Towards the design of a decision support tool for prevention and treatment of Osteoarthritis among Veterans and Active Military

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**Background:**

According to the CDC, not only is arthritis among the most common chronic conditions among veterans and active military, osteoarthritis is, for both men and women, significantly more prevalent among veterans than nonveterans. It is therefore necessary to help prevent or manage at an early stage the progression of this disabling disease. One way is to develop the clinical tools required to accomplish that end. Decision Support is one of those tools as it has the ability to classify individuals into subpopulations that differ in their susceptibility to diseases or their response to a specific treatment. Preventive or therapeutic interventions can then be focused on those who will benefit, sparing expense and side effects for those who will not. Thus, it is the tailoring of medical treatment or prevention to the individual characteristics of each patient and their susceptibility to various chronic diseases.

Big Data analytics will empower physicians at the point of care to diagnose early arthritis stages, choose treatment approaches, decide when to refer to a subspecialist, and mitigate co-morbidities. The aim of this project is to develop a clinical decision support system to study the clinical and genomic factors responsible for causing and exacerbating arthritis. Based on these findings, educate clinicians about how certain clinical and genomic factors are responsible and how to alter their impact. Such a system can also be helpful for clinicians to prescribe the most appropriate medical drugs for treatment.
Methods:

There have been many studies in the area of data mining which determine the occurrence of OA. It would be indeed helpful to have a decision support system that studies various patterns and trends of clinical and genetic factors increasing the risk of occurrence of this chronic and disabling disease. Data analysis indicate that an ACL tear increases the risk of having OA by twenty fold.

Furthermore, most genetic variations among people is a result of single nucleotide polymorphisms (SNPs), which are differences in a single nucleotide within a stretch of DNA. SNPs can result in the production of different RNA molecules and proteins, thus altering the body’s metabolism and physiology. With approximately 10 million SNPs in the human genome, “big data” analytical methods are the most efficient means for discovering which SNPs are associated with a particular disease, including osteoarthritis. Candidate gene studies and genome-wide association studies (GWAS) serve a similar purpose on a much smaller scale, but are infeasible for analyzing large amounts of data.

Design and Methodology:

- a. From established databases, such as the VINCI VA database, extract records of persons with osteoarthritis and develop a cohort.
- b. Obtain information about SNP known to be a risk.
- c. Integrate clinical and genomic data to obtain a universal feature vector.
- d. Perform feature extraction to extract relevant attributes.
- e. Run data mining algorithms to obtain clusters of patients and study similarity.

Conclusion:

The proposed framework will enable an osteoarthritis decision support tool for precision medicine in treatment and prevention of at risk persons in the military.

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