Syuzanna Matevosyan Research Portfolio

Master Student in Erasmus Mundus in Biomedical Engineering

This research portfolio showcases my research achievements and projects in the areas of Biomedical Engineering, done during my studies and work experiences. Portfolio includes Articles, Projects or Laboratory reports pertaining to topics such as Signal Processing, Image processing, Biomechanics and Bioinformatics.

INTERESTS

- Signal Processing
- Image Processing
- AR/VR
- Biomechanics

PERSONAL INFORMATION

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CONFERENCE POSTER ON EUROPEAN SYMPOSIA ON BIOMEDICAL ENGINEERING (ESBME)

Development of an EMG Signal Acquisition System for Hand Gesture Classification

Development of an EMG Signal Acquisition System for Hand Gesture Classification

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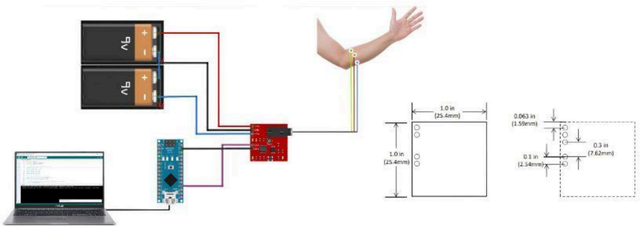
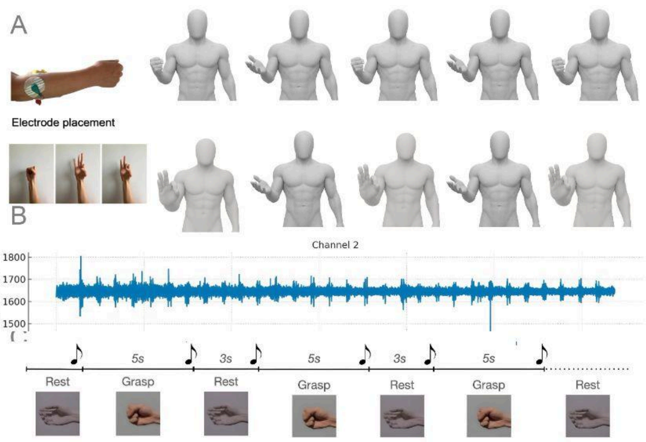
BACKGROUND

Electromyography (EMG) records muscle activity and is widely used for diagnostics, rehabilitation, and controlling prosthetic limbs. Myoelectric prostheses use EMG signals to enable natural hand movement, but accurate movement classification remains challenging due to signal variability and noise. Improving EMG signal acquisition and analysis is essential for developing more effective, user-friendly prosthetic devices. This work Developed a three-channel EMG signal acquisition system with three electrodes and evaluated various machine learning algorithms for classifying three distinct hand movements. SVM with RBF kernel achieved up to 72.6% classification accuracy; increasing electrode channels is recommended for improved precision

METHOD

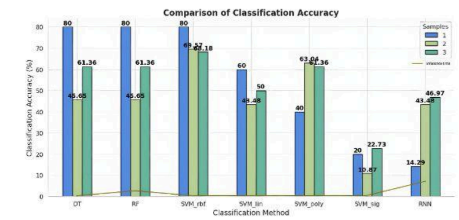


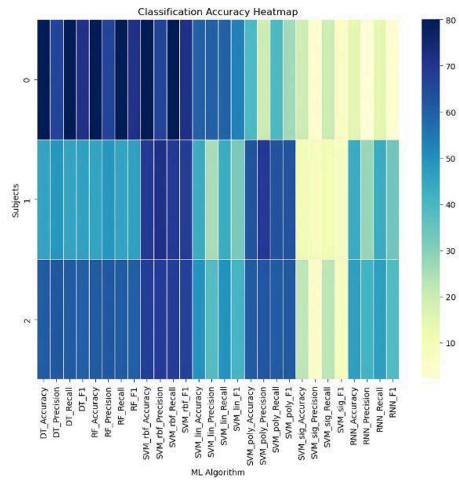
The schematic view of proposed EMG acquisition system.



Three healthy volunteers participated in the study. Surface electrodes were placed on the forearm, and EMG signals were recorded while each subject performed three different hand movements (finger flexion patterns). Each movement was repeated 30 times, with 3s. rest periods in between, and the signals were digitized and labeled for further analysis

RESULTS





Classification accuracy for distinguishing hand movements using various algorithms (SVM, Random Forest, Decision Tree) across three subjects.

CONCLUSIONS

The developed EMG system with three electrodes can classify basic hand movements using machine learning, with SVM (RBF) performing best (72.6%). However, classification accuracy varied between subjects. Increasing the number of electrodes and individual model tuning are needed for better performance in prosthetic control.

REFERENCES

1. Latour, D. Advances in Upper Extremity Prosthetic Technology: Rehabilitation and the Interprofessional Team. Current Physical Medicine and Rehabilitation Reports, 2022
2. Toledo-Pérez, D. C., Rodríguez-Reséndiz, J., Gómez-Loenzo, R. A., & Jauregui-Correa, J. C. 2019. Support Vector Machine-Based EMG Signal Classification Techniques: A Review. Applied Sciences, 2019
3. S. Pancholi and R. Agarwal, “Development of low cost EMG data acquisition system for arm activities recognition,” 2016

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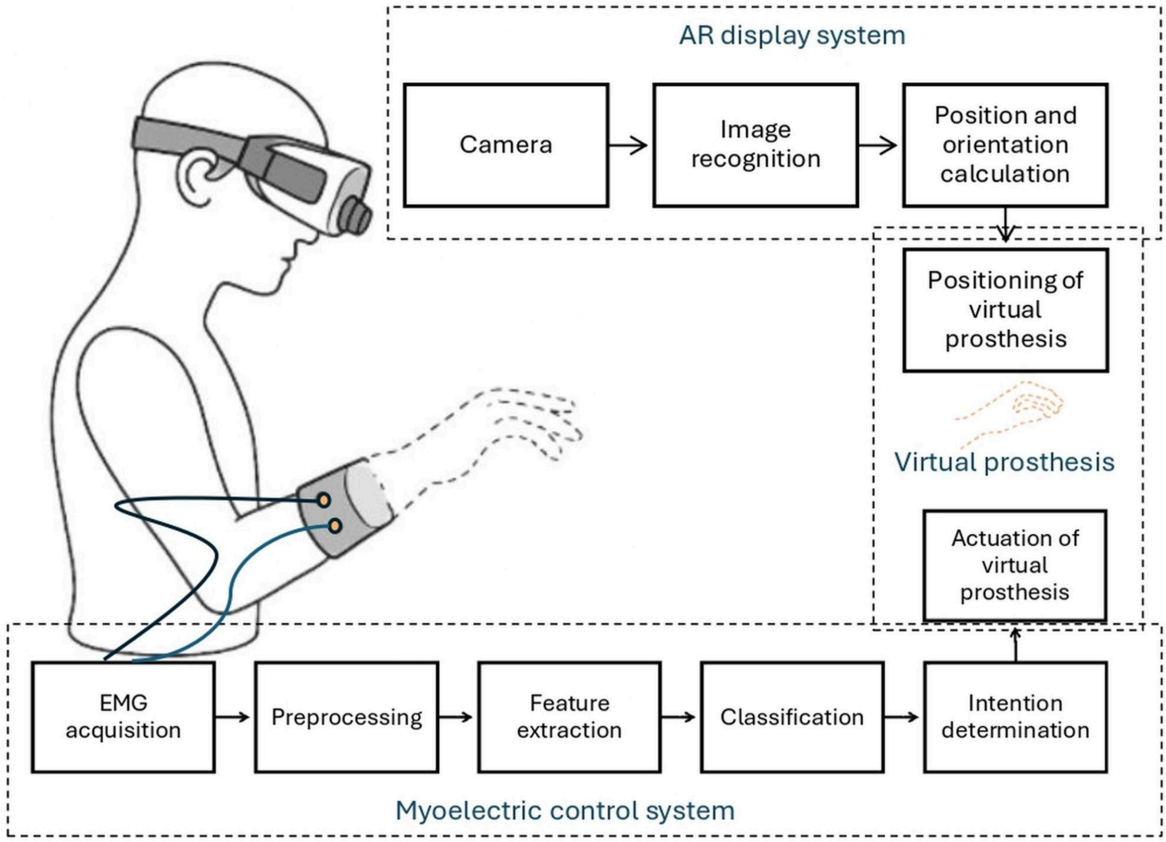
Augmented Reality Based System for Myoelectric Prosthesis Training *(ongoing)*

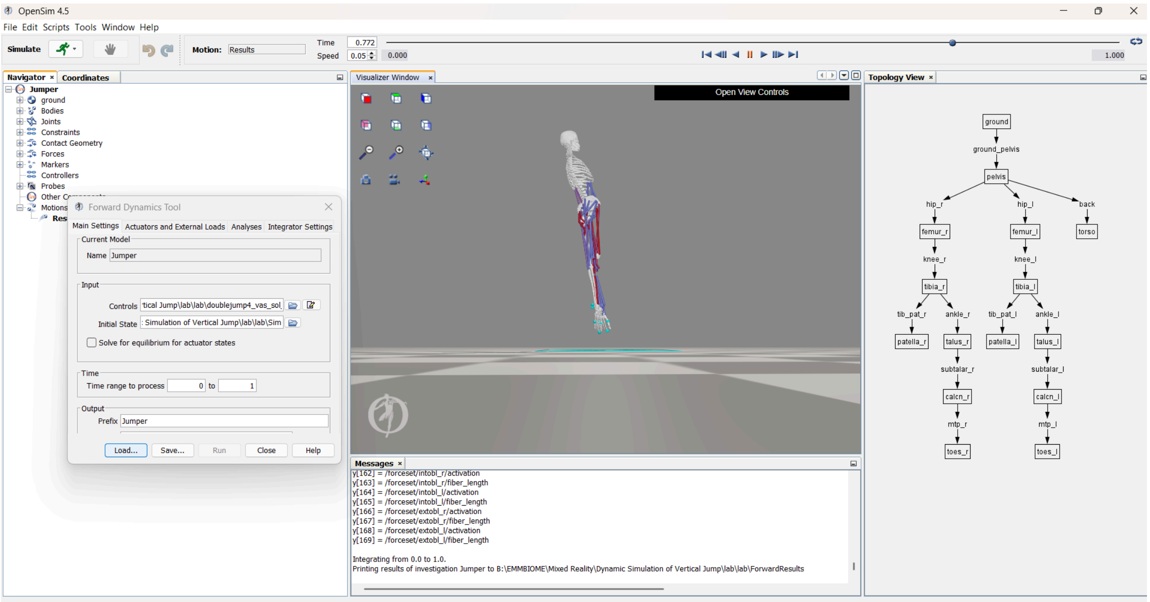
Abstract

The loss of an upper limb has a significant effect on amputees' functional capabilities and quality of life. At present, advanced myoelectric prosthetics restore a certain degree of function after amputation. These devices commonly use surface electromyography (sEMG) signals of residual muscles to activate specific motion in the prosthetic arm. While promising, mastering a myoelectric prosthesis remains a challenging task. Users require extensive training to be able to generate distinctive signals from residual limb. Traditional training approaches to master prosthesis are often characterized by monotony, limited feedback, and lack of engagement. This reduces motivation and ultimately contributes to high rates of prosthesis abandonment. AR represents a promising frontier in rehabilitation, offering a more engaged system to improve motor learning and training. This paper introduces an AR-based platform to help individuals master myoelectric prosthesis control.

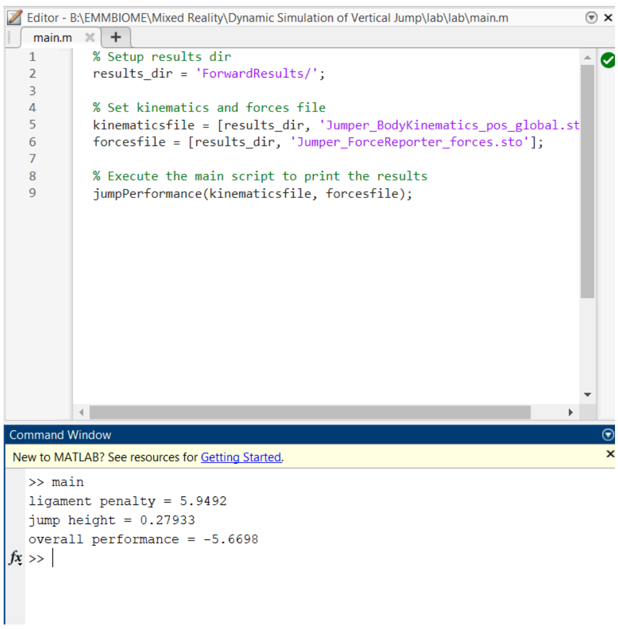


Musculoskeletal modeling for maximum jump height using openSIM

The project involves using the OpenSim platform to analyze and optimize a jumper model's performance through manual adjustments of muscle excitation patterns. The primary objective is to achieve a well-coordinated jump that maximizes jump height. Key workflow components include working with a model file (Simulation.osim), a setup file that defines simulation parameters (Simulation_Setup_Forward.xml), a muscle controls file (Simulation_controls.xml), and an initial states file (Simulation_initial_states.sto). The process consists of iteratively editing muscle excitations for major groups such as the vastus group (VAS), soleus (SOL), gastrocnemius (GAS), and gluteals (GMAX), running forward dynamic simulations in OpenSim, and analyzing the results using a MATLAB.



MATLAB script computes jump height and any associated ligament penalties. Through informed adjustments and simulation feedback, the goal is to refine the excitation strategy and achieve optimal jump performance by effectively coordinating muscle contributions during different jump phases.



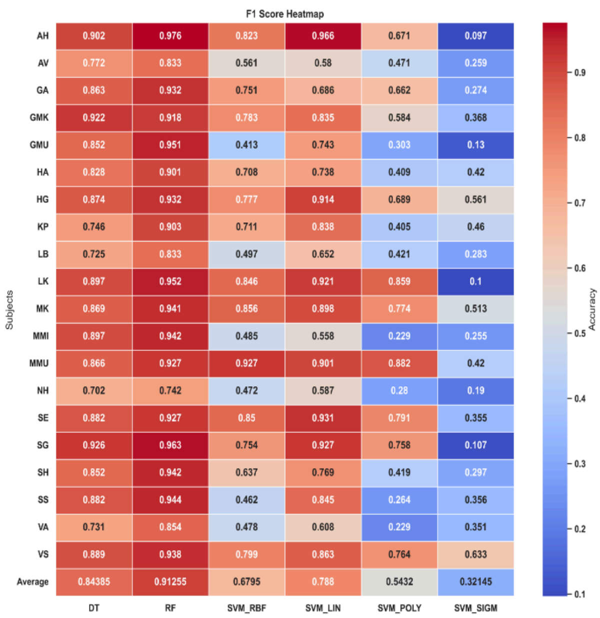
COMPANY: ARMBIONICS
CODE: EMG-SIGNAL-CLASSIFICATION

EMG Signal Classification for Upper Limb Prostheses: A comparison of Machine Learning Algorithms

Abstract

Electromyography (EMG) signal classification is widely used in the development and control of bionic devices, particularly in myoelectric prostheses. By accurately interpreting EMG signals, myoelectric control devices can be further improved, consequently enhancing the quality of life for individuals with limb disabilities. In this paper, we compare various machine learning techniques of EMG signal classification to identify the most effective method boosting the performance of myoelectric limb prostheses. Initially, EMG data from 20 healthy individuals were collected and processed using Discrete Wavelet Transform (DWT). Consequently, DWT was applied together with Symlet 4 extraction filter and ten decomposition levels which allowed an optimal balance between capturing sufficient details and avoiding noise. The preprocessed data was then used to train different traditional machine learning models, including Support Vector Machine, Random Forest classifier, and Decision Tree. The performance of the models was evaluated using cross-validation. Our results showed that Random Forest achieved the highest classification accuracy with the highest F1 score of 0.98 when differentiating between six different movement classes.

PREVIEW:

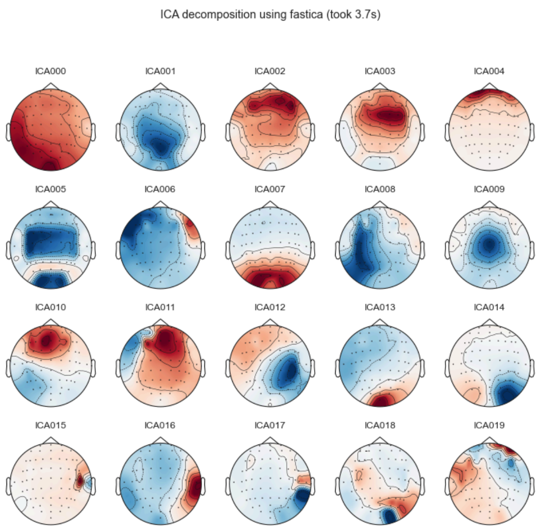


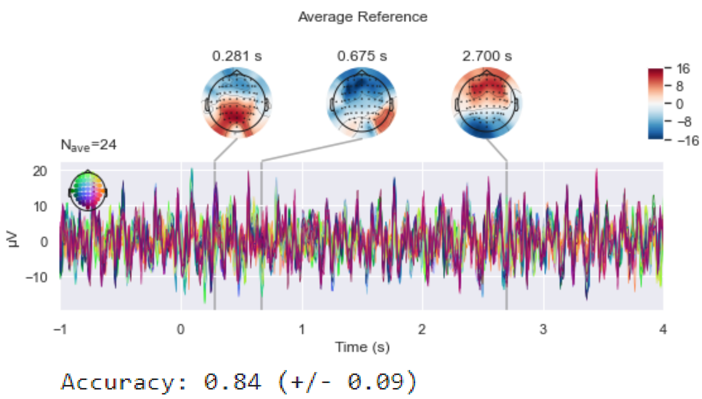
COMPANY: TUMO-LABS TECH INCUBATION PROGRAM
CODE: [CHEST-X-RAY-MASS-DETECTION]
PREVIEW:

RadiCue - AI powered software assistant simplifies X-ray interpretations for radiologists and increases operational productivity of private hospitals. Our mission is to empower radiologists and healthcare professionals by providing an intelligent, efficient, and user-friendly assistant that enhances diagnostic accuracy and streamlines the radiology workflow, ultimately leading to improved patient outcomes.

EDUCATIONAL-CENTER: 42 SCHOOL YEREVAN
CODE: [BRAIN COMPUTER INTERFACE WITH MACHINE LEARNING BASED ON ELECTOENCEPHALOGRAPHIC (EEG) DATA.]
PREVIEW:

Processing of cerebral activity data using machine learning algorithms. The data originated from a motor imagery experiment, where participants were instructed to either physically perform or mentally visualize hand or foot movements in response to specific symbols displayed on a screen. The recorded results are cerebral signals, accompanied by labels indicating the moments when subjects were tasked with a specific movement.





Educational-center: laboratory of bioinformatics and genome BIOLOGY, JAGIELLONIAN University

Code: [comparison-of-transcriptomic-and-protemic-data-using-r]

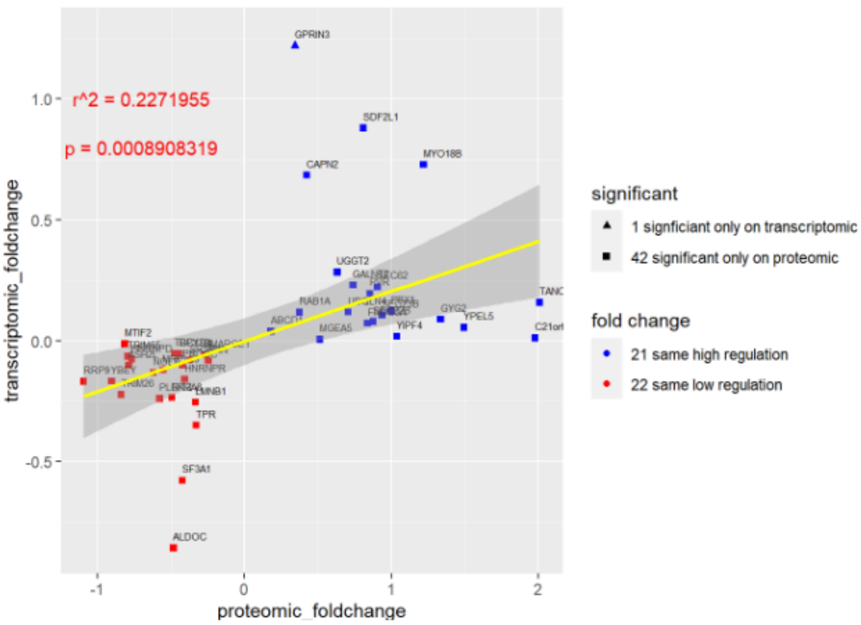
Preview:

Comparison of transcriptomic and proteomic data using R

2022-05-27

Introduction

The analysis is based on transcriptomic and proteomic data from healthy (control) and dystrophin-deficient (DMD) cardiomyocytes human (samples are from 2 patients). Applying data analysis methods to the transcriptomic and proteomic data of the same sample has the goal to check if the results from proteomics are consistent with the data from transcriptomic analysis. Having a list of genes (witch foldchange (Fch) and adjusted p-values) from the transcriptomic part where we compare disease vs. controls and a list of proteins (also characterized by foldchange and p-values) from the proteomic part where the same comparison was done.



BIOINFORMATICS GROUP AT INERNATIONAL SCIENTIFIC AND EDUCATIONAL CENTER OF NATIONAL ACADEMY OF SCIENCES OF THE REPUBLIC OF ARMENIA

Journal: [In the World of Science" Journal 2, 2022]

Preview:

TCL Programming Language in Bioinformatics

"In the World of Science" Journal 2, 2022

Being a hybrid science, bioinformatics links the storage, distribution and analysis of biological information with technology, contributing to the advancement of scientific research in many fields. The word "bioinformatics" itself was first used in 1968, and the definition was first given
in 1978.

The development of bioinformatics has led to major successes in recent years. it has played a unique role in the analysis of vast numbers of genomes. Intensive studies of protein evolution, genomic sequence, and expression patterns ensued. It began a period in which it became widely used, especially in medicine, to identify correlations between gene sequences and diseases, to predict protein structures from amino acid sequences, to help design new drugs, and to tailor treatments to individual patients based on their DNA sequences.