Possibilities of Predicting Arterial Pressure by Means of Heart Rate Variability

Anton Yu Dolganov[a]
Ural Federal University Yekaterinburg, Russian Federation

Keywords: Arterial Pressure, Heart Rate Variability, Machine Learning, Genetic Programming, Regression.

Abstract: The paper shows results of the study which aims to predict values of arterial pressure by means of heart rate variability features. A total list of 64 features was tested, which included features in time and frequency domain, as well as non-linear features. As a means of feature selection, the genetic programming was used. In particular binary encoding was used for generation of features in combinations as well as degree of the polynomial. Data of 50 students-volunteers recorded in sitting position was used. Results of the study suggests that certain heart rate variability features can be used for prediction of the change of arterial pressure. Perspectives and future plans for results improvement were described.

1 INTRODUCTION

Arterial hypertension is one of the most common diseases of the cardiovascular system worldwide. Sharp fluctuations in blood pressure can lead to a deterioration in the patient's condition. It is especially worth noting that the rate of change of pressure has a great influence. Therefore, the task of continuous monitoring of blood pressure becomes extremely important and in demand (WHO, 2018).

Currently used long-term monitoring systems are usually invasive (and can only be carried out under clinical conditions), or intrusive (and do not allow continuous measurements due to the influence of residual occlusion). Therefore, methods of indirect, non-invasive and non-intrusive assessment of blood pressure are becoming more common.

Blood pressure depends on several factors, heart rate is one of them. However, many other variables also affect blood pressure, such as arterial stiffness, blood viscosity, volume of blood pumped into the aorta, microcirculation impedance, etc. Artificial intelligence methods based on using the capabilities of machine learning can help solve this problem. Such an approach allows not only to formalize the description of complex living systems and conduct prognostic analysis, but also to find implicit patterns in the data.

Most of the work in this area comes down to using plethysmogram signals or a combination of plethysmograms with an electrocardiogram, where standard parameters are calculated, such as the arrival time of the pulse, the period of the pulse ejection, the pulse propagation time, and the pulse wave velocity (Anisimov et al., 2014; Kurylyak et al., 2013; Sannino et al., 2015). However, approaches that combine several signals are not practical for everyday use.

At the same time, the possibilities of using only electrocardiogram signals in the task of indirectly assessing blood pressure have not been sufficiently studied. Available works, as a rule, are limited to a rough prediction of the level of pressure (high, normal or low) and do not allow to obtain accurate estimates (Simjanoska et al., 2018, 2019).

In previous works, a study was carried out of the found complexes of significant parameters of heart rate variability to assess the effectiveness of treatment, which showed the consistency of the calculated estimates with blood pressure measurements (Vladimir Kublanov & Dolganov, 2019). This indicates the prospects of using the parameters of heart rate variability signals in the task of indirect estimation of blood pressure.

[a] https://orcid.org/0000-0003-2318-9144

Dolganov, A.
Possibilities of Predicting Arterial Pressure by Means of Heart Rate Variability.
DOI: 10.5220/0009183203480354
In *Proceedings of the 13th International Joint Conference on Biomedical Engineering Systems and Technologies (BIOSTEC 2020) - Volume 4: BIOSIGNALS*, pages 348-354
ISBN: 978-989-758-398-8; ISSN: 2184-4305
Copyright © 2022 by SCITEPRESS – Science and Technology Publications, Lda. All rights reserved

2 MATERIALS AND METHODS

2.1 Biomedical Signals Data

Pilot study was performed in Research Medical and Biological Engineering Centre of High Technologies (Ural Federal University, Russian Federation). A total of 50 students volunteers have performed in the study. Prior to the biomedical signals acquisition the participants were informed of the study paradigm and gave the consent to participate in the study.

The diagram of the study is presented on Figure 1.

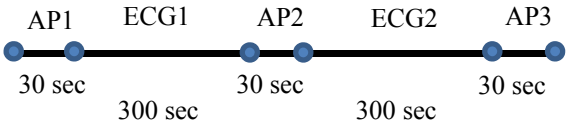

Figure 1: Study Timeline.

All subjects were sitting during the whole Study. Initially, the Arterial Pressure (AP) is measured using a professional tonometer OMRON HEM-907 (Omron Healthcare, Japan). The measurement of AP takes around 30 sec. After that the ElectroCardioGraphy (ECG) signals were registered in the first limb lead by the "Encephalan-131-03" device (manufactured by "Medicom-MTD" company, Russian Federation) for 300 sec. After that the AP is measured again. Follows 300 sec of ECG signals recording. In the end the AP is measured again.

Overall, for each person there were 3 measurements of AP and 2 measurements of ECG signals. The first measurement of ECG is used for Training and Testing, the second measurement is used for the Validation.

The software of "Encephalan-131-03" device allows one to automatically derive the signals of Heart Rate Variability (HRV) from the ECG signals.

2.2 Heart Rate Variability Features

Present work involves list of 64 HRV features, that were in detail described in (Vladimir Kublanov & Dolganov, 2019). Briefly, that list includes commonly used time- and frequency-domain features, non-linear features as well as certain features of wavelet transform. The in-house software in *Python* was used to evaluate these 64 features.

All these features are presented and briefly described below:

Statistical Features

- *M*, the mean value of the *NN* time series;
- *HR*, the Heart Rate, an inverse ratio to the M;
- *SDNN*, the standard deviation of the NN intervals;
- the *skewness* of the dataset;
- the *kurtosis* of the dataset (Zwillinger & Kokoska, 1999);
- *CV*, the coefficient of variation;
- *RMSSD* is the square root of mean of squares of differences between successive elements (Stein et al., 1994);
- *NN*5O, the number of pairs of successive elements that differ by more than 50 ms;
- *pNN*50, is normalized *NN*50 by length;
- *SDSD* is the standard deviation of differences between successive elements (Stein et al., 1994);
- Zero-crossing rate, *ZCR*, the rate of sign-changes. For evaluation of this feature, *M* is substracted from the HRV time-series.

Geometric Features

- M_0, the mode;
- *VR*, the variation range;
- AM_0, the amplitude of the mode.

These three main geometric features comprises following indexes:

- *SI*, the Stress Index
$$SI = AM_0/(2 \cdot M_0 \cdot VR)$$
- *IAB*, the Index of the Autonomic Balance
$$IAB = \mathrm{AM}_0/VR$$
- *ARI*, the Autonomic Rhythm Index
$$ARI = 1/(M_0 \cdot VR)$$
- *IARP*, the Index of Adequate Regulation Processes
$$IARP = AM_0/(2 \cdot M_0 \cdot VR)$$
- Triangular Index, also know as St. George Index (Malik, 1996).

Non-linear Features

The list of nonlinear methods studied in this work includes: Shannon Entropy, Aproximate Entropy (*ApEn*), Sample Entropy (*SampEn*) and Poincare plot features.

Fourier Spectral Features

Spectral analysis is used to quantify periodic processes in the heart rate by the means of the Fourier transform. The main spectral components of the HRV signal are High Frequency – *HF* (0.4 – 0.15 Hz), Low Frequency – *LF* (0.15 – 0.04 Hz), Very Low Frequency – *VLF* (0.04 – 0.003 Hz) (Malik, 1996; Ushakov et al., 2013). Features include spectral power of component, normalized power of component, maximal power and corresponding frequency.

Wavelet Spectral Features

The wavelet transform can be used as an alternative to the Fourier analysis (Addison, 2005). For

evaluation of the continious wavelet transfrom the Gaus wavelet of 8-th order was used (Mallat, 2009). The wavelet transform allows to obtain continious time series, in this case of HF$wt(t)$, $LFwt(t)$ and $VLFwt(t)$ - time series of the *HF*, *LF* and *VLF* spectral components, respectively. The spectral features obtained by the wavelet transform include mean, standard deviation and Shannon Entropy of the wavelet time series.

Moreover, one can study continious function of the *LF/HF* ratio – $(LF/HF)[t]$. In current study the following features of $(LF/HF)[t]$ were used:

- *Nd* - the number of dysfunctions;
- *pNd* - the propotion of the number of dysfunctions divided by the length of the $(LF/HF)[t]$.
- $(LF/HF)_{max}$ the maximal value of dysfunction
- $(LF/HF)_{int}$ the intensity of dysfunction (Egorova et al., 2014).

Prior to the application of genetic programming the features were normalized using z-normalisation.

2.3 Genetic Programming

In the course of the previous study, the genetic programming approach has proven itself to search for significant parameters and select the optimal machine learning method. However, the work was devoted to classification problems. Therefore, during the implementation of this study, solutions will be proposed for the use of genetic programming in regression problems.

For regression task the sklearn library was used. In particular, *LinearRegression* module was used to evaluate the linear regression models. The polynomial models were evaluated using combination of *PolynomialFeatures* and *Pipeline* modules.

The main points that should be determined when using genetic algorithms are the **encoding**, the **initial population**, the **selection criterion**, and the **evolution strategy**.

In this paper, we used the simplest binary encoding. Each “chromosome” consists of 66 genes. For first 64 genes a value of "1" in the chromosome means that a particular HRV feature is included in the combination, a value of "0" means that a particular HRV feature is not included in the combination. Last 2 genes are used to code the degree of Polynomial (from 1 to 5). Empirical evidence had shown that polynomials of higher order were ineffective. Overall each “chromosome” represents list of features in combination and degree of polynomial for a particular combination of features.

As the initial population, it was decided to choose 100 randomly generated chromosomes. It was ensured that first 64 genes contain at least single "1" (there is at least one feature in combination). Additionally, all duplicate chromosomes were removed.

The selection criterion was a minimizing of the following fitness function *f* with the leave-one-out cross validation (LOOCV):

$$f=a*Train+b*Test+c*Validate$$

where *Train* is a term related to a training error (obtained on train using *.score* method on each iteration of LOOCV), *Test* is a term related to a test error (obtained on test point on each iteration of LOOCV), *Validate* is a term related to a validation error (obtained on a validation measurement on each iteration of LOOCV), *a*, *b*, *c* are the weight constants, which are 1, 2, 2 respectfully. Each term consists of median, maximum, minimum and standard deviation of absolute errors.

As a rule, the strategy of evolution is determined by the ratio of the three main genetic operations - copying, crossover and mutation.

In case of copying, the descendant is an exact copy of the ancestor. In our case, 10 representatives of the current generation who have the best ratings by the selection criterion are directly copied to the next generation. In case of crossover, the chromosomes of a child are determined by the interaction between the chromosomes of their parents. In our case, each chromosome is a normalized sum of both parents. 10 representatives of the current generation randomly form 30 pairs of parents, which as a result form 30 descendants with cross chromosomes. Mutations are manifestations of random changes in the chromosome. In our case, the mutation changes the gene to the opposite - “1” to “0” and “0” to “1”, respectively. Each gene on the chromosome has a 5% chance of mutating. In total, 60 mutants obtained from the 10 best representatives of the current generation pass into each subsequent generation. Prior to the further evaluations repeated chromosomes are excluded.

The maximum number of generations in the work is 10. For a greater account of various probabilities, the Genetic algorithm was applied 25 times. Overall diagram of the algorithm is presented on Figure 2.

The algorithm starts with generation of 100 randomly generated chromosomes. After removal of duplicate chromosomes, for remaining chromosomes fitness function *f* is evaluated. All chromosomes are sorted by the value of the *f*. Best 10 chromosomes are used for Copy, Crossover and Mutation operations. As the result, the next generation is formed, and

fitness function *f* is evaluated again. The process of next generation formation and evaluation is repeated for 10 times. The algorithm is repeated 25 times.

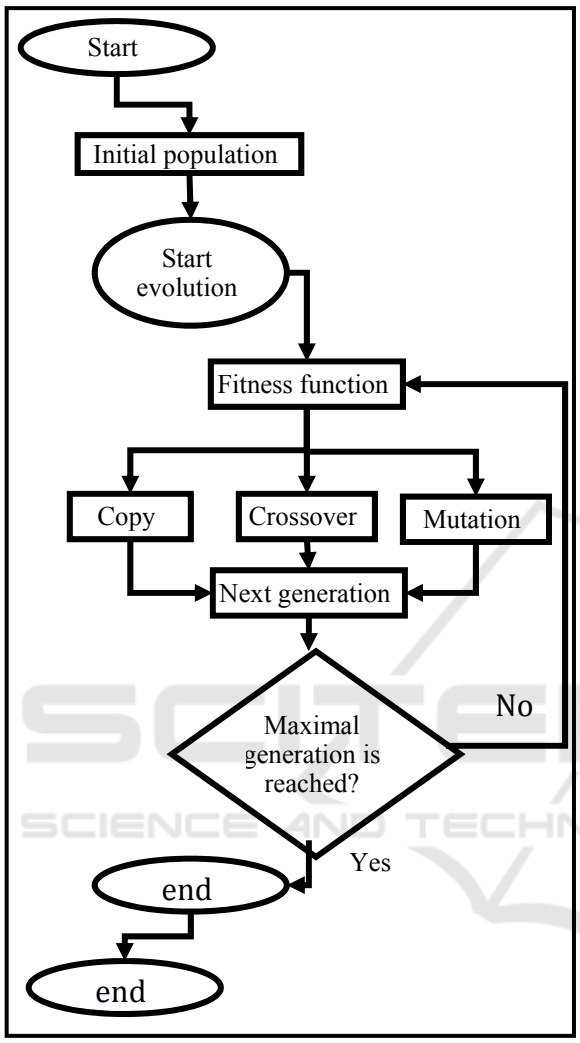

Figure 2: Genetic Programming Diagram (V. Kublanov et al., 2017).

3 RESULTS

At the first step data of AP1 and ECG1 is used for training. Data of AP2 and ECG2 is used for validation. The results of applying the genetic algorithm for all 25 implementations are given in Figures 3 and 4 for Systolic (APS) and Diastolic (APD) AP. Each line represents change of minimal fitness function *f* within a single evolution. Each column represents step of generation within a single evolution. Different lines represent 25 implementations of genetic programming. The value itself is the minimal value of the fitness function *f* for each evolution for each generation.

Relative errors for best representatives among all evolutions are presented in Tables 1 and 2.

4,02	3,82	3,74	3,33	3,33	3,33	3,31	3,30	3,21	3,17
3,85	3,69	3,64	3,57	3,50	3,40	3,24	3,17	3,07	3,07
4,00	3,55	3,52	3,52	3,41	3,25	3,04	3,04	3,04	2,98
4,21	3,84	3,78	3,42	3,20	3,20	3,19	3,16	3,16	3,10
3,77	3,60	3,47	3,27	3,24	3,24	3,24	3,20	3,16	3,13
3,98	3,60	3,35	3,16	3,16	3,16	3,16	3,02	3,02	3,02
4,00	3,59	3,34	3,21	3,18	3,18	3,16	3,12	3,08	3,08
4,14	3,95	3,56	3,49	3,28	3,28	3,08	3,06	3,01	2,99
4,08	3,79	3,71	3,40	3,32	3,32	3,32	3,26	3,26	3,13
3,95	3,95	3,71	3,56	3,54	3,41	3,29	3,24	3,17	3,00
4,10	3,86	3,86	3,74	3,63	3,48	3,43	3,43	3,21	3,11
4,15	3,80	3,80	3,54	3,54	3,38	3,36	3,34	3,34	3,34
3,99	3,85	3,83	3,69	3,69	3,65	3,51	3,51	3,31	3,31
4,07	3,70	3,50	3,28	3,05	3,05	2,97	2,86	2,86	2,86
4,05	3,85	3,76	3,56	3,50	3,31	3,27	3,13	3,11	2,84
4,07	3,77	3,74	3,74	3,58	3,51	3,30	3,30	3,30	3,30
3,98	3,90	3,76	3,55	3,49	3,33	3,29	3,24	3,19	3,09
4,05	3,57	3,57	3,45	3,31	3,23	3,23	3,23	3,22	3,11
4,08	3,94	3,68	3,55	3,55	3,52	3,50	3,37	3,37	3,19
3,97	3,59	3,41	3,40	3,21	3,02	2,94	2,94	2,94	2,82
3,93	3,69	3,49	3,47	3,08	3,08	3,08	3,04	3,02	2,95
4,12	3,80	3,34	3,34	3,34	3,08	3,08	2,89	2,89	2,89
3,68	3,60	3,22	3,22	3,07	3,07	3,07	3,01	3,01	3,00
4,02	3,76	3,47	3,44	3,35	3,31	3,16	3,14	3,10	3,10
3,64	3,57	3,47	3,22	3,20	3,20	3,05	3,02	3,02	3,02

Figure 3: Genetic Programming Results for APS.

Table 1: Errors for APS.

	median	max	min	std
test	8.23%	24.09%	0.62%	6.15%
validate	7.93%	33.97%	0.00%	7.68%

Table 2: Errors for APD.

	median	max	min	std
test	5.60%	26.35%	0.18%	6.71%
validate	6.32%	34.45%	0.01%	7.05%

As it can be seen, the best median results on test data is around 8% for APS and 6% for APD. In addition, alternative variant was considered: to the feature vector values of HRV features of arterial pressure on a previous segment were added. In

particular AP1 and ECG1 were used for prediction of AP2. At the same time validation was performed on data of AP2 and ECG2 for prediction of AP3.

Results of such alternative approach are presented on Figures 5 and 6, and on Tables 3 and 4.

3,34	3,34	3,26	3,26	3,23	3,15	3,01	2,95	2,86	2,74
3,48	3,38	3,27	3,14	3,03	3,03	3,03	3,03	2,92	2,88
3,46	3,24	3,21	3,21	3,18	3,09	3,09	3,09	3,08	3,08
3,50	3,41	3,14	3,14	3,14	3,12	2,90	2,90	2,89	2,87
3,37	3,37	3,29	3,26	3,18	3,18	3,00	2,92	2,92	2,92
3,43	3,24	3,24	3,05	3,05	3,05	3,05	3,05	3,00	3,00
3,42	3,38	3,27	3,27	3,15	2,92	2,92	2,92	2,92	2,92
3,35	3,23	3,13	3,07	2,97	2,92	2,84	2,84	2,84	2,82
3,42	3,29	3,25	3,17	3,10	3,10	3,10	3,10	3,10	3,10
3,30	3,09	3,05	2,91	2,77	2,55	2,55	2,54	2,48	2,48
3,34	3,17	3,16	3,11	3,03	3,03	2,99	2,95	2,86	2,83
3,42	3,32	3,23	3,16	3,14	3,05	3,04	2,99	2,98	2,74
3,30	3,16	3,16	3,16	3,07	3,05	3,05	2,93	2,93	2,93
3,21	3,21	3,21	3,21	3,20	3,19	3,13	3,02	2,90	2,90
3,44	3,34	3,27	3,27	3,13	3,07	3,04	3,04	3,04	2,93
3,44	3,23	3,21	2,75	2,64	2,56	2,53	2,53	2,50	2,50
3,46	3,23	3,07	3,07	3,06	2,96	2,96	2,96	2,92	2,92
3,35	3,26	3,26	2,98	2,98	2,98	2,86	2,82	2,81	2,77
3,43	3,22	3,22	3,21	3,02	2,97	2,97	2,70	2,70	2,70
3,29	3,26	3,20	3,16	3,16	3,14	3,13	3,13	3,07	3,07
3,33	3,22	3,22	3,14	3,14	3,03	3,03	3,01	2,94	2,94
3,37	3,26	3,17	3,10	2,92	2,92	2,72	2,72	2,72	2,71
3,36	3,28	3,18	3,12	3,06	3,03	3,03	3,03	3,02	2,96
3,43	3,33	3,33	3,27	3,27	3,20	3,20	3,17	3,11	3,11
3,33	3,07	3,06	2,86	2,81	2,81	2,81	2,81	2,81	2,81

Figure 4: Genetic Programming Results for APD.

It can be seen that alternative approach can significantly improve results. It can be concluded that task of predicting AP by means of only HRV features can be too ambitious. At the same time the proposed approach can be used to evaluate change in AP after a certain time, when the original "calibration" value is known.

It was noted that the best result was obtained for the linear regression (polynomial of 1st degree). Best combinations consist of around 20 features. Which coupled with 1 degree lessen overtraining.

The results, presented in current work are comparable with ones obtained using Pulsation Wave propagation time (Anisimov et al., 2014). In that work authors reported that for a 1/3 of validation set error was less than 1 mmHg, average error was 9%.

1,16	1,10	1,09	1,05	1,05	1,05	1,05	1,05	1,05	1,05
1,21	1,15	1,13	1,08	1,07	1,05	1,05	1,05	1,04	1,04
1,17	1,12	1,11	1,10	1,05	1,05	1,05	1,05	1,04	1,03
1,21	1,18	1,16	1,14	1,12	1,12	1,12	1,09	1,09	1,05
1,15	1,14	1,11	1,11	1,11	1,08	1,06	1,05	1,03	1,03
1,19	1,18	1,15	1,15	1,15	1,10	1,10	1,10	1,08	1,07
1,12	1,07	1,05	1,02	1,01	1,01	1,01	1,01	1,01	0,99
1,18	1,17	1,16	1,10	1,10	1,10	1,10	1,10	1,08	1,08
1,18	1,16	1,15	1,09	1,07	1,05	1,05	1,05	1,05	1,05
1,19	1,14	1,09	1,08	1,06	1,06	1,06	1,06	1,06	1,03
1,19	1,15	1,11	1,07	1,07	1,06	1,06	1,02	1,02	1,01
1,19	1,16	1,16	1,14	1,12	1,12	1,12	1,10	1,10	1,06
1,20	1,16	1,12	1,12	1,11	1,07	1,07	1,06	1,04	1,04
1,21	1,17	1,13	1,13	1,12	1,12	1,07	1,05	1,05	1,05
1,14	1,10	1,09	1,07	1,07	1,04	1,03	1,01	1,00	1,00
1,22	1,18	1,15	1,11	1,11	1,09	1,06	1,05	1,04	1,02
1,18	1,17	1,13	1,05	1,02	1,00	1,00	0,98	0,98	0,98
1,19	1,13	1,12	1,12	1,03	1,03	1,03	1,03	1,03	1,03
1,20	1,17	1,14	1,11	1,08	1,07	1,06	1,06	1,04	1,04
1,18	1,13	1,10	1,09	1,08	1,08	1,07	1,07	1,02	1,01
1,18	1,15	1,12	1,04	1,02	1,02	1,02	1,02	1,02	1,02
1,19	1,14	1,12	1,12	1,10	1,09	1,08	1,08	1,07	1,02
1,13	1,01	1,01	1,00	1,00	0,99	0,99	0,99	0,99	0,96
1,17	1,15	1,11	1,11	1,09	1,07	1,07	1,07	1,07	1,06
1,23	1,22	1,16	1,12	1,11	1,09	1,04	1,03	1,03	1,03

Figure 5: Alternative Genetic Programming Results for APS.

Table 3: Alternative Errors for APS.

	median	max	min	std
test	2.65%	10.07%	0.06%	2.58%
validate	4.04%	13.77%	0.00%	3.62%

Table 4: Alternative Errors for APD.

	median	max	min	std
test	4.72%	13.12%	0.05%	3.46%
validate	5.91%	21.38%	0.00%	4.84%

Results of the current work are also comparable with results application of genetic algorithms for symbolic regression (Dolganov, 2019). Although additional comparison is required.

1,81	1,67	1,67	1,60	1,57	1,52	1,50	1,48	1,47	1,44
1,81	1,74	1,69	1,60	1,57	1,57	1,56	1,56	1,56	1,53
1,82	1,68	1,60	1,51	1,51	1,51	1,50	1,50	1,48	1,42
1,84	1,78	1,74	1,65	1,49	1,49	1,49	1,49	1,49	1,47
1,90	1,83	1,75	1,66	1,66	1,61	1,59	1,57	1,57	1,52
1,76	1,71	1,63	1,56	1,56	1,56	1,54	1,45	1,45	1,45
1,81	1,77	1,68	1,66	1,58	1,57	1,57	1,56	1,55	1,55
1,78	1,73	1,72	1,57	1,57	1,57	1,57	1,50	1,50	1,50
1,88	1,86	1,82	1,73	1,63	1,63	1,62	1,61	1,58	1,57
1,85	1,77	1,73	1,62	1,60	1,56	1,52	1,52	1,50	1,50
1,87	1,80	1,74	1,62	1,61	1,61	1,59	1,59	1,59	1,59
1,79	1,73	1,61	1,54	1,53	1,52	1,49	1,47	1,47	1,46
1,82	1,79	1,71	1,66	1,66	1,66	1,64	1,64	1,64	1,64
1,84	1,79	1,79	1,59	1,55	1,55	1,55	1,52	1,47	1,47
1,82	1,60	1,60	1,57	1,57	1,56	1,56	1,56	1,53	1,52
1,87	1,72	1,65	1,59	1,58	1,49	1,49	1,48	1,48	1,48
1,74	1,66	1,64	1,59	1,59	1,57	1,57	1,51	1,51	1,47
1,72	1,72	1,70	1,64	1,64	1,63	1,58	1,58	1,58	1,57
1,81	1,77	1,67	1,67	1,60	1,57	1,57	1,57	1,53	1,53
1,85	1,77	1,66	1,61	1,59	1,59	1,57	1,54	1,53	1,51
1,74	1,74	1,67	1,63	1,63	1,59	1,59	1,56	1,54	1,54
1,80	1,69	1,62	1,58	1,55	1,51	1,51	1,51	1,51	1,49
1,73	1,73	1,65	1,59	1,57	1,52	1,52	1,52	1,52	1,52
1,76	1,64	1,64	1,63	1,62	1,60	1,57	1,54	1,54	1,54
1,81	1,68	1,60	1,60	1,53	1,51	1,46	1,45	1,45	1,44

Figure 6: Alternative Genetic Programming Results for APD.

4 DISCUSSION AND CONCLUSIONS

The paper describes investigation testing possibility of the indirect AP measurement by means of HRV features. For such task a pilot study was performed on 50 student-volunteers. The study consisted of simultaneous record of ECG signals and measurements of AP. In the following, HRV time-series were derived from ECG signals by software application. A list of 64 HRV was tested.

Proposed modification of previously used approach of genetic programming (V. Kublanov et al., 2017). Previously the approach was used for the classification task in task of arterial hypertension express-diagnosing. In the paper the approach was modified to be applied in the regression task.

Preliminary results have shown that the error of AP prediction using only features of HRV can be relatively high. At the same time, when we add "calibration" data to the HRV features it is possible to predict change of the AP with relatively low error.

Even though the results, presented in the paper, are relatively low, they show that there is a certain relation between HRV features and AP data. It is worthy to point out that no additional data was used in current study. In particular, no data on gender, anthropomorphic features, age was used. In addition, features of raw ECG signals (morphology, features of P-QRS-T complex) were also not yet tested. Addition of such features might improve the results in the proposed approach.

Among the possible future works directions are application of deep neural networks (Belo et al., 2017) in the task which proved to effective in the biomedical signals synthesis.

REFERENCES

Addison, P. S. (2005). Wavelet transforms and the ECG: A review. *Physiological Measurement*, *26*(5), R155–R199. Scopus. https://doi.org/10.1088/0967-3334/26/5/R01

Anisimov, A. A., Yuldashev, Z. M., & Bibicheva, Yu. G. (2014). Non-occlusion Monitoring of Arterial Pressure Dynamics from Pulsation Wave Propagation Time. *Biomedical Engineering*, *48*(2), 66–69. https://doi.org/10.1007/s10527-014-9420-7

Belo, D., Rodrigues, J., Vaz, J. R., Pezarat-Correia, P., & Gamboa, H. (2017). Biosignals learning and synthesis using deep neural networks. *Biomedical Engineering Online*, *16*(1), 115.

Dolganov, A. (2019). Indirect Measurement of Arterial Pressure by Means of Heart Rate Variability Signals. *2019 Ural Symposium on Biomedical Engineering, Radioelectronics and Information Technology (USBEREIT)*, 156–158. https://doi.org/10.1109/USBEREIT.2019.8736632

Egorova, D. D., Kazakov, Y. E., & Kublanov, V. S. (2014). Principal Components Method for Heart Rate Variability Analysis. *Biomedical Engineering*, *48*(1), 37–41. Scopus. https://doi.org/10.1007/s10527-014-9412-7

Kublanov, V., Dolganov, A., & Gamboa, H. (2017). Genetic programming application for features selection in task of arterial hypertension classification. *Proceedings - 2017 International Multi-Conference on Engineering, Computer and Information Sciences, SIBIRCON 2017*, 561–565. Scopus. https://doi.org/10.1109/SIBIRCON.2017.8109954

Kublanov, Vladimir, & Dolganov, A. (2019). Development of a decision support system for neuro-electrostimulation: Diagnosing disorders of the

cardiovascular system and evaluation of the treatment efficiency. *Applied Soft Computing*, *77*, 329–343. https://doi.org/10.1016/j.asoc.2019.01.032

Kurylyak, Y., Lamonaca, F., & Grimaldi, D. (2013). A Neural Network-based method for continuous blood pressure estimation from a PPG signal. *2013 IEEE International Instrumentation and Measurement Technology Conference (I2MTC)*, 280–283. https://doi.org/10.1109/I2MTC.2013.6555424

Malik, M. (1996). Heart rate variability: Standards of measurement, physiological interpretation, and clinical use. *Circulation*, *93*(5), 1043–1065. Scopus.

Mallat, S. (2009). *A Wavelet Tour of Signal Processing*. Scopus.

Sannino, G., Falco, I. D., & Pietro, G. D. (2015). Indirect Blood Pressure Evaluation by Means of Genetic Programming. *Biomedical Engineering Systems and Technologies*, 75–92. https://doi.org/10.1007/978-3-319-27707-3_6

Simjanoska, M., Gjoreski, M., Bogdanova, A. M., Koteska, B., Gams, M., & Tasič, J. (2018). *ECG-derived Blood Pressure Classification using Complexity Analysis-based Machine Learning*. 282–292. https://www.scitepress.org/PublicationsDetail.aspx?ID=I16nQUpZjDw=&t=1

Simjanoska, M., Papa, G., Seljak, B., & Eftimov, T. (2019). *Comparing Different Settings of Parameters Needed for Pre-processing of ECG Signals used for Blood Pressure Classification*. 62–72. https://www.scitepress.org/PublicationsDetail.aspx?ID=tgp8l7PfXkw=&t=1

Stein, P. K., Bosner, M. S., Kleiger, R. E., & Conger, B. M. (1994). Heart rate variability: A measure of cardiac autonomic tone. *American Heart Journal*, *127*(5), 1376–1381.

Ushakov, I. B., Orlov, O. I., Baevskii, R. M., Bersenev, E. Y., & Chernikova, A. G. (2013). Conception of health: Space-Earth. *Human Physiology*, *39*(2), 115–118. Scopus. https://doi.org/10.1134/S0362119713020175

WHO. (2018). *World health statistics 2018: Monitoring health for the SDGs sustainable development goals*. World Health Organization.

Zwillinger, D., & Kokoska, S. (1999). *CRC standard probability and statistics tables and formulae*. Crc Press.

SCITEPRESS SCIENCE AND TECHNOLOGY PUBLICATIONS