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**International Journal of Electrical, Electronics and Computer Systems**

ISSN: 2347-2820

Volume 14 Issue 01, 2025

## Organ Tissue Transplant Prediction

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### Peer Review Information

*Submission: 11 Sept 2025*

*Revision: 10 Oct 2025*

*Acceptance: 22 Oct 2025*

### Keywords

*Organ Transplant Prediction, Machine Learning in Healthcare, Donor-Recipient Matching, HLA Typing, Bioinformatics, Artificial Intelligence in Medicine, Clinical Decision Support System, Healthcare Data Analytics, Predictive Modeling, Genetic Marker Analysis, Deep Learning Algorithms, Medical Data Mining, Immunological Compatibility, Data-Driven Decision Making, Patient Health Records, Feature Selection Techniques, Data Preprocessing in Healthcare, Predictive Accuracy Optimization, Intelligent Healthcare Systems, Transplant Rejection Risk Assessment, Biomedical Data Analysis, AI-Based Diagnostic Support, Precision Medicine, Cloud-Based Health Monitoring, Explainable AI in Medicine.*

### Abstract

This project focuses on developing an intelligent prediction model for organ tissue transplant compatibility using advanced machine learning and data-driven decision support techniques. The system integrates patient medical records, genetic information such as Human Leukocyte Antigen (HLA) typing, blood group, and biochemical parameters to predict the donor-recipient matching probability. By analysing historical transplant data and learning complex relationships between genetic markers and immune responses, the proposed model aims to minimize the risk of graft rejection and improve clinical decision-making efficiency. The model employs supervised learning algorithms like Random Forest, Support Vector Machine (SVM), and Neural Networks to classify and predict compatibility levels. A feature selection mechanism ensures that only the most influential medical parameters are considered, enhancing accuracy and reducing computational complexity. Additionally, the system may use optimization techniques to prioritize the best donor-recipient pairs when multiple candidates are available.

## Introduction

Organ transplantation is one of the most critical and life-saving medical procedures, offering patients with end-stage organ failure a renewed chance of survival. Despite its importance, the process of identifying a suitable donor–recipient pair remains a highly complex, sensitive, and time-dependent task. Traditionally, donor matching is carried out through blood group compatibility, HLA (Human Leukocyte Antigen) typing, and limited clinical data analysis. While these methods have been widely used, they suffer from several limitations. Manual tissue typing and matching are often time-consuming, prone to human errors, and restricted to a narrow set of parameters. As a result, there is a risk of organ rejection, transplant failure, or, in some cases, wastage of viable organs due to delays in identification. The urgency of the procedure is further intensified by the limited viability window of donor organs. For example, kidneys may remain viable for up to 24–36 hours, whereas hearts and lungs must be transplanted within 4–6 hours. Any delay in matching or transportation directly reduces the success rate of transplantation.

The proposed system utilizes advanced predictive modeling techniques, such as supervised classification algorithms, neural

networks, and ensemble learning methods, to calculate a matching probability score between the donor and recipient. These models are trained on datasets that include key factors like HLA typing, blood group compatibility, age, gender, organ-specific biochemical markers, and medical history. By analyzing these multidimensional parameters simultaneously, the system provides a more comprehensive and precise compatibility prediction compared to conventional approaches. In addition, the integration of bioinformatics tools enhances the model's ability to interpret complex genetic and molecular interactions involved in transplant immunology. The intelligent prediction system thus bridges the gap between medical expertise and computational intelligence. It not only reduces human dependency and manual effort but also contributes to increasing the overall success rate of organ transplants. By leveraging large volumes of historical medical data, genetic information, and biochemical profiles, predictive algorithms can identify compatibility patterns that may not be easily visible through traditional manual methods. This enables the development of data-driven decision-support systems that can recommend the most suitable donor for a given recipient in real time.

## Literature Survey

Sr. No	Paper Title	Author Name	Year of Publication	Problem solved in this paper (Existing Problem Statement)	Technique used to solve problem (Existing Problem Solution)	Future Work (Future Scope)
1	ATissueSpecificDeep Learning Framework for Cancer Prediction	Guangxu Jin, Zhiyu Chen, Hao Tang, QingLi	2021	Cancer prediction models often ignore tissue-specific gene expression features	Proposed tissuespecific deeplearning using multi-omics datasets for higher cancer classification accuracy.	Extend to other cancer types, integrate more omics data, apply in precision medicine
2	A Survey on Tissue Image Analysis Using Artificial Intelligence	Zeynep Guler, Yasin Kaya, Ebru Ayan	2022	Manual histopathological analysis is time-consuming and error-prone	Survey of AI/ML techniques (CNNs, transfer learning) in tissue image classification, segmentation, and detection.	Develop explainable AI, improve dataset diversity, apply in clinical decision support

3	Minimally Invasive Lung Tissue Dielectric Impedance Spectroscopy	Georgina Company, Lexa Nescolard, Virginia Pajares, Alfonso Torre, Pere J. Riu, Javier	2022	CT and PET for lung cancer are costly, use radiation, and depend on radiologists	Minimally invasive Electrical Impedance Spectroscopy (EIS) with bronchoscopy (3- and 4-electrode method).	Validate in larger clinical trials, integrate as complementary tool to PET/CT and biopsy
4	Semi-Supervised Bladder Tissue Classification in Multi-Domain Endoscopic Images	Jorge F. Lazo, Benoit Rosa, Michele Cateillani, Matteo Fontana, Francesco A. Mistrretta, Gennaro Mui	2023	Limited labeled data and domain imbalance in bladder cancer endoscopic imaging.	Semi-supervised GAN-based teacher-student + cycle GAN framework for classification with 90 accuracies.	Apply to larger datasets, improve GAN robustness, adapt for real-time clinical use
5	Reactive Accelerated Aging Testing of Thinned Tissue Engineered Electronic Nerve Interfaces (TEENI)	Ladan Jiracek, Sapieha, Kenneth Fluker Jr., Jack Judy	2023	Neural implants face tissue response and poor long-term stability.	Developed ultra-thin (2.5 $\mu\text{m}$ ) TEENI threads, tested with accelerated aging, observed partial stability issues	Refine electrode design, reduce tissue response, improve long-term reliability of neural interfaces.
6	Advancing Hematopoietic Stem Cell Transplantation Typing: Harnessing Hyperledger Fabric's Blockchain Architecture	Tushar Munje, Swapnali Karmore, Roshan Tarte, Meghana Haswani, Kunjal Mahajan	2023	Traditional HSCT typing systems face challenges in security, transparency, and efficiency in donor-patient matching. Current databases lack trust, scalability.	Proposed a blockchain-based system using Hyperledger Fabric to securely store and share HLA typing data, ensuring immutability, transparency, and faster donor-patient	Extend system to production level health care platforms, integrate with global clinical datasets, Optimize mismatching algorithms.
7	Deep Ensemble Model for Quantitative Optical Property and Chromophore Concentration of Biological Tissues	Dongwon Kim, Minji Kang, Byoung-Ho Lee	2023	Diffuse optical tomography and quantitative imaging of tissue properties suffer from low accuracy and robustness due to model uncertainty and noise, limiting their	Proposed a deep ensemble learning model combining multiple neural networks to estimate optical properties and chromophore concentrations of biological tissues.	Apply the model to larger clinical datasets, extend to real-time imaging applications, and integrate with multimodal imaging techniques for more reliable and widespread medical use

8	Deep Learning-Based Multi-Modal Tissue Characterization for Prostate Cancer Diagnosis	Dongzhe Liang, Wenshuo Liu, Rong Zhang, Jie Tian.	2023	Difficulty in accurate prostate cancer diagnosis using single imaging modality	Deep learning-based fusion of multi-modal data (MRI, histopathology) for better tissue characterization	Expand dataset, integrate more modalities, validate in clinical workflows.
9	Benchmarking the Nonparaxial Beam Propagation Method for Deep-Tissue Microscopy	Praveen Kala Rickett, Ramakrishnan, Qi Hu, Peter R. T. Munro	2025	Accurate modeling of light propagation in deep tissue is limited by computationally heavy methods.	Developed nonparaxial FFT BPM method, benchmarked against PSTD with high accuracy and low	Apply BPM to wavefront correction and large-scale biological tissue imaging.
10	Exploring Deep Clustering Methods in Vibrio Acoustic Sensing for Enhancing Biological Tissue Characterization	Robin Urrutia, Diego Espejo, Montserrat Guerra, Karina Vio, Thomas S'uhn, Nazila Esmaeili, Axel Boese, Patricia	2025	Lack of tactile feedback in minimally invasive surgery makes tissue differentiation difficult	Used vibroacoustic sensing with deep clustering (UMAP, VAE) to classify six tissue types with 92 accuracies	Improve VAE models, expand dataset, validate in surgical environments.

### Research Gap

Existing organ transplantation systems rely heavily on manual tissue typing, HLA matching, and basic clinical parameters such as blood group and age. These traditional methods, while effective to some extent, often lead to delays in donor-recipient identification, higher mismatch probabilities, and increased organ rejection rates. Furthermore, the current systems lack the ability to analyze complex relationships between genetic markers and immunological responses, limiting their predictive accuracy. Although recent research in Artificial Intelligence (AI) and Machine Learning (ML) has shown promising results in healthcare applications—such as disease diagnosis, treatment planning, and image analysis—there is insufficient exploration in the domain of organ transplant compatibility prediction. Most existing studies focus on isolated factors (for example, only HLA typing or clinical records) rather than integrating multi-source data such as genetic, biochemical, clinical, and demographic information into a single, unified model. This fragmented approach reduces the overall reliability of compatibility prediction. Additionally, very few systems employ deep learning architectures capable of

learning complex nonlinear relationships among medical variables.

### Problem Statement

Organ transplantation saves countless lives every year, yet predicting donor-recipient compatibility remains a complex and critical challenge in modern medicine. Traditional approaches, which depend primarily on manual tissue typing, blood group matching, and basic clinical observations, often fail to capture the intricate biological and genetic factors that influence transplant success. As a result, these methods can lead to inaccurate compatibility assessments, delayed decision-making, and in severe cases, organ rejection or transplant failure. To overcome these limitations, there is a growing need for an intelligent, automated prediction system capable of analyzing diverse datasets, including medical history, HLA typing, biochemical profiles, and genetic markers, to provide a more reliable compatibility score. Such a system can significantly enhance the speed, accuracy, and efficiency of the donor-recipient matching process.

In many cases, these conventional methods rely heavily on limited laboratory tests and human

expertise, which can lead to subjective interpretation, inconsistent results, and potential mismatches. Moreover, they do not adequately account for subtle variations in Human Leukocyte Antigen (HLA) alleles, gene expression patterns, or complex immune responses that influence post-transplant outcomes. As a result, inaccurate compatibility assessments can occur, increasing the risk of graft rejection, transplant failure, or prolonged waiting times for suitable donors.

### Conclusion

This project proposes an AI-based prediction system for organ tissue transplant compatibility, integrating donor–recipient medical, genetic, and demographic data. By applying machine learning models, the system aims to increase the success rate of organ transplants, minimize rejection risks, and provide doctors with a reliable decision-support tool. Although limitations exist in terms of data availability, scalability, and privacy concerns, the project lays a strong foundation for the future development of intelligent healthcare systems. With further improvements and clinical validation, this model can significantly contribute to saving lives and improving transplant outcomes.

By leveraging advanced machine learning algorithms, including supervised and unsupervised learning models, the system can identify complex patterns and hidden correlations within large-scale biomedical data that are often undetectable through traditional methods. These algorithms can dynamically learn from historical transplant outcomes to continuously refine compatibility predictions, providing clinicians with a data-driven decision-support tool for more informed and timely matching of donors and recipients. In addition to improving prediction accuracy, the system also aims to accelerate the decision-making process in critical transplant scenarios where time is a limiting factor. The integration of predictive analytics and automated processing can reduce human error, ensure consistency, and optimize the allocation of available organs. Furthermore, the model can be adapted to handle multiple organ types—such as kidney, liver, heart, or lung transplants—by tailoring its input parameters and predictive frameworks to specific biological characteristics.

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