Impact of AI and ML on Bioinformatics (Healthcare)/ Medicine Precision using AI and ML

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Abstract. Impact of Artificial Intelligence has remarkable witnessed in the various areas today and is not limited to just computing fields, but also in the scope of medical assistance. Application of pharmacogenomics in medicine shows a promising future, that has so far been unfulfilled, hopes of improvement and new discoveries that can perform spectacularly in favor of mankind in terms of health and medicine. In this paper we would be presenting a framework which can provide a roadmap for the future of precision medicine in cardiac arrest risk factors (blood pressure); which will be braced with methodologies like classifications, subcategorizing of types of patients based on risk factors and fatality via AI and ML which can prove a boon to achieve better medical efficiency. The framework is based on treatment strategies classified based on receptors, drug composition as a personalized approach. The extent to which information is justified depends on the clinical scenario, particularly the ease with which blood pressure can be controlled.

Keywords: Personalized medicine, Artificial Intelligence, Machine Learning, Cardiac Arrest, Pharmacogenomics.

Introduction

After centuries of identifying the major causes of deaths of patients that foreshadow prognosis of major diseases, it was found that heart diseases, precisely cardiac arrest among various heart diseases was most plethoric. Fig.1[1] provides the visualization about the causes of death in last ten years.

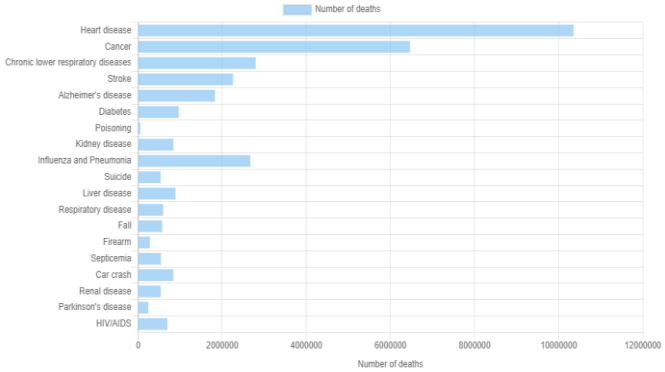

Fig 1. Above graph represents Count of Death and death causes in this decade.
This information concludes how serious heart diseases are.

After rigorous risk analysis of the causes of cardiac arrest, the fact was derived that blood pressure is the major one. Elevated blood pressure is a leading risk factor of death and disability[2] and is predicted to be a major factor till 2040[3]. Though we have treatments available to control blood pressure as various therapies evolved over the time with evolution of technology and our knowledge among the diseases precisely as a result in addition to this therapies that have been evolved of which the physicians treat the patients with an abundance of choice, which makes it more reasonable for physicians to explore and look beyond single agent trials to maximize the individual medical success. The relevance of precision medicine is justified as this approach emphasizes that patients with same disease are nonetheless different from one another, hence their response also varies for the same treatment. Here we had tried to demonstrate that highly effective interventions can be undertaken with the knowledge of individual patient traits thus increasing the medical efficiency.

To achieve this proposal of finding an efficient solution for precision medicine artificial intelligence, machine learning and deep learning are the key tools as they are the most powerful and trending systems which mimics human intelligence to perform tasks which can itself improve with time as they collect more information. Powerful and complex algorithms make it easier to understand the data in better way and accurate prediction could also be done using data irrespective of the type of data that is image or tabular data etc. Use of such methodologies for biological development opens the scope of finding plethora of approaches to counter a problem which are logically justified and can be tested on clinical scenarios.

Biology of Cardiac Arrest

Cardiac arrest also called as cardiopulmonary arrest or circulatory arrest is the state of heart in which abrupt loss of heart function in an individual who may or may not have been diagnosed also it indicates a sudden stop in effective and normal blood circulation due to failure of the heart to pump blood. Historically, the etiologies of cardiac arrest have been dichotomized as cardiac or non-cardiac[4]. The dispensaries and physicians often exist between clinical and postmortem diagnoses, the causes of cardiac arrest are uncertain very often though few frequent causes of cardiac arrest are myocardial infarction, arrhythmia, or heart failure which a prevalence of approximately 50% to 60%[5,6] followed by respiratory insufficiency as the second most common cause.

In contrast with heart attacks that are caused by blockage that stops the blood flow to the heart which is a “circulation” problem, cardiac arrest is caused when the heart’s electrical system malfunctions, heart’s pumping function is “arrested”. Focusing on what happens in cardiac arrest, once the blood circulation stops, oxygen delivery to all vital organs is also stopped and the organ which is most quickly. The patient loses consciousness and breathing is shallow and minimized.

If the cardiac arrest persist over five minutes permanent brain damage may occur. The pulse that is usually seen in the carotid artery in the neck as well in the wrist and ankles is lacking. Even a little damage to primary centers of brain causes a lot of distortion within its complex structure and it develops serious disorders which may vary as per the medication dosage Discussing how this effect takes place is very complex and beyond the scope of this paper. In addition to this genetic factor are also very responsible for this to occur hence understanding the genetic behavior becomes crucial to generate a framework. Due to these, it becomes very important that analyzation and identification of the causes of cardiac arrest should be done, considering all the effective parameters and risk factors because it emphasizes that potential reversible causes should be identified. Artificial Intelligence and machine learning plays very important role in identification of such factors and as per our findings these causes could be categorized, and it comes with a possibility of creating a base of framework to provide precision medicine in such medical scenarios which we are going to discuss up next.

Categorizing Cardiac arrest and Risk Analysis

Importance of identification can be justified as it can improve the outcomes and that could be enhanced by further categorization also it has implications if return of spontaneous circulation in the body is achieved because post-cardiac dysfunction is partly dependent on the underlying cause and post-cardiac should be tailored accordingly[7].

Hence it becomes very important to create a useful and precise framework for the classification of cardiac arrest, and AI & ML are very helpful and handy powerful tools to serve this purpose. As per our proposed framework the cardiac arrest can be classified into two different subcategories on the basis of symptoms for this mendelian disease and can be labeled as high fatality risk and low fatality risk. In general, it is already in understanding of the physicians still the reason why no precise approach has considered for such diseases on contrast with naïve and trial and error medication approaches has yet been unknown. *Fig2.1 & 2.2* represents the visualization of categorical classification of cardiac arrest disease

Type1(High fatality)

- No breathing
- Collapse
- No pulse
- Loss of consciousness

Fig2.1

Type2(Low Fatality)

- Chest Discomfort
- Shortness of breath
- Weakness
- Palpitation (fluttering)
- Faster breathing

Fig2.2

(Represents the classification in which the cardiac arrest can be categorized)

Considering these two classifications approach for medication can be reconsidered as well as classified, although to resolve the problem of more precise approach risk analysis could be and major risk factors can be identified before we talked about correlation of these risk factors, first let us know about what are the risk factors which leads to cardiac arrest and that can be listed as follows,

- Gender of the patient
- If the patient is Chain-smoker
- If the patient consumes other tobacco products
- High Blood pressure
- If the patient has obesity
- If the patient has diabetes
- Metabolic syndrome
- Use of stimulant drugs
- Family history
- History of preeclampsia
- CABG history
- Respiratory illness
- Under Risk

These factors must be variegated congruously to understand the correlation between these risk factors, and by following the process rigorously. We applied logistic regression to understand the correlation between the risk factors mentioned above. *Fig 3* represents the visualization of our findings as a heat map where darker the color higher is the effect of that particular risk factor.

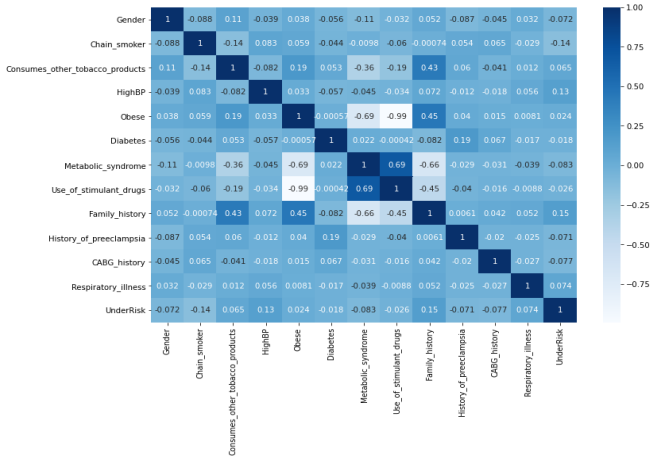

Fig.3. Represents the correlation of Risk Factors.
(Darker the color greater is the effect and if we observe High BP and Diabetes, are the major factors.)

Framework For Understanding Personalized Treatment Approach

In general, there is a trade-off between simplicity and the incorporation of affluent information about individuals in clinical decision making. More personalized strategies prove to be more valuable for patients in whom simple strategies with low information burden proved to be ineffective. The added complexity of additional information enlarges the likelihood of good decision making and improved outcomes and handling the complexity without increasing the calculation burden on the clinician becomes imperative. Therefore, we suggest application of artificial intelligence and machine learning algorithms as they are very capable and effective in such conditions.

We propose a framework as an approach to classify cardiac arrest disease and apply precision medicine on it by understanding the genetic behavior of patient's body and generalizing it, and also understanding the drug compositions of the available drugs in the market which currently used in a naïve methodology for treatment though it sounds complex but as discussed it increases the likelihood of better decision making. Idea behind this methodology is that if we could understand the response of our body for different drugs or different therapies

via genetic factors this can be a boon to medical domain. To discuss this in brief, it is already known that people inherit variations in genes and even a slight change can affect how a body responds to certain drugs. Current drugs are metabolized by the enzyme cytochrome P450 (CYP 450). Once a drug enters in our body either it activates the closed receptors in our body due to the disease or even sometimes boosts its efficiency to cure the disease but vice versa could also happen if wrong dosage or any other medicines are provided for treatment it can lead to numerous disorders in body and can also block the receptors leading to worst case outcomes. Since we are focused on blood pressure, there are six different categories of medicines available which physicians recommend for treatment (Ace inhibitors, ARBs, Alpha blockers, Beta Blockers, Calcium Channel blockers & Diuretics) but trial and error approach contains risk of blocking the receptors leading to worst case outcomes. Hence, we tried an approach to gain better understanding of pharmacogenetics though it is a mendelian approach for this era, but it can provide us better understanding of genetic behavior and its response towards various therapies in best way. In this road we discovered on genetic analysis via GWAS using BP as a quantitative trait by binary definition of hypertension polygenic pathways of BP regulation and Hypertension[8] and on pharmacological testing it was concluded that various receptors agents in our body responses variously on different therapies and drug compositions. *Fig 4*[9] represents and idea about how polygenetic pathways can be generated considering multifold genetic factors to control blood pressure and thus its behavior can be studied for different drug compositions and this information can be utilized to prioritize functional genes and variants.

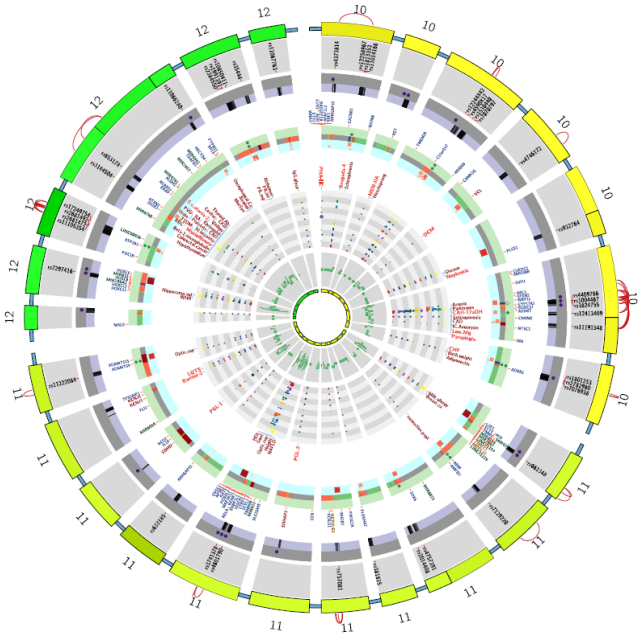

Fig 4[9]. Genetic landscape of monogenic and polygenic blood pressure/hypertension syndromes, casual genes, GWAS loci and information used to prioritize functional genes and variants tagged by GWAS SNPs.

In our proposed framework steps to achieve this goal are, performing risk analysis on the individual patient for identification of the disease by logistic regression and to utilize this algorithm for understand the correlation of risk factors to find out the major risk factors though our findings are high blood pressure and diabetic are major risk factors 55% and genetic factors are the second most after these two up to 20%. So, we will be targeting blood pressure in this paper as diabetes also leads to irregular blood pressure in our body. As a second step for this proposed model, we will use convolutional neural networking to classify the cardiac arrest issue based on their fatality ratios once the identification is confirmed. Once the disease type is classified now medical approaches for treatment can be varied and steps for precise treatment can be carried forward which requires genetical diagnosis and analysis in order to analyze whether the body contains receptors and if they are contained within then in which state the receptors are (blocked or unblocked which responses for blood pressure treatment methodologies). As genes comprises of abundant information which are irrelevant in our case hence, cardiomyopathy is a better method to target specific properties of the genes which responds to drug compositions already available. We found out that in G- proteins receptor Arg-389 responds better in alpha therapies in comparison with Gly- 389 which do not responds in effective for alpha therapies.

Similarly, the receptor Gly-389 which responds better for beta therapies[10] hence we can conclude from the fact that if we have data of genetic receptors and their responses to various therapies. DNA classification can be done and based on the DNA alignment it will be possible to suggest which medicine can be effective precisely for an individual patient.

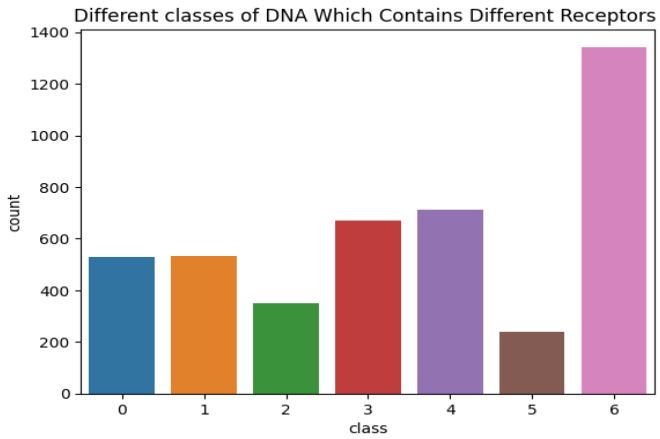

Fig 5. Classification of DNA Alignment based on different receptors contained in genes, the information can be then aligned with different classes of drugs as per their responses.

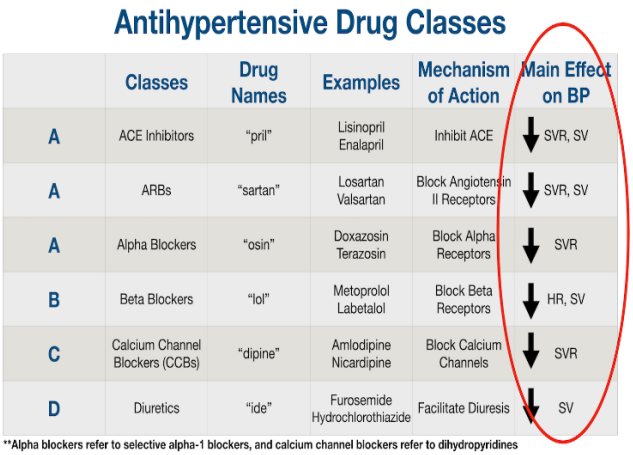

Fig 6. Drugs for blood pressure control based on their classes major receptors for which they are effective.

Also, if you observe *fig 6 it* represents the drugs which are effect for different classes based on therapies hence it derives the conclusion that on the base of their classes' major receptors for which a particular drug is effective can be observed and hence this information can be aligned with the genetic data which contains information about which receptors are active in particular DNA sequence. Thus, a recommendation can be provided with an accuracy that which medicine will be competent for patient's body to control the blood pressure, leading to a controlled clinical scenario for cardiac arrest. Thus, major risk effects of medication for cardiac patients that is uncontrolled behavior of mind (temporary memory loss, uncontrolled anger, development of obesity, emotional weakness, stress or hypertension) can be checked by using this effective method. Based on such controlled treatment, the scopes of finding a logical explanation for the condition of NDE (Near-death experiences) in cardiac arrest survivors[11].

Conclusion

From this research we can conclude the facts that there are two possible classifications of cardiac arrest based on fatality risks, and it can be identified and subclassifies by using Machine Learning algorithms. Considering the major common risk factor in both subclasses of cardiac as blood pressure and by genetic analysis via GWAS using blood pressure as a quantitative trait by binary definition of hypertension polygenic pathways of bp regulation and hypertension, and on pharmacological testing we found that various receptor agents in body responses variously on different therapy methodologies and drug compositions.

Hence based on these receptors with we can classify the DNA patterns that in two segments protein-coding variants and non-coding variants, because it comprises with a scope of new drug development too. In general, from the DNA class of an individual we will be able to make recommendation which drug composition will be more effective in such alignment. Thus, leading to a better medical success rate and an effective advanced treatment methodology.

Limitations

Although our proposed model generates a framework of precision medicine but it yet in future scopes to be generalized for various other diseases. It is yet limited to cardiac arrest identification, classification and effective control over blood pressure considering it as a major risk factor in cardiac arrest. Also, the genomic factors considered are limited since it is very complex process to extract targeted information of DNA and process on it. There is a possibility to enhance this framework and algorithm for recommending the medicine by adding the data of more complex genomic factors for example adding more receptors or response of body based multi-activated receptors in body which leads for a scope to study polymorphed behavior of receptors for a therapy.

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