

[AB1047] TOWARDS THE DESIGN OF A DECISION SUPPORT TOOL FOR PRECISE CARE FOR ARTHRITIS

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Background: Decision Support requires 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 to the individual characteristics* of each patient and their *susceptibility to various chronic diseases*.

Objectives: 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.

Co-morbidity refers to *co-occurrence of more than one disease* in a person at a time. Examples include Diabetes, Cardiovascular diseases, renal diseases, Arthritis, etc. These diseases can occur by chance or there can be *complex pathological associations*. These indirect causal factors are only partially understood. It has been observed that the *number of hospital admissions*, as well as the *mortality rate of comorbid patients*, is *significantly high*. Hence, there is a *need for early detection* of these diseases. The aim of this project is to develop a clinical decision support system to *study the clinical and genomic factors* responsible for causing these diseases. Based on these findings, *educate clinicians* about how certain *clinical and genomic factors* are *responsible for causing these diseases*.

Methods: *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. 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.

Results: Design and Methodology:

From a large EMR database extract records of persons with arthritis.

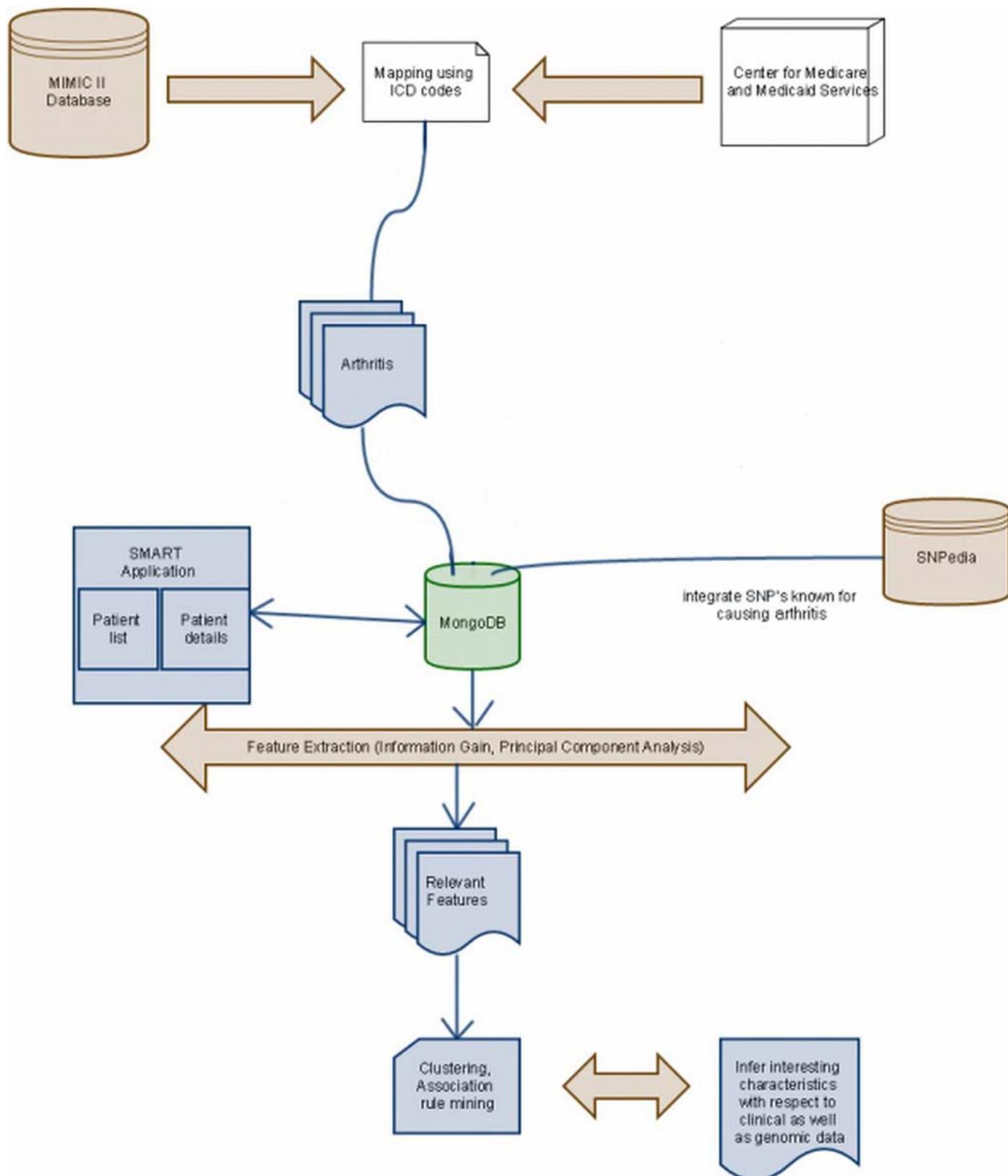
Obtain information about SNP known to be risk causing from SNPedia, dbSNP.

Integrate clinical and genomic data to obtain a universal feature vector.

Perform feature extraction to extract relevant attributes.

Run data mining algorithms like simple k-means to obtain clusters of patients and study similarity between them.

The application systems interconnection logic is depicted in the diagram.



Conclusions: The proposed framework will enable a decision support tool for precision medicine in treatment of persons with arthritis.

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