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Comparison of computational models in prediction of adverse drug reactions

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Computational pharmacology is the application of bioinformatics and computational biology with relevance to pharmacology including understanding of drug action, adverse drug reaction, identification of drug targets and drug design. Early and accurate identification of Adverse Drug Reactions (ADR) is critically important for drug development and clinical safety. Often times the adverse effect of drugs are not discovered until years later after the drugs' release to the market. The post hoc analysis is usually unable to detect rare or delayed on-set ADR until clinical evidence accumulates. The process of drug development and ADRs discovery takes years, meaning that a lot of harm would have been caused to lives before evidences are accumulated, therefore developing a computational pharmacology model that can be used to make informed decisions to decrease attrition rate in the process of drug development with improve number of drugs having an acceptable benefit and risk ratio is paramount. This paper reviews and compares computational methods of the few works that has been done so far to address this issue and hence looks at the applicable methods that can be used in drug to ADR prediction.

Biography

Jumoke Soyemi completed her BSc (Computer Science) at Obafemi Awolowo University, Ile-Ife in 1999, MSc (Computer Science) at University of Ibadan in 2004 and is presently pursuing her PhD (Bioinformatics) at Covenant University, Ota under the Covenant University Bioinformatics Research cluster (CUBRe). Her PhD is supported by h3abionet grant.

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