



## The Role of Biomolecular Techniques in Physical Rehabilitation

Naga Swetha\*

Department of Biochemical Sciences, Andhra University, Andhra Pradesh, India

### DESCRIPTION

Physical rehabilitation is crucial in the management of individuals with disabilities induced by age-related muscle loss or those who have been affected by catastrophic conditions such as trauma, surgery, cancer or other severe pathologies. These instances all share an extended period of physical inactivity. Patients who are placed on bed rest for an extended period of time commonly experience a number of complications such as muscle loss which can exacerbate which was before conditions caused by sarcopenia and as a consequence severely limit physical functions.

The basic goal of this work is to synthesize key strategies for the physiotherapeutic management of physically inactive patients, regardless of the reason for their prolonged bed rest with a particular emphasis on physical rehabilitation, nutrition and forest-bathing. The significance of adequate nutrition in trying to prevent muscle mass loss and successive function is mentioned, along with a characterization of the main nutrients needed for muscle regeneration. From a bio molecular point of view a few particular molecular mechanisms associated with physical rehabilitation have been noted only in the context of physical therapy but also in environment techniques such as forest bathing and body self-healing. Combining a focused hydrotherapy strategy with an appropriate diet and nature-based therapy could therefore aid in the recovery of patients.

Following that and in order to propose salivary protein profiles with greater sensitivity, bioinformatics applications i.e., toolboxes provide an integrated software environment for better proteome analysis. It gives the access to proteomic data formats, analysis

techniques and specialized proteogram visualizations. Experion™ Automated Electrophoresis System i.e., the system offered directly by the manufacturer has been used for multiple clinical applications due to its usefulness in quickly providing a graphical visualization of proteomic bands. It can be used as an out-of-the-box feature for biomarker research. It does, however, lack better tools for data visualization and exploration. In contrast, high-level computing platforms enable cost-effective and tailored data analysis.

Several application tools have been created to enable interactive data mining and visual analytics. These applications benefit greatly from their readiness and low coding effort. The current study prefers to directly implement the computing code for more effective in machine learning-related applications. It includes a molecular analysis using a data mining solution to overcome the lack of discriminative and quantification power provided by a simple molecular biology method namely capillary electrophoresis. Capillary electrophoresis data is typically expressed in kDa and refers to the Molecular Weight (MW) of proteins that migrate in the electrophoretic gel.

In summary, three main functions data visualization, exploration, and mining is used in this to analyses electrophoretic data of neuro typical young adults. The Expectation-Maximization (EM) iteration provides data visualization of the electrophoretic profiles in order to investigate unobserved latent variables in our dataset. Data mining on our dataset, comparing individual molecular profiles to the entire sample, and allows for better visualization of the homogeneous separation of salivary peptides.

**Correspondence to:** Naga Swetha, Department of Biochemical Sciences, Andhra University, Andhra Pradesh, India, E-mail: swetha@gmail.com

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