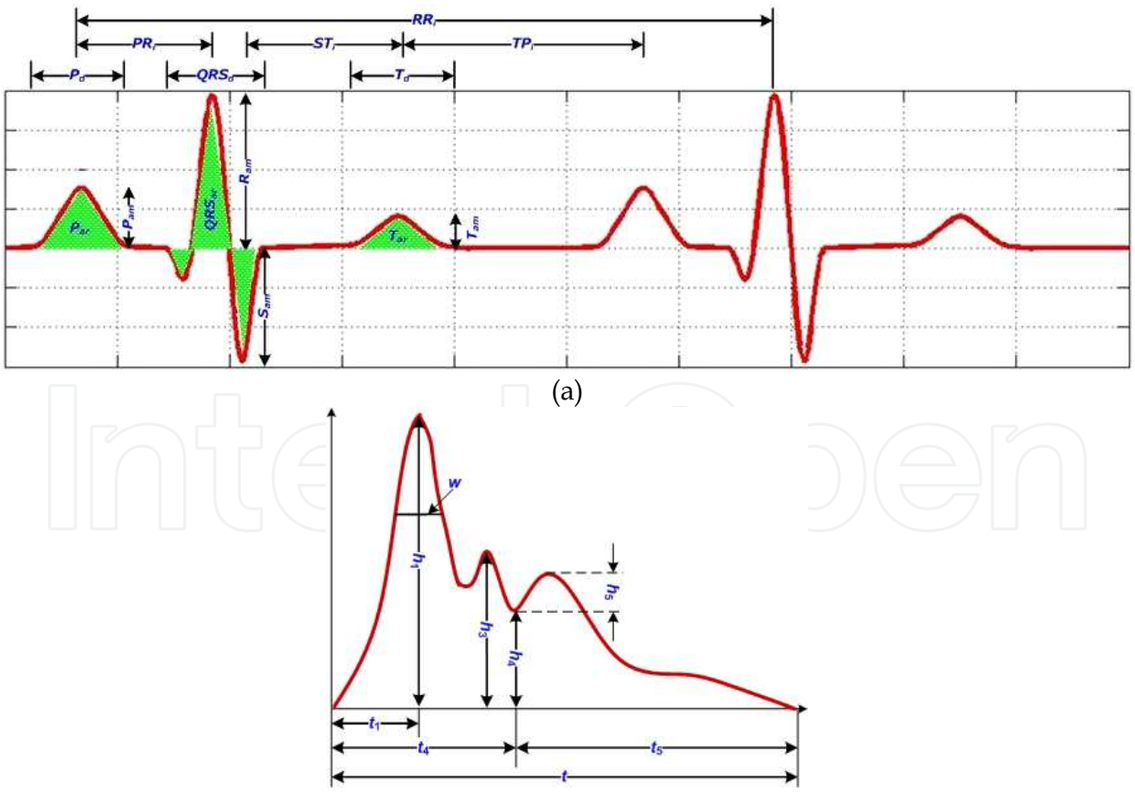

Fig. 6. Physiological waveform analysis (a): ECG; (b): ABP

The pioneer investigators were interested in pulse waveform analysis and pattern recognition in the beginning of computerized ABP interpretation (Fei 2003). However, unlike ECGs, there is a lack of authoritative ABP benchmark with beat-by-beat annotations. In addition, it is extremely difficult to convert the qualitative, ambiguous knowledge in traditional Pulse Diagnostics into computer languages. The investigators were hereby more interested to associate ABP waveforms with other quantitative risk factors for cardiovascular health prognosis (Table 2). However, by means of those techniques, the ABP waveforms had to be calibrated with ABP values that were recorded separately. Additional errors and biases would be introduced in above procedure (Li et al., 2008). Consequently, there were still a few, although not so many, investigators working on ABP morphological analysis (Martin et al., 1994; Li et al., 2008).

It is difficult to calibrate non-invasive physiological signals with regard to the accidental instrumental inaccuracy and human artefacts as well. Thus many investigators chose to normalize those physiological signals and concentrated on morphological analysis (Weiben et al., 1999; Lagerholm et al., 2000; Linh et al., 2003; Chazal et al., 2004; Osowski et al., 2004; Christov et al., 2005). Moreover, it has been reported that the morphological features from normalized ECGs are comparable to those from original ones in computerized interpretation (Chazal et al., 2004).

To normalize physiological signals, several common filters were firstly applied to remove baseline wandering, muscular tremor, electrical line interference, and other noises (Lagerholm et al., 2000; Chazal et al., 2004; Christov et al., 2005). After the basic filters, those physiological signals were then normalized, in a beat by beat manner, to the amplitudes within [-1, 1] and the intervals within [0, 1]. Then the same group of physiological signals, no matter ECGs or ABP waveforms, turned to more consistent and amenable to computational interpretation. Following the strategies in reference (Chazal et al., 2004), it is possible to derive the morphological features out by nonlinear sampling. As to ECG signals, the sampling was carried out within two windows (Fig. 7a). The first one (150ms) attempted to characterize the QRS complex while the other one (350ms) for the T wave. Within each window, 10 points of physiological signals were uniformly sampled. In terms of ABP waveforms, the unique sampling window (500ms) was oriented to the region between systolic and diastolic complexes (Fig. 7b). Similarly, there were totally 20 points sampled

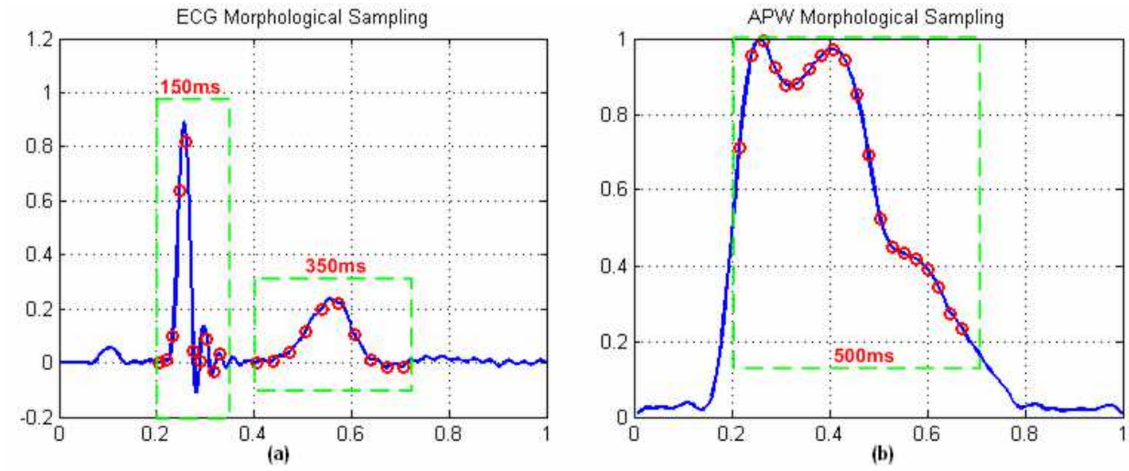

Fig. 7. Nonlinear sampling for morphological feature characterization (a): ECG; (b): ABP

from each beat of ABP waveforms. Those sampling points formed the morphological features for subsequent computerized recognition and classification.

3.2 Adaptive physiological signal modelling

The conventional strategies, including signal regularization and morphological analysis, are helpful to suppress physiological signal variability in some sense. It seems the results are amenable to computerized interpretation, too. However, it is meanwhile observed that morphological feature sets are not sparse and not robust enough. Actually, signal representation in time domain is legible but redundant, which may be evidenced by means of PCA (Geva 1998; Stamkopoulos et al., 1998). As a consequence, morphological analysis was generally combined with domain transformation, such as Hilbert transform (Bolton & Westphal 1981), HD (Rasiah et al., 1997; Lagerholm et al., 2000; Linh et al., 2003) and WT (Senhadii et al., 1995; AI-Farhoum & Howitt 1999; Saxena et al., 2002; Engin 2007), in those published paradigms of computerized physiological signal interpretation.

Domain transformation, unlike direct morphological analysis, attempts to characterize physiological signals in an alternative space, where the genuine signal components are more discernible from noises and artefacts. For instance, the well-known spectral analysis is exactly based on a classical domain transformation, namely Fourier transform. It is hereby possible to suppress baseline wandering by a high-pass filter, or remove electrical line interference with a notch filter.

In domain transformation, the recorded physiological signals are alternatively characterized by a set of singular basis functions. In general, those basis functions, either orthonormal or not, have no explicit physical meanings, which make them abstract for understanding. But lots of refractory problems may turn resolvable in those alternative function spaces. Take computerized ECG arrhythmia interpretation for an example. It has been confirmed that Hermite basis functions (HBFs) and wavelet energy descriptors are among those most competitive ones for feature characterization in discrimination analysis (Senhadii et al., 1995; Rasiah et al., 1997; AI-Farhoum & Howitt 1999; Lagerholm et al., 2000; Saxena et al., 2002; Linh et al., 2003; Engin 2007).

3.2.1 Hermite decomposition

It is possible to carry out domain transformation and signal modeling by orthonormal basis functions or not. But the orthonormal basis functions are usually preferred due to the fast implementation. It is hereby desired to find out a series of orthonormal basis functions for compact physiological signal modeling. Nevertheless, to be orthonormal, the basis functions have to meet a set of rigorous mathematical regularities. In other words, most orthonormal basis functions, such as cosine basis functions for Fourier Transform, are not efficient for physiological signal modeling. On the contrary, it has been found that HBFs share the resembling waveforms with electrocardiograms (ECGs). Thus they can be utilized to model ECG waveforms compactly (Rasiah et al., 1997; Lagerholm et al., 2000; Linh et al., 2003).

In mathematics, HBFs are derived from Hermite polynomials:

$$\mathbf{\Phi}_m = \frac{1}{\sqrt{2^m m! \sqrt{\pi}}} e^{-t^2/2} \mathbf{H}_m(t), \tag{1}$$

where $\mathbf{H}_m(t)$ is the m^{th} Hermite polynomial:

$$\mathbf{H}_m(t) = 2t\mathbf{H}_{m-1}(t) - 2(k-1)\mathbf{H}_{m-2}(t)\,, \tag{2}$$

where $\mathbf{H}_0(t)$=1 and $\mathbf{H}_1(t)$=2t. Hermite polynomials are a classical orthogonal polynomial sequence, and with common usages in probabilistic analysis and physics.

To cope with physiological signal variability, two modulating parameters, σ and τ, were applied to the conventional HBF in this dissertation. So they turned to be:

$$\mathbf{\Phi}_m = \frac{1}{\sqrt{\sigma 2^m m!\sqrt{\pi}}} e^{-t^2/2}\mathbf{H}_m(t)\,, \tag{3}$$

where t was modulated as $(n\text{-}\tau)/\sigma$ (σ and τ are dilation and translation factors respectively). Then it is possible to approximate and model a physiological signal compactly as:

$$\mathbf{S}' = \sum_{m=1}^{M} c_m \mathbf{\Phi}_m(n)\,. \tag{4}$$

The object is to find out the appropriate model order M, the optimal modulating parameters σ and τ in HBFs, as well as the according weight c_m.

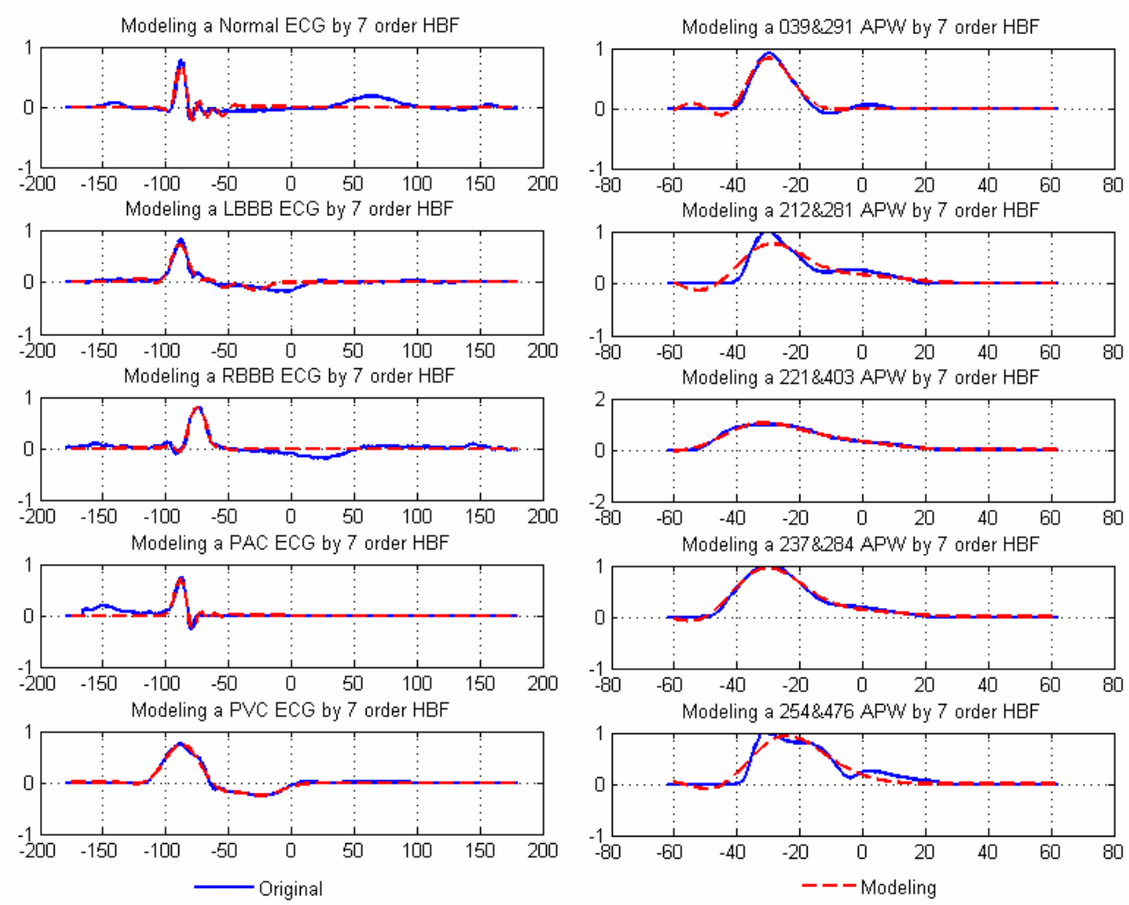

Fig. 8. Modelling physiological signals by 7 order HBFs (a): ECG; (b): ABP

However, in practice, it has been found that physiological signal modelling by the modulated HBFs often suffers from excessive computing. The heuristic gradient descent

algorithms have been advocated for this problem (Rasiah et al., 1997). Here a special algorithm was adopted to achieve fast implementation. In summary, the algorithm strives to find an approximately optimal solution in the fixed transformation grids. Firstly, it adaptively estimates the spans of dilation and translation in accordance with the incoming physiological signal. In the second, that limited transformation space is segmented into M-by-M grids (M was designated in advance). Then, the algorithm generates an estimate in each transformation grid, and evaluates it against the original physiological signal. Such procedure iterates throughout the entire transformation grids (M^2). The final results are taken as those parameters leading to the minimum approximation error. As shown in Fig. 8, such fast algorithm performed fairly well, and a few low-order HBFs have been able to approximate those physiological signals.

3.2.2 Wavelet analysis

The advantages of wavelet transform over other techniques lie in its unified time-frequency analysis. In other words, by wavelet transform it is possible to characterize a physiological signal with its temporal and spectral features simultaneously. Thus a variety of successful applications have been reported on physiological signal processing and analysis, covering from adaptive denoising, compression, delineation to feature characterization, pattern recognition, and others. In terms of feature characterization, the investigators paid substantial attention on wavelet energy (Senhadii et al., 1995; AI-Farhoum & Howitt 1999), wavelet entropy (Rosso et al., 2001) and other energy-dense wavelet coefficients (Senhadii et al., 1995).

In essence, wavelet transform can be considered as a kind of multirate filter banks. The signal components within distinct spectra emerge at different scale levels of wavelet transform. The investigators in reference (Senhadii et al., 1995) hereby proposed to characterize ECG signals by a feature vector containing energies at different wavelet scales. The DWT with 10 levels was employed there. The authors in reference (AI-Farhoum & Howitt 1999) further investigated on the relative wavelet energy, which was concerned with both spectral and temporal aspects of wavelet transform. A 6-element feature vector was formed with the wavelet energies at scale 2, 3, 4 and before, within, after the QRS complex in each beat of ECG.

The results of wavelet transform manifest the resemblance of a physiological signal and the modulated wavelets at different scales and shifts, which is quite similar to spectral analysis by Fourier transform. Therefore, taking a signal's wavelet transform as $W_{a,b}$, it is possible to define the total wavelet energy as:

$$Er_{tot} = \sum_a \sum_b \left| \mathbf{W}_{a,b} \right|^2 = \sum_a Er_a \ , \tag{5}$$

where Er_a is the wavelet energy at scale a:

$$Er_a = \sum_b \left| \mathbf{W}_{a,b} \right|^2 \ . \tag{6}$$

The relative wavelet energy at each scale is then defined as:

$$REr_a = Er_a \ / \ Er_{tot} \ , \tag{7}$$

which reflects the probability distribution of energy scale by scale. Then, coming to wavelet entropy, it will be defined as in the reference (Blanco et al., 1998):

$$Ep = -\sum_a RErr_a \cdot \ln(RErr_a) \,. \tag{8}$$

Wavelet entropy may serve as a measure of order/disorder degree of a physiological signal. Thus it provides useful information about the underlying dynamical process associated with that signal.

Another kind of features comes from the energy-dense components of wavelet transform. Two different strategies have been proposed and validated to derive them (Senhadii et al., 1995; Christov et al., 2005). The first one was desired to find out them by matching pursuits from time-frequency dictionaries, which will be elucidated in next chapter. The second one was based on the fast DWT. Given the results of DWT as $\mathbf{W}_{\mathrm{AM}}(n/2^{\mathrm{M}})$ and $\mathbf{W}_{\mathrm{D}m}(n/2^{m})$ (m=1,2,…M), the feature sets were derived from the maximum coefficients at $\mathbf{W}_{\mathrm{AM}}(n/2^{\mathrm{M}})$ and each scale band $\mathbf{W}_{\mathrm{D}m}(n/2^{m})$. Hereafter those extrema at different scales will be termed as wavelet scale maxima.

In this chapter, the feature sets based on relative wavelet energies, regional wavelet entropies and wavelet scale maxima were evaluated for physiological signal variability. It is noteworthy that wavelet transform by different mother wavelets, owing to their distinct properties (e.g., support, regularity, and vanishing moments), generally lead to different analytical results. Here the 3-order Gaussian derivative was chose as the mother wavelet. The energy of ECG QRS complexes have been identified within 5~15Hz approximately (Pan & Tompkins 1985). Obviously, the energies of ECG P and T waves concentrate within a spectral band less than 5Hz. Meanwhile, it has been found in our practice that, no matter ABP systolic or diastolic complex, their spectral energies are in a region less than 5Hz. The spectral resolution of 3-order Gaussian wavelet is obviously appropriate for ECG and ABP analysis.

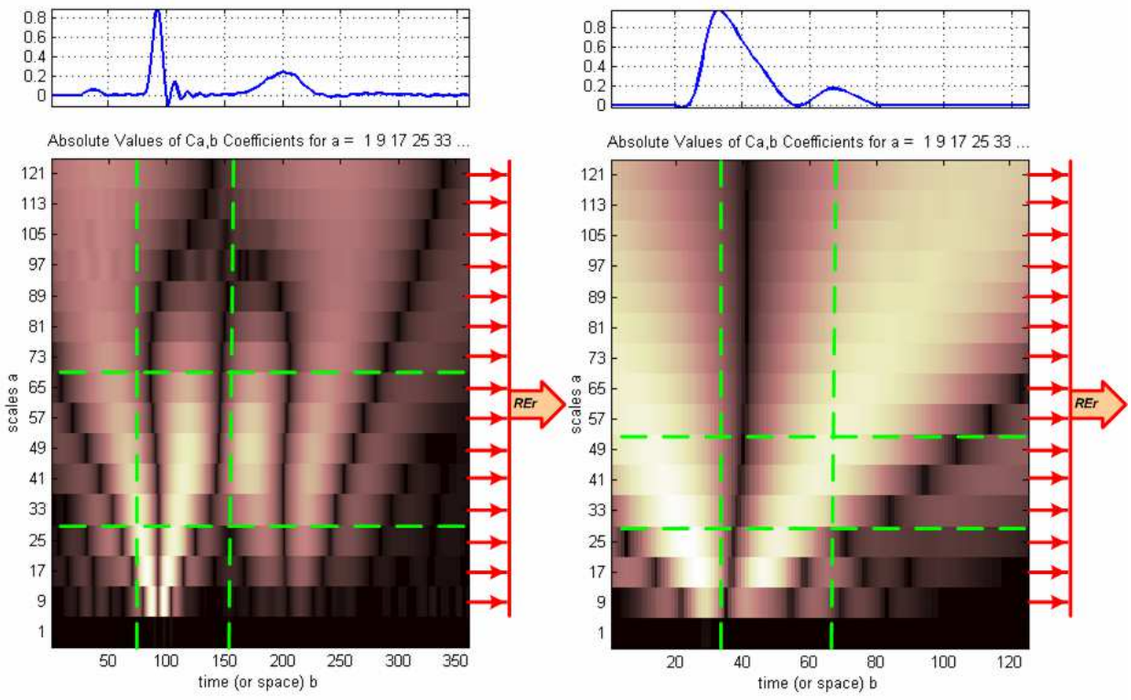

Fig. 9. Feature characterization by wavelet-based time-frequency analysis (a): ECG; (b): ABP

In terms of physiological signal characterization, the ratios of all wavelet scales, except the first one, were chosen for relative wavelet energy (Fig. 9). Then, the results of wavelet transform were partitioned into 9 segments based on wavelet spectral bands and temporal fiducial marks (Fig. 9). Coming to ECG signals, wavelet spectral bands were chosen as the scales {9; 17; 25}, the scales {33; 41; 49; 57; 65} and the left scales till 121. They were desired to characterize the spectral energies of QRS complex, P and T waves respectively. The temporal partition took advantage of a 200ms window (50ms before and 150ms after the R point). The entropy in each segment was computed and rated for regional wavelet entropies. With regard to APW signals, the spectral bands were chosen as {9; 17; 25}, {33; 41; 49} and the left scales. The temporal fiducial marks were based on the systolic peak and diastolic peak of ABP waveforms (Fig. 9).

3.2.3 Matching pursuits

In view of the advantages of fast implementation, it is attractive to screen the energy-dense wavelet coefficients and model physiological signals under the frameworks of fast DWT. As a matter of fact, the abovementioned paradigm of wavelet shrinkage was exactly by means of this idea. However, it is noteworthy that orthonormal wavelet basis functions (WBFs), due to their mathematical regularity, are not efficient for physiological signal modeling. The authors in reference (Mallat & Zhang 1993) hereby proposed a technique of matching pursuits based on WP analysis, by which it is possible to adaptively select the appropriate wavelet coefficients out from a large and redundant dictionary of time-frequency atoms.

In fast DWT, a signal is split into an approximation part and a detail one by a pair of quadrature mirror filters (QMF). Then the approximation part will be iteratively separated by that pair of QMF. Unlike DWT, WP analysis splits both parts of approximation and detail iteratively. Such paradigm preserves the advantages of fast implementation, but incurs the risk of redundancy in time-frequency representation. It rewards the extra flexibility for noise suppression and signal compression (Mallat 1998). There have been standard algorithms for WBF selection, based on information entropy minimization, from the redundant dictionary of time-frequency atoms (Coifman & Wickerhauser 1992). Nevertheless, they are not oriented to compact signal characterization. Under the framework of WP analysis, the technique of matching pursuits attempts to characterize a complicated signal concisely with several adaptive WBFs.

Physiological signal decomposition and modelling by matching pursuits is similar to the standard WT:

$$s(n) = \sum_{m=1}^{\mathrm{M}} < R^m f, \boldsymbol{\psi}_m > \boldsymbol{\psi}_m + R^{\mathrm{M}+1} f \ , \tag{9}$$

where $\boldsymbol{\psi}_m$ is the modulated orthonormal wavelet, and $R^m f$ is the decomposition residue at level m. However, unlike the common WBF, the $\boldsymbol{\psi}_m$ here is characterized as [4.3]:

$$\boldsymbol{\psi}_m(n) = \frac{1}{\sqrt{2^j}} \boldsymbol{\psi}\left(\frac{n}{2^j} - \left(p + \frac{1}{2}\right)\right) e^{i 2\pi \cdot n \cdot 2^{-j} (k + 1/2)} \ , \tag{10}$$

where $0 \le j \le \log_2 \mathrm{N}; 0 \le p \le 2^{-j}\mathrm{N}; 0 \le k \le 2^j$. It was in essence a discrete mother wavelet dilated by 2^j, centred at $2^j (p+1/2)$ and modulated by a sinusoidal wave with frequency $2\pi 2^{-j}$ $(k+1/2)$. By matching pursuits, those wavelets best matching the residue at each scale level

would be chosen for physiological signal characterization. In other words, the technique of matching pursuits here is greedy and locally optimized in contrast to those globally-optimizing algorithms based on information entropy.

The authors in reference (Mallat & Zhang 1993) demonstrated the competence of matching pursuits for complicated signal modelling by means of Gabor wavelets as an example. Actually, matching pursuits is a general technique under the framework of WP analysis (Suppappola & Suppappola 2002). For instance, the symmlet wavelet with 8-order vanishing moments has been proved effective (Christov et al., 2005). In this chapter, the Daubechies wavelet with 8-order vanishing moments was evaluated for physiological signal modelling. The pending decisions include the desired number of wavelets, the tuning parameters of wavelets, and the level of WP decomposition.

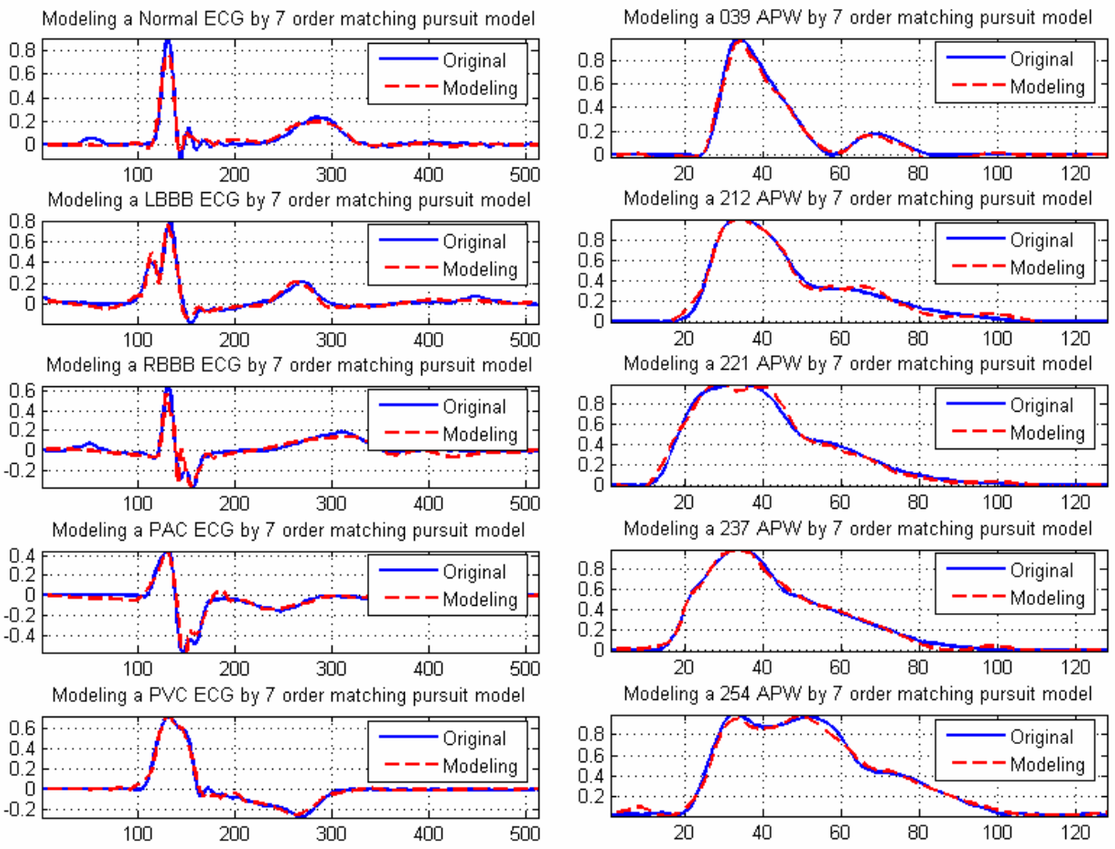

Fig. 10. Modelling physiological signals by 7 order matching pursuits (a): ECG; (b): ABP

We are interested in modelling physiological signals by adaptive wavelets. The first of all, to accomplish the dyadic WP analysis, the signal length should be equivalent to a power of two, such as 128 (2^7), 512 (2^9) and 1024 (2^{10}). In this chapter, all physiological signals were re-sampled or interpolated, instead of zero-padding, to approach those standard lengths. In the second aspect, the resultant models should be as compact as better. It has been reported in reference (Suppappola & Suppappola 2002) that, by matching pursuits, 10-order WBFs were generally enough to characterize the ECG signals in MIT/BIH Arrhythmia Database (Moody 1997). Nevertheless, 5 orders of them seem not enough. As a consequence, the order

of WBFs is empirically chosen as 7 for compact physiological signal models with fair performance. In the third aspect, by referring to their octave spectral bands, 8 level of WP analysis seems appropriate to capture most of the essential components of cardiovascular physiological signals. Then, the WBFs are adaptively traced and tuned by matching pursuits. Compared with those HBF models, no matter for ECG signals or ABP waveforms, the WBF models (Fig. 10) are obviously better than them.

4. Adaptive clustering and classification

The underlying objective of non-invasive cardiovascular monitoring is to tell 'normal' or 'abnormal' health conditions. If possible, it is desired to further elucidate the causes of 'abnormal' health conditions, for example, left ventricular hypertrophy, aortic valve stenosis, arteriosclerosis, or others. The physiological signals, either ECGs or ABP waveforms, bring important messages of blood circulation within cardiovascular system. Thus it is a tradition of interest to observe their properties as well as variations from normal subjects and the patients with various symptoms. Recording effective physiological signals is not an easy task in respect to pathophysiological variability, instrumental inaccuracy and manual inconsistency. On the other hand, it is even more challenging to interpret those recorded physiological signals clearly. As a matter of fact, even clinical physicians have to take long-term career training in order to obtain and maintain their skills, let alone electronic computers.

The most intuitive ways for computerized physiological signal interpretation come into being as knowledge engineering and expert systems. By them, it is possible to formulate and convert medical experts' knowledge and experience into computer-compatible data and information (MN ECG Coding Center 2009). Nevertheless, it has been found that the abstract and qualitative medical knowledge is not so amenable to nonclinical computer engineers. For instance, most clinical physicians are good at coping with various physiological signal variations and artefacts, but they are generally not able to elucidate their extraordinary capability to nonclinical engineers in a quantitative manner. On the other hand, computer engineers are good at constructing knowledge base and inference machines, but lack of proper medical knowledge and diagnostic experience. Without their thorough cooperation, those computerized medical expert systems are not robust enough with regard to physiological signal variability.

As a consequence, nonclinical scientists and engineers attempted to resolve such challenge from another aspect. Suppose there are lots of recorded physiological signals with credible annotations by a group of medical experts. The investigators are concerned with the methods and techniques by which those physiological signals may be related to their annotations automatically. In this regard, a good many of computational methods, including template matching and statistical analysis in hard computing (Long et al., 1997; Gerencsér et al., 2002), Artificial Neural Networks (ANNs) and Fuzzy Logics (FL) in soft computing (Suzuki 1995; Tatara & Gnar 2002; Lei et al., 2008), have been proposed and validated for computerized physiological signal interpretation.

In general, those techniques do not simply resort to the empirical thresholds of amplitudes and rhythms any more. In stead, the advanced signal processing methods, such as wavelet analysis and HD, are utilized to find out the underlying properties of physiological signals. Whereas their results are not intuitive to visual inspection, it is deemed that the alternative features are more suitable than original physiological signals for computerized

interpretation. In above sections, some of signal processing techniques, including morphological sampling, adaptive HBFs, relative wavelet energies, regional wavelet entropies, wavelet scale maxima and adaptive WBFs, have been investigated carefully to attack physiological signal variability.

It is noteworthy that, in those alternative feature spaces, the conventional medical knowledge accumulated in clinical medicine does not hold any more. The new rules and explanatory statements have to be established in order to recognize and classify physiological signals. We are concerned with the autonomous organization and clustering of physiological signals in this section. Actually, if those physiological signals could be organized together for similar groups but separately for different groups, it is not so difficult any more to classify them by computational methods. In addition, it is extremely difficult or expensive to request medical experts to carefully review and annotate so many physiological signals. Take the MIT/BIH Arrhythmia Database (MAD) at PhysioNet (Moody 1997) for an example. Whereas each recording lasts 30 minutes only, there have been over tens of thousands of beats with variant annotations in it.

As a consequence, the techniques of self-organizing and data clustering receive much attention in computational intelligence. A variety of them, including fuzzy c-means (FCM) (Lei et al., 2008) and self-organizing maps (SOM) (Lagerholm et al., 2000), have been extensively investigated for physiological signal analysis. By them it is possible to fuse the advantages of wavelet analysis and computational intelligence for self-organizing physiological signals.

4.1 Self-organizing physiological signals

As mentioned above, annotating physiological signals by hands is an extremely challenging task. Unfortunately, it is even more challenging at present to carry out fully-automated recognition and classification by computers. However, at least, it is possible to organize and cluster physiological signals by computers in an autonomous manner. The results may serve as a reference to medical experts in analyzing and annotating physiological signals. Unsupervised classification, also known as data clustering, is exactly the techniques designed to find out the intrinsic distributions of unknown signals or data (Jain et al., 2000). The metrics of similarity and the criterion function, but not human intervention, determine the final results of data clustering.

There have been a variety of clustering algorithms, most of which are based on either iterative error minimization or hierarchical clustering (Duda et al., 2001). Hierarchical techniques organize signals or data in a nested sequence of groups which can be displayed in a dendrogram. In contrast, the error minimizing algorithms desire to work out a systemic partition that minimizes the internal variances and maximizes the mutual discrepancies. The latter paradigms are more frequently utilized in computerized physiological signal interpretation.

4.1.1 Self-organization by error minimization

The issue of data clustering can be elucidated in a formal language: Given N feature vectors in a d-dimensional metric space, determine one of their distributions in K groups, so that the members in the same group are more similar to each other than to those in different groups. The value of K may or may not be specified, but a clustering criterion function must be designated for optimization. In essence, the error minimization is a kind of local criteria

because it is sensitive to the initial clustering, the similarity metrics and the criterion function. The interested readers are advised to look through the reference (Jain & Dubes 1988) for details on algorithms and techniques in this field.

Take the classical algorithm of *k*-means for an example. It seeks to assign N patterns, based on their attributes and the designed metrics, into K groups $\{C_1, C_2, \ldots, C_K | \ K<<N\}$. Then, each cluster C_k has n_k members and each member is in exactly one cluster. The results are comprised of prototyping templates and the pattern affiliation to each group. In *k*-means, the prototyping template for each group is defined as its centroid:

$$C_k = \sum x_i^k \Big/ n_k , \tag{11}$$

where x_i^k is the *i*th pattern belonging to the group *k*. Error minimization seeks to reduce (12) as a criterion function:

$$J = \sum \ e_k^2 \ , \tag{12}$$

where e_k is the Euclidean norm or a similar metric within each group

$$e_k = \sqrt{\sum_{i=1}^{n_k} (x_i^k - C_k)^T (x_i^k - C_k)} \ . \tag{13}$$

The ideal results of a *k*-means algorithm will minimize the internal variance within each group but maximize the mutual discrepancies between different groups.

In the *k*-means algorithm, each pattern is limited to one and only one of K groups, which is often not true in computerized physiological signal interpretation. As a matter of fact, the physiological signals from cardiovascular health monitoring are subject to multifold effects of cardiac functions, vascular elasticity and even blood viscosity. In other words, it is usually not appropriate to simply assign a physiological signal to a single group. To this issue, two kinds of paradigms, namely FCM and SOM, have been proposed and practiced with success.

FCM applies a membership degree μ_{ij} to indicate the belongingness of the *j*th pattern to the *i*th group. The criterion function of FCM is similar to that of *k*-means:

$$J = \sum_{n=1}^{\mathrm{N}} \sum_{k=1}^{\mathrm{K}} \mu_{kn}^m \left\| x_n - C_k \right\|^2 \ , \tag{14}$$

where μ_{kn} represents the membership degree of feature vector x_n in the *k*th group, C_k is the *k*th group centroid, and *m* (*m*>1) is a constant controlling the resultant fuzziness.

There are constraints oriented to the normalization of probabilistic distribution. By that, it has been proved in reference (Duda et al., 2001) that data clustering in the light of maximum likelihood is equivalent to a centriod-based clustering by their averages. Then, in accordance with Equations (15) and (16), the membership degrees μ_{kn} and the centroids C_k are updated iteration by iteration respectively:

$$\mu_{kn} = \frac{\left\| x_n - C_k \right\|^{-2/(m-1)}}{\sum_{k=1}^{K} \left\| x_n - C_k \right\|^{-2/(m-1)}} \ ; \tag{15}$$

$$C_k = \frac{\sum_{n=1}^{N} \mu_{kn}^m x_n}{\sum_{n=1}^{N} \mu_{kn}^m}. \quad (16)$$

The algorithm is optimized when the patterns close to their group centroids are assigned with high membership degrees, and those far away from their centroids are with low membership degrees.

4.2 Neural computation

SOM is another popular paradigm for adaptive data clustering. It follows the strategies of ANNs instead of that of FCM. ANNs are generally comprised of various computational models originated from biological neural networks. In neuroscience, a neural network describes a population of physically interconnected neurons whose inputs and outputs define a recognizable network (Figure 11a). Communication between different neurons often involves electrochemical processes abstracted as synapses. In general, a neuron will trigger an action potential and further transmit it to the associated neurons if it perceives the incoming stimulations over a certain threshold (Hebb 1949). Similarly, a computational ANN model takes an ensemble of simple processing elements as neurons, and linear connections between them as synapses (Figure 11b). Each neuron merely carries out a simple linear or nonlinear transform, but their aggregation with linear connection often exhibits complex global behaviours. In other words, the functional characterization of an ANN relies not only on its basic processing elements but also on the systematic connections.

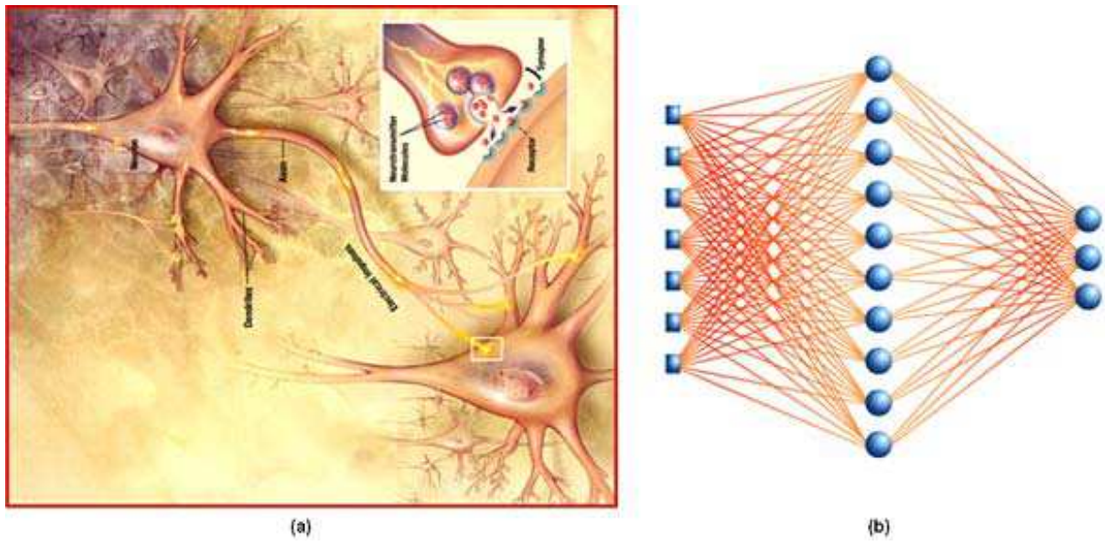

Fig. 11. Biological vs. artificial neural networks (adapted from www.neurevoluion.net 2009)

ANNs are claimed for their competence in nonlinear mapping as well as self-adaptation. Suppose the ANNs input space is comprised of the N-dimension continuous or discrete feature vectors $\{\boldsymbol{X} \in d^{\mathrm{N}}\}$, its output space consists of the M-dimension continuous or discrete responses, categories or decisions $\{\boldsymbol{Y} \in d^{\mathrm{M}}\}$. It has been proved that an ANN, with appropriate infrastructure and controlling parameters, may establish a nonlinear map $f(\boldsymbol{X} \Rightarrow \boldsymbol{Y})$ approaching their genuine relationships arbitrarily well. Take computerized ECG interpretation for an example. The incoming feature vectors may be the 20-dimension

morphological sampling, the 10-dimension HBFs, the 15-dimension relative wavelet energies, the 9-dimension regional wavelet entropies, or the 7-dimension WBFs. The output vectors may be "normal" and "abnormal" in one dimension, the 5-dimension AAMI heartbeat classes, the 15-dimension MIT/BIH arrhythmia types (Moody 1997) or even hundred-dimension cardiovascular diseases. Then the ANN may be configured and tuned by means of the annotated physiological signals. The popular paradigms include (Jain et al., 2000) multilayer perceptrons (MLPs), radial basis function (RBF) networks, probabilistic neural networks (PNNs), and so forth. In contrast, there are also many ANN paradigms specially designed for the cases of no prefixed responses. SOM and adaptive resonance theory (ART) are the typical examples of them. It is deemed that their outputs may reflect the intrinsic properties of physiological signals in some sense.

An ANN may be characterized by its basic processing elements and the connections between them. Different from conventional analytical models, the controlling parameters in an ANN are unknown in advance, and have to be identified by self-adaptive learning. The underlying discrepancies of abovementioned paradigms exactly lie in their learning mechanisms. Those supervised ANNs often rely on error minimization. Namely, the ANN parameters are tuned step by step in order to minimize mapping errors. On the contrary, the unsupervised ANNs generally adopt the strategies of competitive learning. Merely those most similar nodes to network inputs will be updated accordingly. In a nutshell, their underlying mechanisms of self-adaptation are utterly different:

- ***Error Minimization***: In supervised ANN learning, an input $\boldsymbol{X}$ is presented to that ANN with unknown parameters $\{\boldsymbol{\theta} \mid \Theta_i^k ; w_{ij}^k\}$, its actual output $\boldsymbol{Y}^*$ will be evaluated against the target output $\boldsymbol{Y}$. An artificial objective function J, usually as the square of the errors, is introduced to relate $\boldsymbol{\theta}$ and network performance $|\boldsymbol{Y} - \boldsymbol{Y}^*|$. As the ultimate target is to reduce $|\boldsymbol{Y} - \boldsymbol{Y}^*|$ to the minimum, it is a reasonable choice to update those parameters in the gradient descent direction. Of course, a prerequisite assumption is that J is smooth and differentiable everywhere. The topics worthy of investigation in this field include how to arrive at the global minimum but local minima, how to speed up evolution while avoiding oscillation, and so forth.
- ***Competition and Resonance***: Competitive learning is complementary to above supervised learning by means of error minimization. A central point of this kind of systems is pattern matching that searches and updates the internal memories of a network against an external input. The common SOM networks compete for an updating in a prefixed feature space. In other words, even the outliers may stimulate the internal behaviours of a SOM network. On the contrary, the ART networks lead either to a resonant state or to a parallel memory. If pattern matching ends at an established node, the prototyping template may either remain the same or incorporate information from matched portions of new input. Otherwise, if ends at a new status, the ART network learns the new input. Anyway, such match-based learning stands for a totally new style of network self-adaptation.

The rationale of supervised ANNs is built on an underlying assumption: any complex relationship or association can be modelled as a function, and meanwhile, that function can be approximated by a linear combination of simple linear or nonlinear basis functions. The essence of supervised learning means utilizing some form of quantitative algorithms to reduce the errors or costs on a set of known training data. At present, a good many of gradient descent or conjugate gradient algorithms, and their variants, have been well established to evolve ANNs for reducing the specific errors or costs. Suppose a function can

be characterized by its unknown parameters $f(\Theta | \theta_k, k=1, \ldots, K)$. Then, on a training dataset, the incoming pattern $s_j(n)$ and the desired response y_j should have been confirmed. However, if the function response from f does not equal to the desired one, there is an empirical error $e_j=|f(s_j(n))-y_j|$. The idea of ANN evolution is to minimize the error square by means of the gradient information.

In above paradigms of supervised learning, the optimization is oriented to minimize the apparent errors or costs. However, there is no any warranty that the final results are optimal and reside at the global optimum. Even after different enhancing strategies are incorporated, the optimum can be guaranteed with respect to the available training dataset only. If the training dataset is representative enough to cover the whole space of interest, it is safe to convey the optimality of ANNs to the unknown testing dataset. However, it is often not the case. The problem is, what we are really interested in is the optimality in testing but not training dataset. The relevant research is mainly focused on the generalization and expectation risk minimization. Based on the concept of margin, Vapnik proposed the optimum separation hyperplane for classification and recognition (Vapnik 1998). The margin can be modeled as the shortest distance of training data to a separation hyperplane. In a word, to a linear classification problem, the optimum separation hyperplane is the one with the maximal margin among all possible separation hyperplanes. Vapnik and his colleagues also proposed the technique of Support Vector Machines (SVMs) for hunting that optimum separation hyperplane. Nowadays SVMs are considered as one of the most promising techniques in computational intelligence.

After decades of years of development, there has been a variety of ANN models with successful applications to adaptive clustering, function learning, pattern classification and nonlinear prediction. SOM, multilayer perceptrons (MLPs), radial basis function (RBF) networks, recurrent (Hopfield) networks and adaptive resonance theory (ART) networks are all well-established and have been widely validated in various real-life applications [6.15]. MLPs originate from linear perceptrons, which is one of the earliest ANN models. The rationale of utilizing MLPs for classification is quite intuitive: it is possible to approximate any function by a linear combination of simple basis functions. Then, in MLPs, there are a layer of input neurons, one or several layers of hidden neurons and one layer of output neurons. If we take each output neuron as a target function, to a specific incoming pattern, the neuron with the biggest response in the output layer is then assumed as the one representing the expected result. To define the MLPs, it is necessary to decide the number of hidden layers and the number of neurons in each hidden layer. Generally speaking, one or two hidden layers have been powerful enough, provided enough neurons in each layer, to approximate a function with any complexity. The adaptation or optimization of MLPs mainly relies on the algorithm of error backpropagation. Its essence is similar to gradient descent algorithm. The rationale of RBF networks for classification is similar to that of MLPs. Furthermore, their architectures are quite similar, too. However, the localization of neuronal transfer functions determines many unique properties of RBF networks. Firstly, there is always a single layer of hidden neurons in RBF networks. In other words, it is comparatively manageable to develop RBF networks. Secondly, there are merely several hidden neurons covering a specific incoming pattern; hence merely those involved neurons will adapt themselves accordingly. Namely it is easier for RBF networks to arrive at their optima than MLPs if the target space is appropriately covered by initial RBF neurons. However, due to the localization of response, more hidden neurons are also necessary for RBF networks at the same time.

5. Simulations

The part of experiments in this chapter was built on a workbench dataset (Fig. 12)., which was excerpted from the recording 207 of the MAD workbench. The different types of arrhythmia ECGs often intertwine together. At the same time, the single group of arrhythmia ECGs often has diversified morphologies, too. The dataset consists of 2 leads of synchronous ECG recordings, namely MLII and V1. There are 6 types of arrhythmia patterns identified by medical experts. All data have been normalized before adaptive modelling in order to suppress physiological signal variability. The feature descriptors, including HBFs, relative wavelet energies, wavelet scale maxima and matching pursuits, were utilized for physiological signal modelling. Those descriptors were then transferred to a subsequent FCM or SOM for adaptive clustering. In addition, the supervised MLP and PNN were taken advantages for physiological signal classification. The performance of all paradigms were evaluated quantitatively.

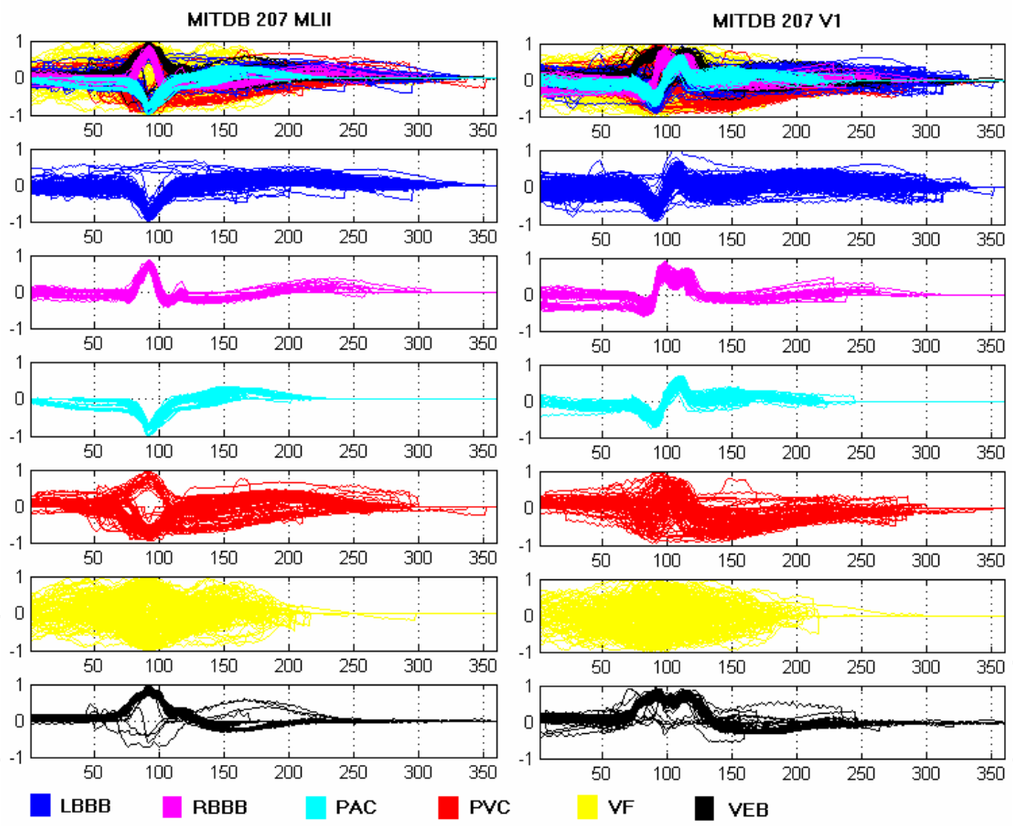

Fig. 12. Selected arrhythmia ECG beats from MAD

The orders of Hermite modeling, relative wavelet energies, wavelet scale maxima and matching pursuits were set as 7, 15, 16 and 7. The subsequent FCM or SOM adapted the input layer in accordance with the incoming patterns, while had a fixed output layer with 12 nodes. In other words, 12 clusters eventually came into being. Note that it is necessary to assign a larger cluster number than the genuine one. In most cases, patterns vary even within a same group. As shown in Fig. 13, the ECG beats are classified in accordance with their abstract model parameters but not the intuitive morphological features any more.

In Fig. 13, the ECG beats within each same cluster have been identified by their canonical annotations. For computerized interpretation, it is desirable to have those within-cluster ECG beats being the same group, for example, the LBBB beats. However, many of them are mixed together in most cases. It degrades the quality of computerized interpretation substantially. Without the priori knowledge on the incoming ECG beats, we have to take those in a cluster as a single type of arrhythmia. We hereby took a strategy of majority voting to evaluate the performance of adaptive clustering quantitatively. As shown in Fig. 13, the majority beat of the first and second clusters is VF (!) while the one of the forth cluster is PVC (V). In other words, the 339 beats of the first two clusters will be taken as VF while the 70 beats in the forth cluster are PVC. Then, based on the following confusion matrix, it is possible to calculate the quantitative accuracy of adaptive clustering.

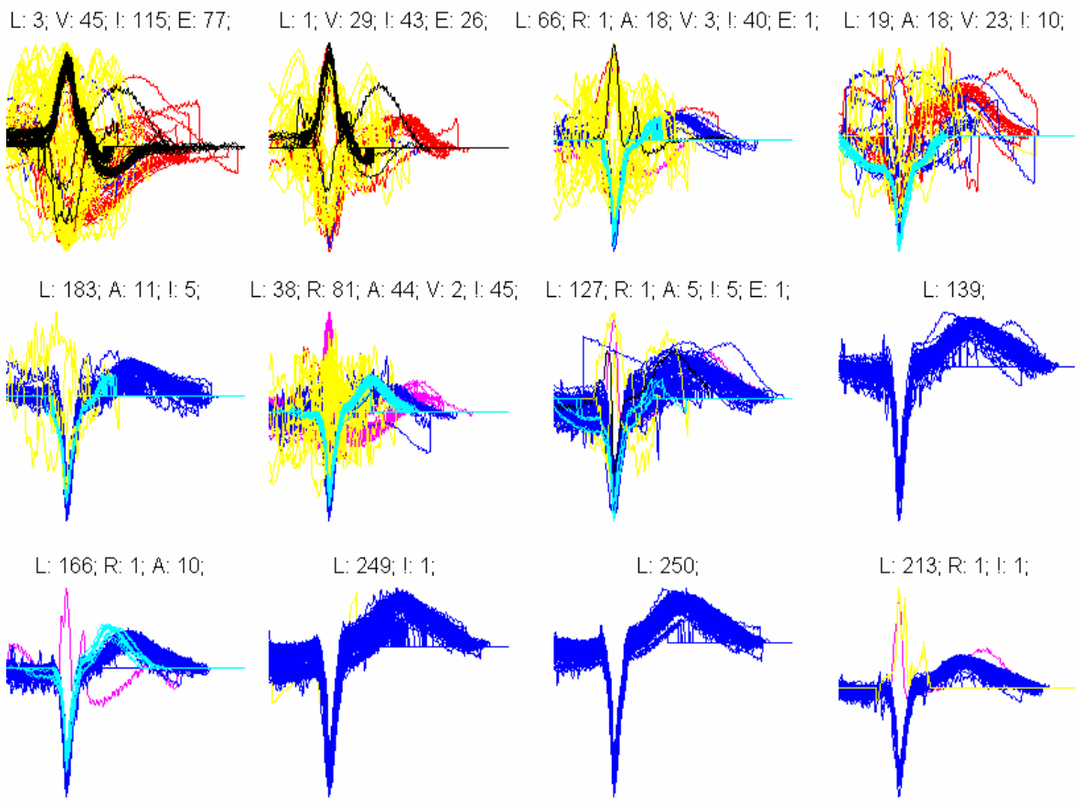

Fig. 13. Adaptive ECG arrhythmia clustering with WSM and SOM

	LBBB	RBBB	APC	PVC	VF	VEB	*total*
LBBB	1393	4	44	3	52	2	1498
RBBB	38	81	44	2	45	0	210
APC	0	0	0	0	0	0	0
PVC	19	0	18	23	10	0	70
VF	4	0	0	74	158	103	339
VEB	0	0	0	0	0	0	0
total	1454	85	106	102	265	105	2117

Table 3. The confusion matrix of adaptive clustering by the system in Fig. 13

The sensitivity *Se* may be defined as (Lagerholm et al., 2000):

$$Se = \frac{\mathrm{TP}}{\mathrm{TP} + \mathrm{FN}}, \tag{17}$$

and the accuracy is based on the quantitative error rate:

$$Error(\%) = \frac{\mathrm{FP} + \mathrm{FN}}{\mathrm{TP} + \mathrm{FP}}, \tag{18}$$

where TP stands for the amount of true positives, FN for false negatives, and FP means false positives. By means of above indices, the performance of various wavelet networks for clustering can be evaluated quantitatively, as listed in the following Table 4.

	TP	FP	FN	*Se*	*Error* (%)
HBF-SOM	1519	598	598	0.718	56.5
HBF-FCM	1560	557	557	0.737	52.6
RWE-SOM	1576	541	541	0.744	51.1
RWE-FCM	1605	512	512	0.758	48.4
WSM-SOM	1655	462	462	0.782	43.6
WSM-FCM	1695	422	422	0.801	39.9
MP-SOM	1574	543	543	0.744	51.3
MP-FCM	1564	553	553	0.739	52.2
PCA-SOM	1627	490	490	0.769	46.3
PCA-FCM	1666	451	451	0.787	42.6

Table 4. Clustering performance comparison of wavelet networks

There are several points worthy of noting in Table 4. The first of all, no any method achieved a good result as expected due to the intrinsic harshness of the selected ECG recording. Among various paradigms of computational intelligence for clustering, the one by WSM is most competitive. In the second aspect, the clustering results of FCM are better than those of SOM, although the improvement is not so much. In the third aspect, FP and FN are same in all cases. No matter FCM or SOM, it attempts to assign an incoming pattern to a specific cluster even though that pattern may be far away from all clusters. Therefore, any inaccurately assigned pattern is both false positive for other clusters and false negative for the right cluster. Finally, it seems that the energy-oriented models (e.g., relative wavelet energies (RWE) and WSM) are better for adaptive clustering than the morphology-oriented ones (e.g., HBFs and matching pursuits (MPs)).

There are six groups of ECG beats with known arrhythmia in Fig. 12, namely LBBB, right bundle branch block beat (RBBB), premature atrial contraction (PAC), premature ventricular contract (PVC), ventricular flutter (VF) wave and ventricular escape beat (VEB). Each group has different number of normalized ECG beats, namely 1454 LBBBs, 85 RBBBs, 106 PACs, 102 PVCs, 265 VFs and 105 VEBs.

In essence, each ECG beat after normalization could be characterized as a 360-dimensional multivariate vector. Obviously it is not a good idea to apply them directly for network interpretation due to the "curse-of-dimensionality" and the inter-dimensional crosstalk. As a consequence, the modelling parameters instead of the original signals were imported for

training and evaluation. It is not only contributive to concise network architecture but also more robust against physiological signal variability (Li et al., 2009).

To train and test the computational paradigms for classification, each group of the dataset was randomly divided into two subgroups with the ratio 0.8:0.2. In other words, 80% ECG beats were utilized to train the classifiers, while the left 20% were reserved for network validation. Such procedure was repeated for five times, hence each computational paradigm was trained and evaluated five times independently. The final performance was based on the averaged recognition rate and classification accuracy. It is hereby possible to estimate the generalization capability of a computational paradigm by means of such "leave-one-out" strategy.

Three types of ANN were implemented and evaluated for supervised classification, that is, a MLP, a PNN and a kNN. Both MLPs and PNNs attempt to approximate the prototype of the specific group of physiological signals with the neurons and associated weights. The category of an incoming pattern is assigned according to the output neuron with maximal response (MLPs) or the winner neuron in competitive learning (PNNs). Their performance has been reported in the following Table 5.

		MLPs	PNNs	*k*NN
HBFs	mean (μ)	19.11	7.42	8.56
	std (σ)	2.29	1.59	1.49
RWE	mean (μ)	19.44	9.13	8.89
	std (σ)	1.58	1.18	0.98
WSM	mean (μ)	17.53	6.9	8.56
	std (σ)	1.23	1.24	1.09
MPs	mean (μ)	26.9	13.9	13.29
	std (σ)	3.21	0.91	1.05

Table 5. Performance evaluation of three types of supervised classifiers

Obviously the PNN classifier performed better than the MLP one in most cases. For instance, no matter by means of which kind of physiological signal modelling, the classification error rates of the MLP classifier range from 17.53% to 26.9%. On the contrary, the worst result of PNN classifier is 13.9% only. Furthermore, the results in Table 5 indicate that, although methodologically simple, kNNs achieved the competitive classification performance for uneven datasets. The classification error rates are comparable to those by PNNs in most cases. As a matter of fact, if with a narrow spread of Gaussian basis functions, a PNN classifier can be in essence considered as a kNN one. Nevertheless, the PNNs are generally with comparatively abstract neurons for category prototyping. In contrast, kNNs rely on the isolated training patterns only. Theoretically speaking, after supervised training, the PNN classifiers with appropriate configuration run faster than the kNN ones.

From the viewpoint of physiological signal modelling, the best performance of recognition and classification should be attributed to WSM. No matter by which kind of supervised classifier, the WSM models always lead to a minimal error rate in comparison with other kind of adaptive models. Note that the energy-oriented modelling strategies, including relative wavelet energies (RWE) and WSM, are inefficient for physiological signal representation. However, they performed well for adaptive clustering and supervised classification. It is exactly opposite to those morphology-oriented modelling schemes, for

example, HBFs and MPs. In summary, the energy-oriented modelling schemes are better than those morphology-oriented ones for computerized recognition and classification.

6. Conclusion

The central idea of this chapter is focused on computerized interpretation of cardiovascular physiological signals, including ECG and ABP waveforms. Both of them are easily accessible by means of contemporary biosensors and transducers. However, their computerized interpretation has to confront the intrinsic variability due to pathophysiological artefacts, instrumental inaccuracy and inconsistent measurement. The techniques based on domain transformation and signal modelling, including RWE, WSM, HBFs and MPs, were elaborated and evaluated carefully in this chapter. In addition, the paradigms of adaptive clustering and supervised classification were introduced for computerized physiological signal interpretation. A few computerized paradigms were carried out by combining them and evaluated on a real-world workbench database. Although intriguing, the results indicate that there is no any prevailing paradigm for computerized interpretation of cardiovascular physiological signals yet. It hereby calls for more sophisticated paradigms, for example, wavelet networks, wavelet SVMs, wavelet ARTMAP, and so on.

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This book by In-Tech publishing helps the reader understand the power of informed decision making by covering a broad range of DSS (Decision Support Systems) applications in the fields of medical, environmental, transport and business. The expertise of the chapter writers spans an equally extensive spectrum of researchers from around the globe including universities in Canada, Mexico, Brazil and the United States, to institutes and universities in Italy, Germany, Poland, France, United Kingdom, Romania, Turkey and Ireland to as far east as Malaysia and Singapore and as far north as Finland. Decision Support Systems are not a new technology but they have evolved and developed with the ever demanding necessity to analyse a large number of options for decision makers (DM) for specific situations, where there is an increasing level of uncertainty about the problem at hand and where there is a high impact relative to the correct decisions to be made. DSS's offer decision makers a more stable solution to solving the semi-structured and unstructured problem. This is exactly what the reader will see in this book.

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