# OGMIOS: An Intelligent System for Supporting Clinical Decisions in Precision Medicine

Ana León[1,*,†], José Fabián Reyes Román[1,†], Mireia Costa[1,†], Alberto García S.[1,†] and Oscar Pastor[1,†]

[1]*Valencian Research Institute on Artificial Intelligence (VRAIN), Universitat Politècnica de València, Camí de Vera S/N, Valencia, 46022, Spain*

**Abstract**

The goal of precision medicine is to provide each patient with the best diagnosis and treatments possible using their genomics information. Integrating this information together with the clinical data of the patients is the key to establishing Precision Medicine as a reality in clinical practice. Nevertheless, the huge amount of genomics data repositories, their heterogeneity, and their dispersion make this integration a challenge. The objective of this project is to generate a platform for the interpretation of genomics data to help clinical experts in the prevention, diagnosis, and treatment of human disease. This objective is achieved through the alignment of the interests and perspectives of the different work contexts (clinical and genetic) under a common conceptual model that facilitates the standardization and interoperability of data, and the use of Explainable Artificial Intelligence techniques. The project involves a research team from the UPV that provides technological knowledge, a sequencing company that provides genomics knowledge, and three hospitals that provide clinical knowledge. The system is validated in the context of genetic predisposition to pediatric cancer and cardiovascular disease.

**Keywords**

Precision Medicine, Conceptual Modeling, Explainable Artificial Intelligence

## 1. Introduction

Advances in sequencing technologies (Next generation sequencing, NGS) offer the possibility of obtaining individual genomes with increasingly reduced times and costs. Personalized Medicine (PM) is based on the genomics knowledge of each patient in order to select the best diagnosis and design the best treatment for each one. Integrating this information together with the clinical data is the next step to establishing PM as a reality in clinical practice [1, 2]. In this way, we will be able to both anticipate the development of diseases and establish more effective therapies, knowing in detail the genomics origin and the possible response to drugs. All this

*RPE@CAiSE'23: Research Projects Exhibition at the International Conference on Advanced Information Systems Engineering, June 12–16, 2023, Zaragoza, Spain*

*Corresponding author.

†These authors contributed equally.

aleon@vrain.upv.es (A. León); jreyes@pros.upv.es (J. F. R. Román); micossan@vrain.upv.es (M. Costa); algarsi3@pros.upv.es (A. G. S.); opastor@dsic.upv.es (O. Pastor)

0000-0002-0877-7063 (A. León); 0000-0002-9598-1301 (J. F. R. Román); 0000-0002-8614-0914 (M. Costa); 0000-0001-5910-4363 (A. G. S.); 0000-0002-1320-8471 (O. Pastor)

will save costs both in diagnosis and treatment, and will undoubtedly have an impact on the patients' quality of life. This impact can be summarized in the following points:

1. Better understanding of the development of the disease.
2. Direct patient care:
    a) Adaptation of medical treatment avoiding the adverse effects of the application of therapies that may not be appropriate for the type of disease presented.
    b) Less treatment-related toxicity, to find out if there is a greater susceptibility of the patient to presenting them after some chemo-therapies.
    c) Adaptation of surgical treatment.
    d) Correct selection of donors (e.g., for transplant in leukemia).
3. Family genetic advice.
4. Ability to provide more detailed information about the forecast.
5. Detection of associated problems that may require early intervention.
6. Help to cope with the psychological burden of the diagnosis.
7. Help in decision-making for other subjects and families with the same genetic profile.
8. Make it possible to discharge family members who are not affected and who are not carriers of the variant considered related to the disease, avoiding unnecessary follow-up and psychological pressure.
9. Provide updated knowledge in accordance with new research and evidence that is emerging.

In this process, the participation of three fundamental actors is necessary:

- An advanced sequencing service that performs the processing of the samples and the initial study in accordance with the highest quality standards associated with the processing of this type of information.
- Professional experts in data science who provide the necessary knowledge to manage and integrate all the information generated through a data ecosystem that allows standardization and interoperability.
- Clinical experts with the ability to interpret the patient's genetic and clinical information, and generate new knowledge.

The objective of this project is to generate a platform (OGMIOS) for the interpretation of genomics data to help clinical experts in the prevention, diagnosis, and treatment of the disease. To achieve the main objective of this project, it is required the use of advanced Explainable Artificial Intelligence (XAI) techniques [3, 4, 5] that, based on conceptual models [6, 7], allow to determine the origin of the decisions made in each context and thus facilitate the data analysis process. Specifically, the platform will be developed for the study of genetic predisposition to pediatric cancer and cardiovascular diseases (familial heart disease with risk of sudden death), generating a basic infrastructure that, beyond the project, aspires to be extended to other diseases and contexts. The project is financed by the Valencian Innovation Agency and Innovation, started on July 2021, and is expected to be finished by September 2023.

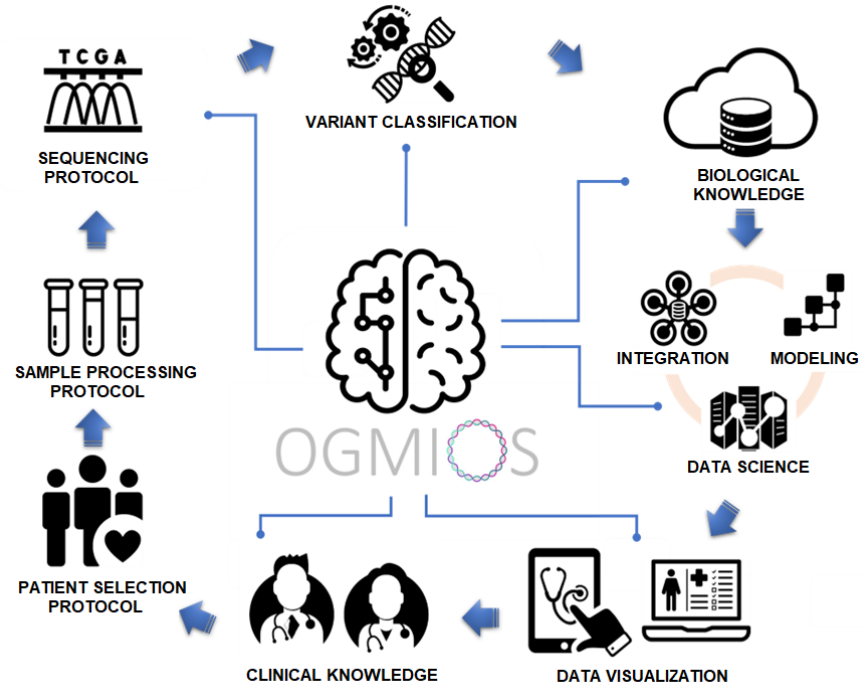


**Figure 1:** Functional Architecture of the OGMIOS Platform.

## 2. Project Objectives and Tangible Outputs

To achieve the main objective of the project, our team integrates leading researchers in Artificial Intelligence from the Polytechnic University of Valencia (UPV), medical services from the most important hospitals in the Valencian Community (La Fe, Clínico and Alicante) and a leading company in its sector (Bionos Biotech). This objective will be achieved through the design and development of an intelligent platform, aligning the interests and perspectives of the different work contexts (clinical and genetic) under a common conceptual model that facilitates data standardization and interoperability (see Fig. 1).

Through the design and development of the platform, the project provides the following outputs:

- An automated process of interpretation and classification of variants based on current standards used by the scientific community.
- An intelligent analytical support that, using Data Science and Artificial Intelligence technologies, allows scientific evidence to be compared with clinical data to accurately identify those variants directly involved in the development of the symptoms presented by a patient.
- User interaction mechanisms that guide the entire diagnostic process and facilitate decision-making.

To this end, the following milestones are established:

- An ontological characterization of the clinical/genomics domain.
- Definition of the required protocols to include the patients that will validate the platform results.
- Definition of a systematic process for the management and analysis of genomics data.
- Design and development of the data analysis platform.

As a final result of the project, there will be a technological platform, which will allow the integration and analysis of clinical and sequencing data obtained from different groups of patients affected by any of the phenotypes to be studied (pediatric cancer and cardiovascular disease). Through this platform, it will be possible for the research groups to analyze the stored information, solve the pertinent knowledge questions, and generate valuable knowledge for the different groups of patients. Once validated, the platform can be adapted to other clinical domains (exploration of different diseases).

## 3. Relevance for CAiSE

This project is aligned with the following CAiSE topics:

- IS for healthcare: This project is focused on developing a platform expected to have effects and impacts on healthcare procedures, work practices, and treatment outcomes. This topic is currently gaining importance for the scientific community due to the improvement of diagnostic methodologies and the vast amount of data that current biomedical devices are generating. With this project, we introduce the best practices for developing sound Information Systems to a new domain of knowledge with a high impact on society.
- Conceptual modeling, languages, and design: The core of this project is based on the application of conceptual modeling to the different stages of its design and development, from the modeling of the business process to the requirements analysis and the representation of the domain knowledge. Following a model driven-development process, the platform is prepared to evolve by adding new functionality and allowing the management of new knowledge guaranteeing the quality of the data.
- Artificial Intelligence and Machine Learning: Artificial Intelligence is a trending technology to automate and optimize the analysis of genomics and clinical data. Nevertheless, AI solutions are accepted to be a black box. This raises concerns, and people have become skeptical about how AI technologies can improve human decision-making. To reduce uncertainties, more transparency is required so that resulting decisions are explainable. This is why an Explainable Artificial Intelligence (XAI) approach has been followed to guide the data analysis in this project.

## 4. Current Project Status

The project is currently in its final phase, where the different experts involved are validating the results of the platform in two fundamental aspects:

1. Evaluation of the functionality of the data collection platform through a systematic process of testing and test cases.
2. Evaluation of the precision of the results derived from the variant classification process through a series of comparative studies with previously obtained results.

This validation process allows the platform to be improved through a series of iterations with the experts. Preliminary results have been published in:

- García, A., León Palacio, A., Reyes Román, J. F., Casamayor, J. C., and Pastor, O. (2021). A Conceptual Model-Based Approach to Improve the Representation and Management of Omics Data in Precision Medicine. IEEE Access, 9, 154071-154085. DOI: 10.1109/ACCESS.2021.3128757.
- León Palacio, A., García, A., and Pastor, O. (2022). An Advanced Search System to Manage SARS-CoV-2 and COVID-19 Data Using a Model-Driven Development Approach. IEEE Access. DOI: 10.1109/ACCESS.2022.3169268.
- García S, A. et al (2021, April). CitrusGenome: Applying User Centered Design for Evaluating the Usability of Genomic User Interfaces. In International Conference on Evaluation of Novel Approaches to Software Engineering (pp. 213-240). Springer, Cham. DOI: 10.1007/978-3-030-96648-5_10.

## Acknowledgments

We wish to thank the IIS La Fe, INCLIVA, ISABIAL, and BIONOS for their huge contribution to this project and their willingness to help. This work was supported by the Valencian Innovation Agency and Innovation through the OGMIOS project (INNEST/2021/57), by the Spanish Ministry of Universities and the Universitat Politècnica de València under the Margarita Salas Next Generation EU grant, and co-financed with ERDF and the European Union Next Generation EU/PRTR.

## References

[1] K. Lu, M. Wood, American society of clinical oncology expert statement: Collection and use of a cancer family history for oncology providers, Journal of clinical oncology 32 (2014) 833–841.
[2] C. Kesserwan, L. F. Ross, A. Bradbury, K. Nichols, The advantages and challenges of testing children for heritable predisposition to cancer, Am Soc Clin Oncol Educ Book 35 (2016) 251–269.
[3] W. Samek, Explainable ai: interpreting, explaining and visualizing deep learning, Springer Nature 11700 (2019).
[4] D. G. et al., Xai—explainable artificial intelligence, Science Robotics 4 (2019).
[5] S. Spreeuwenberg, AIX: Artificial Intelligence needs explanation: Why and how transparency increases the success of AI solutions, Amsterdam: LibRT: the Lab for Intelligent Business Rules Technology, 2019.

[6] A. Olivé, Conceptual Modeling of Information Systems, Springer Berlin Heidelberg, 2007.
[7] O. Pastor, Conceptual modeling of life: Beyond the homo sapiens, in: C. Springer (Ed.), Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics), 2016, pp. 18–31.