Baština Akademije nauka i umjetnosti Bosne i Hercegovine

The Industry of the Future: From Industry 4.0 to Industry 5.0 – Integration of Humans and Technology: New Technologies

Karabegović, Isak

2025

Akademija nauka i umjetnosti Bosne i Hercegovine

https://bastina.anubih.ba/handle/123456789/837

Preuzeto s Baštine Akademije nauka i umjetnosti Bosne i Hercegovine

https://bastina.anubih.ba/

DOI: 10.5644/PI2025.220.15

Accelerating Innovation in Healthcare Through High-Performance Computing: Applications and Future Perspectives

Adna Softić[*1,2], Sarah Spahić[1], Amra Džuho[1], Ana Lalović[1,3], Adna Ašić[1], Lejla Gurbeta Pokvić[1,3,4]

Abstract: *The healthcare sector is undergoing a profound transformation driven by the convergence of data-intensive biomedical research and advanced computational technologies. High-Performance Computing (HPC) has become a cornerstone infrastructure for addressing the growing complexity, volume and heterogeneity of health data. This paper explores the multifaceted role of HPC in modern healthcare, focusing on its integration with artificial intelligence, medical imaging, genomics and simulation-based modeling. HPC accelerates tasks ranging from genomic sequencing and drug discovery to organ-level simulations and real-time diagnostics, enabling more precise and personalized interventions. Through case studies, we illustrate how HPC supports large-scale cancer genomics, simulates hemodynamic responses in cardiovascular therapies, enhances image-based diagnostic pipelines and facilitates the development of AI models for clinical decision support. In each of these domains, HPC boosts computational throughput and enhances reproducibility, scalability and predictive power. Despite its transformative potential, several challenges hinder widespread adoption, including limited access to infrastructure, lack of parallelized software and the need for secure and interoperable systems. The paper discusses future directions, including cloud-based HPC democratization, exascale computing and federated learning models that ensure data privacy while promoting collaboration. By positioning HPC as a strategic enabler of innovation, this paper underscores its central role in transitioning from reactive to predictive, precision-driven healthcare. The integration of HPC with AI and biomedical data sciences will continue to shape the future of medicine, bringing scalable and explainable solutions to clinical practice worldwide.*

Keywords: *HPC, AI, biomedical data, healthcare*

1. Introduction

The healthcare sector is undergoing a profound digital transformation driven by rapid advances in data acquisition technologies, biomedical research and

[*1]Verlab Research Institute for Biomedical Engineering, Medical Devices and Artificial Intelligence, Sarajevo, Bosnia and Herzegovina
[2]Department of Medical Biotechnologies, University of Siena, Siena, Italy
[3]International Burch University, Sarajevo, Bosnia and Herzegovina
[4]University of Donja Gorica, Podgorica, Montenegro
E-mail: adna@verlabinstitute.com

artificial intelligence (AI). As a result, healthcare professionals and researchers face an unprecedented deluge of data generated from diverse sources such as electronic health records, imaging modalities, wearable devices and omics platforms. Managing, processing and analyzing this complex, high-volume data requires computational capabilities far beyond those of conventional systems. High-Performance Computing (HPC) has emerged as a cornerstone technology that enables timely, accurate and scalable analysis, thereby reshaping the landscape of modern medicine [1-3].

High-Performance Computing refers to the aggregation of computing power, through parallel processing, distributed systems, or specialized architectures, to perform complex computations at high speed and precision. Traditionally used in fields such as physics and climate modeling, HPC has become increasingly integral to biomedical research and clinical practice [4]. Its applications span genomic sequencing, drug discovery, image analysis, predictive modeling and real-time decision support systems, with the common goal of improving patient outcomes through speed, accuracy and personalization. One of the most transformative impacts of HPC in healthcare is seen in genomic medicine [5]. The sequencing of the first human genome, which took over a decade and billions of dollars, can now be accomplished in less than a day thanks to integrated HPC platforms [6]. Similarly, during the COVID-19 pandemic, HPC-enabled simulations of the virus's spike protein binding mechanisms contributed significantly to vaccine development [7]. Beyond genomics, HPC is revolutionizing diagnostics and treatment planning. In cancer research, petabyte-scale data analysis is employed to link tumor composition with genetic profiles, leading to individualized treatment plans. Moreover, AI models powered by HPC systems are used to predict cardiovascular disease risks using retinal image analysis, while supercomputers simulate blood flow dynamics to optimize prosthetic heart valve designs [8,9].

The integration of HPC in clinical workflows is further supported by national and regional HPC competence centers across Europe, including initiatives under the EuroHPC Joint Undertaking and projects such as EuroCC. These centers assist academic and industrial users in leveraging HPC resources for healthcare innovation, demonstrating that democratized access to HPC infrastructure is crucial for translating scientific advances into medical applications. This paper explores the multifaceted applications of HPC in healthcare by presenting examples that illustrate its transformative role. It also discusses the benefits and future directions, emphasizing the need for secure, accessible and interoperable HPC solutions that align with the goals of personalized and precision medicine.

2. The Role of High Performance Computing in Modern Genomics

The field of genomics has witnessed a data explosion, driven by next-generation sequencing (NGS) technologies capable of producing terabytes of data in a single run. Analyzing such complex and voluminous datasets requires computational power far beyond what conventional systems can provide. HPC has emerged as a fundamental enabler of genomic discovery, offering the scalability, speed, and efficiency needed to process, analyze, and interpret massive genomic datasets. Its applications have become particularly prominent in pan-genomics, single-cell transcriptomics and large-scale population sequencing studies. Despite its growing relevance, the integration of HPC into genomics still faces significant challenges, including high data complexity, substantial memory requirements and suboptimal scalability of certain algorithms [10].

The analysis of genomic data demands computationally intensive methods for efficient storage, transmission, and processing which makes HPC an essential tool. Since conventional tools often fall short in handling such complex data, modern HPC infrastructure, including GPUs, TPUs, and multi-core systems, enables the use of machine learning (ML) and deep learning (DL) algorithms in tasks such as gene classification, prediction of functional DNA regions, enhancer-promoter interaction mapping and alternative splicing analysis. This synergy between HPC and ML/DL significantly contributes to the development of precision medicine by allowing therapeutic approaches to be tailored to a patients genetic profile. Beyond enabling the processing of large-scale data, HPC in genomics allows for the application of sophisticated deep learning models that are transforming how genetic information is analyzed and interpreted. For instance, convolutional neural networks (CNNs) are used to classify DNA sequences, while recurrent neural networks (RNNs and LSTMs) model genetic sequences as biological languages. These methods pave the way for novel approaches to predict genomic functional elements, protein localization, and gene expression regulation. They significantly outperform traditional statistical methods and support automated analysis of heterogeneous and high-dimensional omics data [11].

According to Patil et al. (2024), leveraging HPC for AI-driven genomics research, significantly outperforms conventional methods, achieving up to 216× faster data processing, 10% higher accuracy in variant calling and notable improvements in scalability, data security and computational efficiency, highlighting its potential for real-time clinical applications in genomics [12].

The exponential growth of genomic data has created significant computational challenges, particularly in detecting complex genetic interactions such as epistasis. Traditional computing systems are often inadequate for handling the vast number of possible SNP-SNP interactions, which can reach into the billions

even in moderately sized datasets. HPC provides a viable and necessary solution to this challenge, enabling the parallelization of computationally intensive tasks and dramatically reducing analysis time. For instance, an epistatic analysis that would take over a year on a single processor can be completed in a matter of days using hundreds of CPU cores or GPU-based architectures. By leveraging HPC infrastructures through distributed memory models like MPI, shared memory models like OpenMP, or cloud-based solutions, researchers can now conduct exhaustive genomic interaction analyses at scales that were previously impractical, thus accelerating discoveries in genomics [13].
Applications of HPC are particularly critical in population genomics, cancer genomics and single-cell sequencing, where datasets are not only large but also highly multidimensional. Despite the clear advantages, the integration of HPC into genomics research poses challenges such as software optimization for parallel architectures, high memory demands and the need for robust data storage and transfer solutions [12].

3. Simulation and Modeling of Biological Systems Using HPC

HPC has become a tool for simulating and modeling complex biological systems, offering unprecedented capabilities for understanding the dynamic behavior of biological processes across multiple scales. From molecular interactions and protein folding to organ-level physiology and whole-body systems biology, HPC enables researchers to perform highly detailed simulations that would be computationally prohibitive on standard computing platforms. By leveraging parallel processing, large memory capacities and specialized architectures such as GPUs, HPC facilitates the use of advanced methods like molecular dynamics (MD), agent-based modeling and finite element analysis (FEA) to replicate biological phenomena with high temporal and spatial resolution. These simulations are not only critical for hypothesis testing and systems-level understanding but also for predictive modeling in personalized medicine, such as simulating drug interactions with target proteins or modeling tumor growth under different therapeutic strategies. As biological data becomes increasingly complex and voluminous, the integration of HPC with biophysical modeling stands at the forefront of computational biomedicine, enabling virtual experiments that complement and often guide laboratory and clinical research. Simulating complex biological systems (cellular networks or molecular interactions) requires both high precision and substantial computational resources. HPC frameworks like CODES, built upon the ROSS parallel discrete-event simulation engine, enable realistic and scalable modeling of systems involving tens or even hundreds of thousands of nodes. These tools support design space exploration and allow researchers to preserve causal relationships between biological events. By replaying traces from real scientific

applications, such simulations can uncover communication bottlenecks and performance patterns in biological systems, much like evaluating interconnect efficiency in supercomputers. This approach brings new depth to biomedical modeling, where theoretical constructs can be validated through high-fidelity virtual experiments. Ultimately, HPC-based simulations are instrumental in advancing personalized medicine and improving our understanding of disease mechanisms at the systems level [14].

Alam et al. (2016) provide an early evaluation of IBM Blue Gene/Q, emphasizing its efficiency in large-scale parallel computing tasks. These capabilities are crucial in the simulation of biological systems, which often involve highly complex, multi-scale models, from molecular dynamics to whole-organ modeling. The study demonstrates how advanced interconnects, high memory bandwidth, and energy efficiency contribute to scalable performance, which directly supports large-volume simulations, such as protein folding, cardiac electrophysiology, or even population-wide epidemiological modeling [15].

Recent advances in computational immunology emphasize the growing need for HPC to model such complexity accurately. Mechanistic models of immune responses now span multiple scales, molecular pathways, cellular interactions, tissue dynamics, and require the integration of vast, heterogeneous data from genomics, proteomics, and imaging. HPC infrastructures are essential for running agent-based simulations, solving large systems of differential equations, and calibrating models through data assimilation and parameter sweeps. These computational tools allow for in silico exploration of immune responses to infection, vaccination, or cancer, enabling personalized simulations that could eventually inform clinical decisions [16].

4. Medical Imaging and AI-Assisted Diagnosis

Medical imaging plays an important role in modern diagnostics, enabling non-invasive assessment of anatomical and pathological conditions. With the rise of high-resolution modalities such as MRI, CT and PET, the volume and complexity of imaging data have grown exponentially. HPC has become indispensable in this domain, providing the computational infrastructure required to process, analyze and interpret vast amounts of imaging data in real time or near-real time.

One prominent example comes from the National Competence Centre of the Czech Republic, where a remote tissue segmentation tool was developed to support radiologists in clinical environments. The tool is based on a hybrid architecture in which a frontend interface at the hospital enables clinicians to interact with imaging data via open-source 3D Slicer, while the backend executes deep learning-based segmentation models on an HPC cluster using

NVIDIA's Clara Train SDK. Only anonymized data in NIfTI format is transmitted and all communication is encrypted, ensuring compliance with privacy regulations. This setup enables rapid and precise AI-assisted segmentation of organs and lesions, significantly reducing the time and subjectivity associated with manual image analysis [17]. Similarly, the Swiss National Supercomputing Centre has demonstrated how HPC can enhance diagnostics and treatment planning by improving the simulation of blood flow in aortic valve replacement procedures. Through massively parallel simulations involving more than 300 million grid points, researchers were able to model turbulent flow patterns around prosthetic valves with unprecedented accuracy. These insights not only improve the design of implants but also facilitate the development of diagnostic tools, such as the HPC-PREDICT pipeline, which integrates 4D Flow MRI with Kalman filters and deep learning to provide automatically annotated, high-resolution imaging suitable for clinical use [18,19]. These cases highlight a broader trend in diagnostic medicine: the convergence of imaging, AI and HPC to enhance speed, accuracy and personalization. In cardiology, ophthalmology, neurology, genotoxicology and oncology, AI models trained on large imaging datasets are being used for risk stratification, disease detection and prognosis prediction. However, their clinical deployment often depends on the availability of sufficient computing power. Training deep learning models for image segmentation or classification, for instance, typically requires powerful GPUs or cloud-based HPC environments [20-24].

Despite this progress, challenges remain. AI models trained on imaging data can exhibit biases due to non-diverse training sets and performance may degrade in real-world conditions. Furthermore, many healthcare institutions, especially in low- and middle-income regions, lack access to HPC infrastructure or secure data transfer systems needed for integration of these tools. There is a growing need for federated HPC platforms and national competence centers to support hospitals and SMEs in adopting AI-assisted diagnostic solutions.

5. Future Perspectives on the Role of HPC in Healthcare

As biomedical research becomes increasingly data-intensive and model-driven, the role of HPC in healthcare will only grow in importance. Future advances are expected in several key directions. Tighter integration of HPC with artificial intelligence and machine learning will enhance predictive accuracy in diagnostics, drug discovery and treatment personalization. These AI-HPC synergies will enable real-time decision support systems trained on multiscale biomedical data, from omics to imaging and clinical records. Second, the expansion of exascale computing and quantum-inspired architectures will allow researchers to simulate biological processes at unprecedented levels of detail,

enabling breakthroughs in areas such as whole-organ modeling, virtual drug screening, and individualized immune system simulations. Democratizing access to HPC resources through cloud-based platforms will help smaller institutions and developing regions participate in cutting-edge medical innovation. Federated models of computation may further support secure, collaborative research across institutions while preserving data privacy. The ethical and regulatory landscape must evolve alongside these technical advances. As patient-specific modeling and simulation enter clinical workflows, transparency, explainability and reproducibility will become critical to ensure trust and clinical adoption.

6. Conclusion

High-Performance Computing has emerged as an important pillar in the digital transformation of healthcare, enabling the biomedical community to meet the computational demands of modern diagnostics, therapeutics and biomedical research. Across domains, from genomic sequencing and molecular simulations to AI-powered imaging diagnostics and clinical decision support, HPC enables high-resolution, scalable and timely processing of increasingly complex biomedical data. This paper has illustrated how HPC is not merely accelerating data analysis but fundamentally reshaping how healthcare problems are approached and solved. In genomics, HPC has made population-scale sequencing and real-time variant interpretation feasible. In simulation biology, it has transformed our capacity to model multiscale biological systems and test hypotheses in silico. In medical imaging and diagnostics, HPC-powered AI models are bringing precision and speed to disease detection that rivals, and in some cases augments, expert-level decision-making. However, realizing the full potential of HPC in healthcare is contingent on several critical factors. These include addressing disparities in infrastructure access, optimizing software for parallel computing, safeguarding data privacy and ensuring model fairness and clinical interpretability. Equally important is the development of human capital, clinicians, researchers and engineers capable of co-creating next-generation tools using HPC. Looking ahead, the convergence of HPC with AI, cloud platforms and emerging exascale and quantum systems will unlock new paradigms in precision medicine. These technologies will enable not just faster analysis but smarter systems: capable of learning, adapting and predicting across diverse patient populations and data modalities. Cloud-accessible HPC frameworks and federated platforms will be essential for bridging the global equity gap, empowering researchers and clinicians in resource-limited settings to harness the same tools as world-class centers.

7. References

[1] Bajwa, J., Munir, U., Nori, A., & Williams, B. (2021). *Artificial intelligence in healthcare: transforming the practice of medicine. Future healthcare journal, 8(2), e188–e194. https://doi.org/10.7861/fhj.2021-0095*

[2] Stoumpos, A. I., Kitsios, F., & Talias, M. A. (2023). Digital Transformation in Healthcare: Technology Acceptance and Its Applications. International journal of environmental research and public health, 20(4), 3407. https://doi.org/10.3390/ijerph20043407

[3] Wu, Y., Xiang, Y., Ge, J., & Muller, P. (2018). High-Performance Computing for Big Data Processing. Future Generation Computer Systems, 88, 693–695. doi:10.1016/j.future.2018.07.054

[4] Zhu, Y., Lyngaas, I., Meena, M. G., Koran, M. E. I., Malin, B., Moyer, D., Bao, S., Kapadia A., Wang, X., Landman, B., Huo, Y. (2025). Scale-up Unlearnable Examples learning with high-performance computing. doi:10.48550/ARXIV.2501.06080

[5] Wang L.T., and Wang H.M., 2024, Big data in genomics: overcoming challenges through high-performance computing, Computational Molecular Biology, 14(4): 155-162 (doi: 10.5376/cmb.2024.14.0018)

[6] Powers, M. E., Mannthey, K., Sebastian, P., Adsule, S., Kiernan, E., Smith, J. T., Way, J., Shifaw, B., Roazen, D., Narvaez, P. (2022). Deploying genomics workflows on high performance computing (HPC) platforms: storage, memory, and compute considerations. bioRxiv. doi:10.1101/2022.04.05.485833

[7] Amaro, R. E., & Mulholland, A. J. (2020). Biomolecular Simulations in the Time of COVID19, and After. Computing in science & engineering, 22(6), 30–36. https://doi.org/10.1109/MCSE.2020.3024155

[8] Kazimierczak, N., Kazimierczak, W., Serafin, Z., Nowicki, P., Nożewski, J., & Janiszewska-Olszowska, J. (2024). AI in Orthodontics: Revolutionizing Diagnostics and Treatment Planning-A Comprehensive Review. Journal of clinical medicine, 13(2), 344. https://doi.org/10.3390/jcm13020344

[9] Wong, D. Y. L., Lam, M. C., Ran, A., & Cheung, C. Y. (2022). Artificial intelligence in retinal imaging for cardiovascular disease prediction: current trends and future directions. Current opinion in ophthalmology, 33(5), 440–446. https://doi.org/10.1097/ICU.0000000000000886

[10] Jiang, M., Bu, C., Zeng, J. et al. Applications and challenges of high performance computing in genomics. CCF Trans. HPC 3, 344–352 (2021). https://doi.org/10.1007/s42514-021-00081-w

[11] Thakre, V., Vedpathak, S., & Sawarkar, S. (2021). Genomics, high performance computing and machine learning. United International

Journal for Research & Technology, 2(8), 149–154. Retrieved from https://uijrt.com/articles/v2/i8/UIJRTV2I80021.pdf

[12] S. Patil, C. P. Lora and P. A, "Genome Analysis at Scale: Leveraging HPC for AI-Driven Genomics Research," 2024 International Conference on Advances in Computing Research on Science Engineering and Technology (ACROSET), Indore, India, 2024, pp. 1-6, doi: 10.1109/ACROSET62108.2024.10743839.

[13] Alex Upton, Oswaldo Trelles, José Antonio Cornejo-García, James Richard Perkins, Review: High-performance computing to detect epistasis in genome scale data sets, Briefings in Bioinformatics, Volume 17, Issue 3, May 2016, Pages 368–379, https://doi.org/10.1093/bib/bbv058

[14] Mubarak, M., Carothers, C. D., Ross, R. B., & Carns, P. (2016). Enabling parallel simulation of large□scale HPC network systems. IEEE Transactions on Parallel and Distributed Systems, 28(1), 87–100

[15] Alam, M., Abedi, V., Bassaganya-Riera, J., Wendelsdorf, K., Bisset, K., Deng, X., Eubank, S., Hontecillas, R., Hoops, S., & Marathe, M. (2016). Agent-based modeling and high performance computing. In J. Bassaganya-Riera (Ed.), Computational Immunology (pp. 79–111). Academic Press. https://doi.org/10.1016/B978-0-12-803697-6.00006-0

[16] Tikotekar, A., Ong, H., Alam, S., Vallée, G., Naughton, T., Engelmann, C., & Scott, S. L. (2009). Performance comparison of two virtual machine scenarios using an HPC application. Proceedings of the 3rd ACM Workshop on System-Level Virtualization for High Performance Computing - HPCVirt '09. doi:10.1145/1519138.1519143

[17] Koch, M., Arlandini, C., Antonopoulos, G., Baretta, A., Beaujean, P., Bex, G. J., Biancolini, M. E., Celi, S., Costa, E., Drescher, L., Eleftheriadis, V., Fadel, N. A., Fink, A., Galbiati, F., Hatzakis, I., Hompis, G., Lewandowski, N., Memmolo, A., Mensch, C., Obrist, D., … Vignali, E. (2023). HPC+ in the medical field: Overview and current examples. Technology and health care : official journal of the European Society for Engineering and Medicine, 31(4), 1509–1523. https://doi.org/10.3233/THC-229015

[18] De Marinis, D., & Obrist, D. (2021). Data Assimilation by Stochastic Ensemble Kalman Filtering to Enhance Turbulent Cardiovascular Flow Data From Under-Resolved Observations. Frontiers in cardiovascular medicine, 8, 742110. https://doi.org/10.3389/fcvm.2021.742110

[19] Vishnevskiy, V., Walheim, J., Kozerke, S. (2020). Deep variational network for rapid 4D flow MRI reconstruction. Nature Machine Intelligence.; 2(4): 228-235.

[20] Bi, W. L., Hosny, A., Schabath, M. B., Giger, M. L., Birkbak, N. J., Mehrtash, A., Allison, T., Arnaout, O., Abbosh, C., Dunn, I. F., Mak, R. H., Tamimi, R. M., Tempany, C. M., Swanton, C., Hoffmann, U.,

Schwartz, L. H., Gillies, R. J., Huang, R. Y., & Aerts, H. J. W. L. (2019). Artificial intelligence in cancer imaging: Clinical challenges and applications. CA: a cancer journal for clinicians, 69(2), 127–157. https://doi.org/10.3322/caac.21552

[21] Nechita, L. C., Tutunaru, D., Nechita, A., Voipan, A. E., Voipan, D., Tupu, A. E., & Musat, C. L. (2025). AI and Smart Devices in Cardio-Oncology: Advancements in Cardiotoxicity Prediction and Cardiovascular Monitoring. Diagnostics, 15(6), 787. https://doi.org/10.3390/diagnostics15060787

[22] Dey, D., Slomka, P. J., Leeson, P., Comaniciu, D., Shrestha, S., Sengupta, P. P., & Marwick, T. H. (2019). Artificial Intelligence in Cardiovascular Imaging: JACC State-of-the-Art Review. Journal of the American College of Cardiology, 73(11), 1317–1335. https://doi.org/10.1016/j.jacc.2018.12.054

[23] Softić, A., Merdović, N., Dlakić, V., Mrđanović, E., Mahmutović, L., Ler, D., & Pokvić, L. G. (2024). Comet Assay in the Digital Era: A Review of the Use of Artificial Intelligence for the Analysis of DNA Damage Based on the Results of the Comet Assay. 9th European Medical and Biological Engineering Conference (pp. 178–185). Cham: Springer Nature Switzerland. https://doi.org/10.1007/978-3-031-61625-9_20

[24] Pallumeera, M., Giang, J. C., Singh, R., Pracha, N. S., & Makary, M. S. (2025). Evolving and Novel Applications of Artificial Intelligence in Cancer Imaging. Cancers, 17(9), 1510. https://doi.org/10.3390/cancers17091510

LIST OF AUTHORS

Ašić Adna
Verlab Research Institute for Biomedical Engineering, Medical Devices and Artificial Intelligence, 71 000 Sarajevo Bosnia and Herzegovina

Banjanović-Mehmedović Lejla
University of Tuzla
Faculty of Electrical Engineering
Dr. Tihomila Markovića 1,
75000 Tuzla, Bosnia and Hezegovina

Biber Nejra
University of Sarajevo,Faculty of Mechanical Engineering, 71000 Sarajevo, Bosnia and Herzegovina

Bičo Ćar Mirha
University of Sarajevo
School of Economics and Business
Trg oslobođenja 1, 71000 Sarajevo
Bosnia and Herzegovina

Bošnjak Basil
Verlab Research Institute for Biomedical Engineering, Medical Devices and Artificial Intelligence, 71 000 Sarajevo Bosnia and Herzegovina

Bratovcic Amra
University of Tuzla,
Faculty of Technology
UrfetaVejzagića 8, 75000 Tuzla
Bosnia and Hezegovina

Dimitrijevic Sonja
"Mihajlo Pupin" Institute,
Belgrade

Dimitrijević Natalija
University of Belgrade, Faculty of Electrical Engineering,
11000 Belgrade, Serbia

Džuho Amra
Verlab Research Institute for Biomedical Engineering, Medical Devices and Artificial Intelligence, 71 000 Sarajevo Bosnia and Herzegovina

Gurbeta Pokvić Lejla
Research Institute Verlab for Biomedical Engineering, Medical Devices and Artificial Intelligence
Ferhadija 27, 71000 Sarajevo
Bosnia and Herzegovina

Hundur Hiyari Madžida
Verlab Research Institute for Biomedical Engineering, Medical Devices and Artificial Intelligence
71 000 Sarajevo, Bosnia and Herzegovina

Husak Ermin
University of Bihać
Technical Faculty, St. Irfana Ljubijankića
77000 Bihać, Bosnia and Hezegovina

Hozdić Elvis
University of Novo mesto, Faculty of Mechanical Engineering, Novo mesto, SI-8000, Novo mesto,Slovenia

Ilić Jelena
University of Belgrade, Institute Mihajlo Pupin,
11060 Belgrade, Serbia

Karabegović Edina
University of Bihać, Technical Faculty
St. Irfana Ljubijankića, 77000 Bihać
Bosnia and Hezegovina

Karabegović Isak
Academy of Sciences and Arts
of Bosnia and Herzegovina
Bistrik 7, Sarajevo, 71000 Sarajevo Bosnia and Hezegovina

Lalović Ana
Verlab Research Institute for Biomedical Engineering, Medical Devices and Artificial Intelligence, 71 000 Sarajevo
Bosnia and Herzegovina

Lemeš Samir
University of Zenica, Polytechnic Faculty
Fakultetska 1, 72000 Zenica
Bosnia and Herzegovina

Lindov Osman
University of Sarajevo
Faculty of Transport and Communications
Zmaja od Bosne 8, 71000 Sarajevo
Bosnia and Herzegovina

Lukić Dejan
University of Novi Sad,Faculty of Technical Sciences,
21000 Novi Sad, Serbia

Mahmić Mehmed
University of Bihać
Technical Faculty, St. Irfana Ljubijankića
77000 Bihać, Bosnia and Hezegovina

Majstorović D. Vidosav
University of Belgrade
Faculty of Mechanical Engineering
Belgrade, Serbia

Merdović Nejra
Verlab Research Institute for Biomedical Engineering, Medical Devices and Artificial Intelligence
71 000 Sarajevo
Bosnia and Herzegovina

Milošević Mijodrag
University of Novi Sad,Faculty of Technical Sciences,
21000 Novi Sad, Serbia

Milenković Aleksandar
University of Belgrade, Institute Mihajlo Pupin,
11060 Belgrade, Serbia

Muminović J. Adis
University of Sarajevo – Faculty of Mechanical Engineering, Sarajevo, Bosnia and Herzegovina

Spahić Lemana
Research Institute Verlab for Biomedical Engineering, Medical Devices and Artificial Intelligence,
71000 Sarajevo, Bosnia and Herzegovina

Spahić Sarah
Verlab Research Institute for Biomedical Engineering, Medical Devices and Artificial Intelligence, 71 000 Sarajevo
Bosnia and Herzegovina

Stosic Dragan
"Mihajlo Pupin" Institute,
Belgrade

Šahić Elvir
University of Sarajevo
School of Economics and Business
Trg oslobođenja 1, 71000 Sarajevo
Bosnia and Herzegovina

Šestić Munira
University of Sarajevo
School of Economics and Business
Trg oslobođenja 1, 71000 Sarajevo
Bosnia and Herzegovina

Todorovic Filip
TE-KO Kostolac, EPS,
Kostolac

Pašić Mirza
University of Sarajevo,Faculty of Mechanical Engineering, 71000 Sarajevo, Bosnia and Herzegovina

Radončić Amina
Internatinal Burch University
Natural and Medical Sciences
Sarajevo, Bosnia and Herzegovina

Rodić Aleksandar
Mihajlo Pupin Institute
Univeristy of Belgrade
11000 Belograde, Serbia

Simeunović Vladimir
"Mihajlo Pupin" Institute
Computer systems, Belgrade, Serbia

Smajlhodžić-Deljo Merima
Verlab Research Institute for Biomedical Engineering, Medical Devices and Artificial Intelligence, 71 000 Sarajevo
Bosnia and Herzegovina

Softić Adna
Verlab Research Institute for Biomedical Engineering, Medical Devices and Artificial Intelligence, 71 000 Sarajevo
Bosnia and Herzegovina

Vojić Samir
University of Bihać
Technical Faculty, St. Irfana Ljubijankića
77000 Bihać, Bosnia and Hezegovina

Vuković Mladen
Elixir Zorka,
15000 Šabac, Serbia