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Prediction model by using Bayesian and cognition-driven techniques: a study in the context of obstructive sleep apnea

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Abstract

This research proposes a mechanism for cost-effective medical diagnostic support for relatively new physical ailments or diseases where there are incomplete data sets available and hence, common parameters are forced to be used for drawing a-priori inferences. We propose a simple but powerful prediction model that combines the advantages of the Bayesian Approaches and Cognition-Driven Techniques such as Expert Reasoning (ER) and Cognitive Reasoning (CR) using Markov Chain analyses. Then, we demonstrate the effectiveness of our approach in predicting Obstructive Sleep Apnea (OSA).

Keywords: diagnostic support; a-priori inferences; Bayesian Approaches and Cognition-Driven Techniques; Expert Reasoning (ER); Cognitive Reasoning (CR); Markov Chain analyses; Obstructive Sleep Apnea (OSA)

1. Introduction

Bio-informatics is now being increasingly used as a means of providing medical diagnostics support. In [20], it was shown that the use of statistical tools and techniques is gaining widespread acceptance amongst biomedical informatics scientists as an aid to decision making. There is a surge in the number of such articles published in the leading medical journals such as the Journal of American Medical Informatics Association (JAMIA) and the International Journal of Medical Informatics [20]. However, the focus in Bio-informatics has been on advanced computational tools and algorithms that can process large and complete data sets efficiently for diagnostic support. For example, in [18], a new program package JAGUC has been developed. It offers cost advantages over other available tools in processing large sequence of raw data sets and supporting biologists in decision making. In the same year and in the similar vein, two software packages to determine which of the two offers cost advantage in processing large data sets and better decision support [19].

Bayesian approach, which is of non-frequentist or non-classical [1], is used when estimation by using frequentist or classical approach (e.g. expert reasoning) is unclear - when parameters are random although data values can be acquired [1, 2, 3, 4 ,5]. This is very appropriate for this OSA research because there are no means to support decisions (i.e. using frequentist approach is unclear) in situations of new diseases (i.e. OSA parameters are random) where phenomenon of interest (i.e. OSA in our research) is relatively new and there are limited data sets (though data values can be acquired) for drawing a-priori inferences. There is a documented evidence of statistical tools and techniques in Bioinformatics for faster and efficient processing of data that

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