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Recent trends in Pharmacogenomics and Bioinformatics

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Abstract
The study of genes and how pharmaceuticals affect a person's reaction is known as pharmacogenomics. In order to establish safe and effective pharmaceutical dosages that are customised for each patient based on their genetic makeup, the science of pharmacogenomics, which is still in its early stages of development, combines pharmacology, the study of drugs, with genomics, the study of genes. In the area of genomics, which is associated with genetics and genomics, computer technology is used to collect, store, analyse, and disseminate biological information and data, such as amino acid and DNA sequences or comments about those sequences. It is mostly used to extract from biological analysis by knowledge using algorithms and software. Applications of bioinformatics and pharmacogenomics in numerous fields were discussed. Additionally, the importance of pharmacogenomics and bioinformatics in medication development was investigated. The most recent developments and needs in pharmacogenomics were also presented.

I. INTRODUCTION
The study of genes and how pharmaceuticals affect a person's response is called pharmacogenomics. In order to offer patients with safe, effective medicine dosages that are tailored to their particular genetic make-up, the science of pharmacogenomics, which is still in its infancy, Study of pharmaceutical for combine pharmacological with genome and study of gene. One of the key programmes in which scientists are discovering and learning how genes relate to the way the body reacts to project of Human Resource to drugs. In the future, it will be possible to forecast a person's medicine effectiveness based on genetic makeup and informative of existence of side effect reaction. Pharmacogenomics is still in its infancy despite advances in science and technology. Pharmacogenomics is only occasionally used, but new methods are continually being tested in clinical settings. Pharmacogenomics will soon make it possible to create treatments that are specifically tailored to treat conditions like neurological, cardiovascular, HIV, cancer, and asthma.[1]

The field of the course of investigates how someone's genetic make-up influences how they react to medicine. Many drugs offered today are "one remedy that suits all," currently they don't all work in exactly the same manner; this field mixes the research of genes and how they operate with the technology behind pharmaceuticals to develop effective, safe medications that can be offered based on someone's genetic makeup. Adverse drug reactions, also known as reactions to medications, are undesirable side effects that may be difficult to predict in patients who will benefit from the medication, who are unlikely to respond at all, and who are likely to suffer them. [2]

It is the study of the Pharmacogenomics is how hereditary variations in adverse effect or pharmacological response related to generic code. Both accessibility and interest are rising quickly. The doctor will be able to multiple of treatment with it best pharmacokinetics, the right drug quantity, and have low chances of adverse effects if they are knowledgeable about the gene-drug pairing for a variety of therapies. Practitioners must understand the fundamental concepts of pharmacokinetics and pharmacodynamics are how to repose the drug response in order to utilise this knowledge. The genetic differences that result in various phenotypes can also be understood once these have been identified. Our review discusses these ideas and provides instances of frequently prescribed drugs and the genes they couple with. Despite the fact that the Food and Drug Administration (FDA) recommendations on pharmacogenomics testing are currently lacking, direct-to-consumer testing is nonetheless freely accessible. In this content, of they discuss the limitations of pharmacogenomic testing, the criteria for testing, and how to evaluate a pharmacogenomic report. The expectation is that by customising treatments and doses to a person's genetic makeup,

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individualised medicine will enable the prediction of a reliable and efficient response.[3]

Using computer technology, the area of genomics, which is connected to genetics and genomics, gathers, stores, analyses, and shares biological information and data, such as sequences of amino acids and DNA, or annotations regarding those sequences. Databases that organise and index these biological data are used by researchers and physicians to gain more knowledge about health and illness, as well as, in certain situations, to aid in the delivery of medical care. Similar to the function of analysis of data in the data-driven and Internet era, bioinformatics plays a crucial part in biological research. Until recently, gaining access to the data was the most difficult obstacle. Because of advancements in reading DNA sequences, it is now considerably simpler to accomplish this. The next issue is to decode the significance of the collected data. Computer-based approaches are becoming the standard since the data forces are utterly enormous, whether that you're discussing figures on traffic to a website or the human genome. The ultimate objective of bioinformatics' use of person's genomes is to get any useful knowledge about how complicated biology affects human health. [4]

Computer science, mathematics, statistics, molecular biology, and genetics are the main academic fields that make up the interdisciplinary field of bioinformatics. From a computational standpoint, large-scale, data-intensive biological concerns are addressed. The two most prevalent problems are modelling molecular Processes in biology and making inroads from the data collected. The following steps typically form a bioinformatics solution: Use scientific information to develop statistics. Make a computer simulation. Put an issue with computational modelling to rest. Evaluate and analyse algorithm computer. A brief introduction is given to his chapter to biological terminology before discussing numerous well-known bioinformatics problems in an orderly fashion based on the various type of sequence analysis, data source, which also includes sub problems including the identification of multiple sequence alignment, homologs, sequence pattern for searching and examine protein sequence and DNA for clues about their function. The three-dimension data have protein sequence are as such, they present challenges in structural alignment, prediction of secondary and tertiary structures, and functional protein structure analysis. In the examination of microarray data, statistical analysis, classification, and clustering techniques are often utilised, and gene expression data is frequently represented as matrices. Such as protein-protein interaction networks, network of biology, regulatory gene network, and metabolic pathway are typically represented as graphs, and problem associated as the building and large analysis of scale network, are addressed using graph theoretic methods. [5]

II. APPLICATIONS OF PHARMACOGENOMICS AND BIOINFORMATICS

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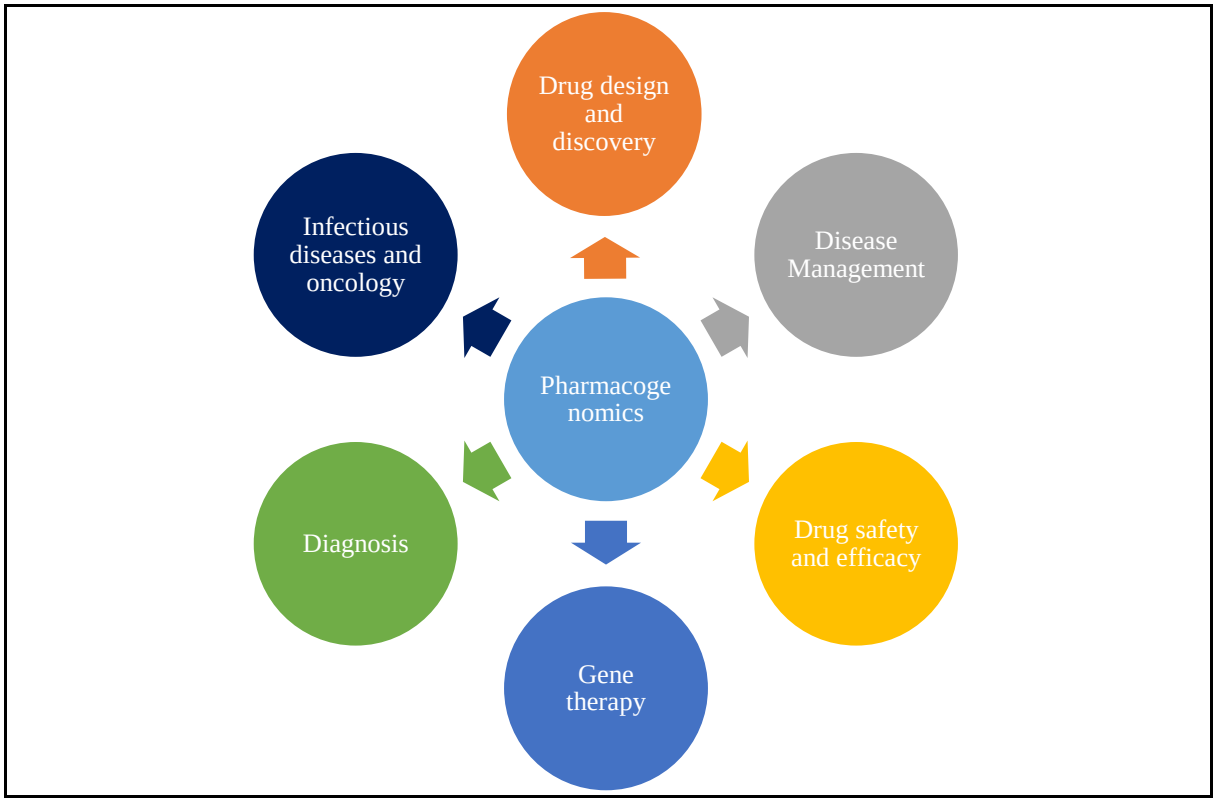

Some of the well-known uses of pharmacogenomics are listed below: -

- Improve drug safety, and reduce ADRs;
- Improve medication discovery for human diseases,
- Find the best dosage for each patient's specific genetic predisposition, and
- Improve proof of concept for effectiveness studies.

Pharmacogenomics can be used in psychiatry, cardiology, oncology, and pain treatment, among other medical specialties. Pharmacogenomics may also be used in forensic pathology to analysis of drug-related death cause when an autopsy cannot provide a clear answer.

Pharmacogenomics tests are used in cancer treatment help identify the people who are more likely to respond to specific cancer treatments. Doctors and caretakers have more choices for better managing drug selection and side effect reduction thanks to pharmacogenomic tests in behavioural health. Companion diagnostics, which refers to tests given along with medications, is another name for pharmacogenomics. KRAS testing with cetuximab and EGFR testing with gefitinib are two examples. In addition to effectiveness, germline pharmacogenetics can aid in the identification of patients who are more prone to experience severe toxicities when given cytotoxic like classical 5-FU, which demonstrate poor detoxification in response to genetic variation. Genetic dysregulations affecting the genes encoding.

The fundamental issue with cardiovascular problems is how patients react to medications like statins, warfarin, and beta blocker. Cardiovascular risk is increased in CYP2C19 individuals on clopidogrel, prompting authorities to revise the medication's package insert. Type 2 diabetes with patient who have genotyping haptoglobin show an adverse effect on cardiovascular disease, at higher risk and vitamin e with Hp2- supplementation lower danger through changing HDL. [6]

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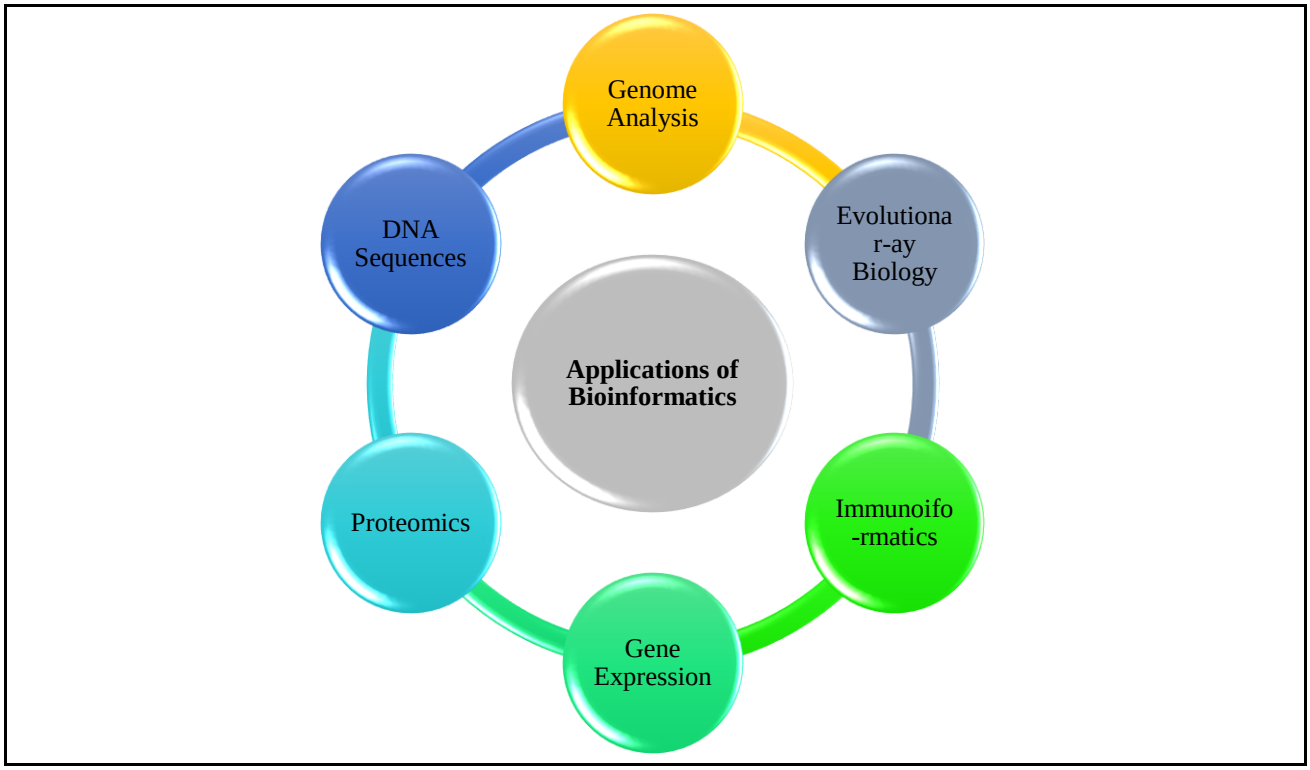
APPLICATIONS OF BIOINFORMATICS



It is mostly used to extract knowledge from biological data using algorithms and software.

The investigation of genomes, proteomics, 3D protein structure modelling, image analysis, medication development, and many more domains regularly use bioinformatics. Bioinformatics is frequently used in preventive medicine and precision, are which largely concerned with develop methods to control, prevent, and treat severe disease infectious. The important objective of biological process was understood to increase the bioinformatics.

Several bioinformatics applications are listed below.

- In Gene therapy.
- In studies of evolution.
- In uses involving microbes.
- In Protein structure Prediction.
- Used in the study of medicine to find novel medications. [7]

III. ROLE OF PHARMACOGENOMICS AND BIOINFORMATICS IN DRUG DEVELOPMENT AND DRUG DISCOVERY

Pharmacogenomic is the study of genes and how medications can alter how each person reacts to a given stimulus. For the creation of effective doses of drugs, it's a novel discipline that combines both pharmacology and genetics. The Project Human Genome is assisting in understanding of the relationship between genes and their impact on the body how to react the drugs. The effectiveness of medications and their adverse drug reactions vary depending on an individual's genetic makeup. Pharmacogenomics is still trailing behind after all these developments. The use of pharmacogenomics is now restricted, but there is a high probability in the near future, it will be used to treat diseases like cancer, HIV, and cardiovascular illnesses that affect a large portion of the population. [8

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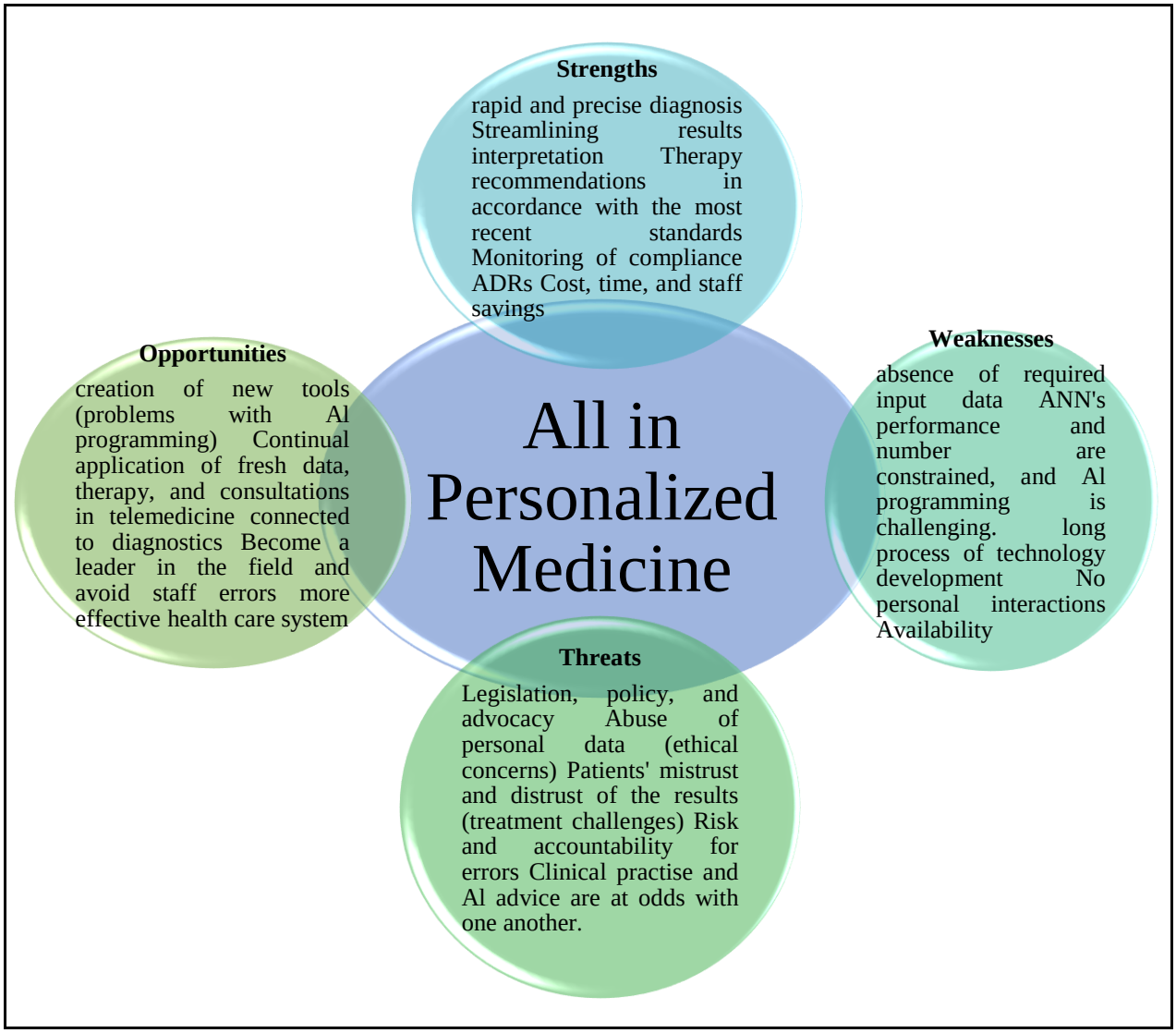
Personalized/effective medication



Recent developments in pharmacogenomics make it easier to identify the various medication effects. Nowadays, personalised medicine is increasingly accessible thanks to advancements in genomics, pharmaceutical technology, pharmaceutical biotechnology, microscopy, and other fields of science. The connection between health and gene is the fundamental tenet of personalised medicine. In personalised medicine, the health histories of the patient's family members have been recorded, and from these records, genetic causes of the specific disease or ailment have been established. [9-10]

Personalised medicine prescribes drugs depending on each patient's genomes. MicroRNA profiling and molecular interaction assist in identifying the illness process. In addition, genomic sequencing, haplotype mapping, and SNP genotyping are crucial in determining the hazards and susceptibility of a given disease or ailment. Implementing personalised medical therapy will enhance the effectiveness of treatment while lowering the toxicity and side effects. A greater comprehension of the variances to their consequences on toxicity, excretion and drug metabolism and will recover the method of error and trial. FDA only mandates Pharmacogenetics testing for a restricted subset of pharmaceuticals, and there is only limited evidence of the therapeutic efficacy of pharmacokinetic testing for a few treatments. [11]

Recent developments in pharmacogenomics are possible to have

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comprehend the drug's causes of a various response. The basis of the drug is a prescribing dosage to a specific patient is provided by the identification of genetic variation and relationship the variable responds to drugs. Genetically tailored design, prescription and administration of improve therapy therapeutic outcomes while reducing is to risk of toxicity and other adverse effect. It is an individual variation of a better understanding and their effect of medicine response, excretion, toxicity and response will take the place of current trial- and error approach to treatment. Only a limited subset of pharmaceuticals has FDA labelling requiring pharmacogenetics testing, and there is scant evidence of the therapeutic value of this technique. There are not various instances pharmacogenomics where affects clinical priority, despite the enormous potential. Numerous genetic variations have not yet been explored; however, some have been linked to various disorders. A label for the uses of that drug may be released based on data relating to the results of therapy with a genetic variant and specific drug. The implementation of personalised medicine's objectives is hampered by numerous restrictions. Future developments in genomics, diagnostic techniques, clinical decision- making and data analysis viable commercial models for personalising treatment may hasten the process of tailoring treatment based on a patient's genetic profile.[12]

Restoration of orphan drugs

Pharmaceutical companies mainly focus on the major drugs which are prescribed for the diseases affecting 20 million people or more. These are called as blockbuster drugs. As a result, we can see that fewer drugs are being produced to treat illnesses that only affect a tiny number of people. These substances are referred to as prospective substances, abandoned substances, or orphan substances. Therefore, if pharmacogenetic genomic strategy could be modified, this would help to develop and revive orphan medications and show who might benefit from them. Pharmaceutical corporations will support the development of orphan pharmaceuticals from a business perspective in order to promote the size of reduction of a population that has to treated, as this is the only way they can abandon blockbuster drugs and promote orphan ones. Pharmacogenomics is now recognised by a number of international food and drug agencies, and its methods of medication development are supported. However, some people are against using these strategies. The notion that the implementation of pharmacogenomics will strategy result in a major less of revenue for the drug market is what is causing this type of resistance. However, some of the workers entirely disagree with this perception and regard it as a MYTH; they claim that the application of these pharmacogenomic technologies would expand the size of the drug market and hold promise for the future. Pharma genomics' Restrictions on Drug Design and Development Progress: Pharmacogenomics research is focused on genetic differences, particularly in coding areas. But in reality, predicting gene variants and coding areas is quite challenging. Single nucleotide polymorphism (SNP) is crucial for the therapeutic response and has a significant impact on it. Between 100 and 300 nucleotides in the 3 billion base Human Genome include SNPs. To determine the role of genetics in drug response, millions of SNPs need to be found and analysed. The lack of awareness and understanding of the attraction between gene variants and variable drug response is one of the key challenges restricting this pharmacogenomics-based drug delivery. Another constraint on this method is how time-consuming and difficult it is. This technique may not be feasible in the near future because numerous genes are anticipated to affect responses, making it difficult to choose the precise genes among them. Each and every doctor and physician involved in this genomic process needs to have a deeper understanding of genetics and take extra steps to identify the optimum medication for each patient. The course of treatment should also vary depending on the patient. Future considerations should also take into account economic factors.

Limitations of Pharma-genomics Progress in Designing Drug and Development of Drug Designing:

Pharmacogenomics research is focused on genetic differences, particularly coding in areas. But in reality, predicting gene variants and coding areas is quite challenging. The single nucleotide polymorphism (SNP) has a significant impact on how the body reacts to drugs. Between 100 and 300 nucleotides in the Human Genome Base for in 3 billion include SNPs. To determine the role of genetics in drug response, millions of SNPs need to be found and analysed. The lack of awareness and understanding of the between connection gene variants and variable response drug is one of the key challenges restricting this pharmacogenomics-based drug delivery. Another constraint on this method is how time-consuming and difficult it is. This technique may not be feasible in the near future because numerous genes are anticipated to affect responses, making it difficult to choose the precise genes among them. Each and every doctor and

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physician involved in this genomic process needs to have a deeper understanding of genetics and take extra steps to identify the optimum medication for each patient. The course of treatment should also vary depending on the patient. Future planning should also take into account economic issues.[13]

The Indian Context of Need for Pharmacogenetics

In the top five India is one of the worldwide pharmaceutical markets as of 2018, accounting for 17.5% of the world's population. The high incidence of drug attrition is one of the primary problems and biggest financial burdens facing the pharmaceutical industry. 54% of the 641 new medications that three-trial entered phase between 1998 and 2008, according to a 2015 study. [14]

One of the 214 medications that entered preclinical research between 1994 and the middle of 2016 was the only one that was ultimately commercialised, according to recall assessment of drug development and drug discovery patterns in India.[15] The most frequently reported causes of medication failure during the development process include high toxicity caused by the molecule's uncertain bioavailability and lack of efficacy.[16] Drugs are frequently removed from the market even after comprehensive clinical studies due to reports of ADRs in particular populations. In India, 6.7% of all hospital admissions result in serious ADRs.[17]

Drug metabolising enzymes (TPMT, NAT2, CYP450s, COMT, GSTs, SULT1A1, and UGTs) and drug transporters (OCT1, MMDR1, and SLCO1B1) with diverse allele frequency distributions among the various Indian subpopulations can be linked to challenges in drug development as well as side effect reaction and inconsistent responses (South Indians, North Indians, and North East Indians). [18]

Bioinformatics and drug discovery

The process of identifying and verifying a disease target and finding and producing a chemical compound to interact with that target is known as the drug discovery process. The pharmaceutical industry requires systems for drug discovery and metabolism, computational chemistry, combinatorial chemistry, ADME informatics, cheminformatics, metabolic modelling, and another multidisciplinary informatics. News and information flow between various departments, such as growth and discovery [19]

Drug target identification

The identification and prediction of biological active candidates, as well as the mining and storage of relevant data, are significant goals of modern bioinformatics techniques. Drugs are typically only created when the specific pharmacological target responsible for their activities has been found and researched. The number of potential targets for drug discovery is increasing dramatically with the help of bioinformatics' mining and warehousing of the human genome sequence, the nucleotide compositions of those genes that code for the target proteins have been defined and categorised, and new targets with greater therapeutic potential have been found predict that the knowledge found in the human genome will be crucial in this field. Drug developers now have an unheard-of choice of luxury as more as gene are found and the drug discovery cycle become more data-intensive. It is anticipated that the number of prospective medications in the pharmaceutical companies of pipelines would significantly expand as a result of bioinformatics' ability to identify and analyse an increasing number of biological therapeutic targets.[20]

Designing of new drug:

One of the most very important steps in the discovery and formulation of novel drugs is drug design. A key part of it is played by advanced bioinformatics. The drug design depends upon various factors such as (a) identification of new drug targets (b) 3D structure of PDB database (c) advance bioinformatics (d) tools for detecting protein-drug interaction. Types of drug design: Basically, there are two types of drugs designing process. (a) Ligand based drug design: Molecules those are binds with target. 3D QSAR and pharmacophore modelling are mostly utilised in ligand-based drug design. (b) Drug design based on structure: The protein structure of a newly found chemical entity is compared with a known protein structure in structure-based drug creation utilising X-ray crystallography.[21]

Drug target validation

Bioinformatics also provides techniques and Algorithms for forecasting novel drug target as well as for storing and maintaining information on current target drugs. After the identification of "potential" therapeutic target, is there hardly ever to need demonstrate a direct connection between a target and the desired disease. The procedure of creating such a major relationship justifies the process of creating new drugs. Target validation is a procedure where bioinformatics is heavily influencing what is happening. Validating drug targets aids in reducing the risk of failure during the clinical testing and approval processes. [22]

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The limits of bioinformatics

Although more difficult studies are now possible thanks to advancements in technology, bioinformatics' potential is constrained. Massive volumes of biological data can be transformed by bioinformatics into patterns that people can read and understand, but those patterns still require interpretation by biologists who have specialised in related fields. In fact, the field of bioinformatics frequently requires bringing specialists from a wide range of disciplines together in order to interact at every stage of the experimental chain. Additionally, the amount and speed of bioinformatics analysis will always be constrained by computational resources. The majority of tools still need to run on large computers and servers that must be in the cloud, even if current projects have come a long way from earlier attempts that relied on user processing power to answer their queries. [23]

Benefits of Bioinformatics:

The following is a brief discussion of the major advantages that bioinformatics tools provide for drug discovery programmes:

According to the Tufts Report, each successful drug that is commercialised now costs $800 million to find and develop. To lessen this financial burden, several companies of biopharmaceutical now use of computation techniques and bioinformatics technologies. Experimental research can be influenced by virtual screening, lead optimisation, and estimations of bioactivity and bioavailability. The early end avoided can be experimental dead by only pursuing the most promising experimental avenues of investigation. The increased use of bioinformatics in the pharmaceutical sector is mainly responsible for the market's expansion. With use of the bioinformatics in medication research and development, it is anticipated that the early of creating a novel drug will fall by 32% annually and that the time required for discovery drug will shorten by 30%. [24]

In the anticipated $25.1 billion worldwide market for drug discovery in 2006, that is a valuable proposition. According to BCC Research, the global bioinformatics industry will grow from its current $1.4 billion to $3 billion in 2010, for a compound annual growth rate (CAGR) of 15.8 percent. This development should be driven by analysis software and services, which should increase from $450 million in 2005 to $1.2 billion in 2010[25]

Time-line-

Drug research programmes can select only the most promising drug candidates with the aid of CADD's predictive ability. Biopharmaceutical businesses can speed up the time it takes for drugs to reach the market by concentrating drug research on particular lead candidates and avoiding possible "dead-end" compounds.[26]

The in-depth knowledge that researchers gain regarding drug-receptor interactions is one of the non-quantifiable advantages of CADD and the usage of bioinformatics technologies Drugs' intricate, atomic-scale binding properties, which are impossible to envision in any other manner, can be seen in detail in molecular models. When we provide researchers with updated molecular models of their potential therapeutic substances, their protein targets, and how the two interact, they usually come up with fresh suggestions for how to change the drug substances for better match. This intangible advantage might make creating study routines easier. [27]

Bioinformatics technologies can be used to acquire all the necessary information about possible targets. Among other things, this data includes information on gene and protein expression as well as information on species distribution, homologous mapping, function prediction, pathway information, illness connections, and variations. Pharmaceutical companies are able to avoid wasting time, money, and resources on bench research on targets that won't succeed thanks to the collection of this data into databases about potential targets.[28]

IV. TOOLS USED IN PHARMACOGENOMICS AND DEVELOPMENT

Bioinformatics Tools for Population Science study

Google Trends

A server was created by the Google corporation to aid in understanding public influenza outbreaks.[29]

It was developed and is used to quickly identify regional influenza outbreaks under the name Google Flu Trends. It quickly gathers and analyses the data, assisting in the quick identification of influenza disease transmission in the population under investigation. There is a lot of potential for Google Trends to be a sensitive, trustworthy, and timely surveillance system. This server is now best suited to tracking disease activity in industrialised nations because it requires large populations of web search users to be most effective. For the

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surveillance of epidemics and diseases with a high prevalence, it is very beneficial. [30-38]

National Electronic Disease Surveillance System (NEDSS)

In order to inform medical professionals and governmental bodies about the prevalence, trends, and outbreaks of infectious diseases in the population under study, the National Electronic Disease Surveillance System (NEDSS) was created. Online disease databases, cutting-edge computing equipment, and bioinformation technology tools are used to run the NEDSS. The capacity of the surveillance systems is increased by each of these elements, including the National Electronic Telecommunications System for Surveillance (NETSS), HIV/AIDS reporting systems, immunisation campaigns, and tracking systems for tuberculosis and other infectious diseases among the general population. This helps underdeveloped countries keep infectious diseases under control, which is very advantageous. [39]

HealthiManage

With the help of the iPhone bioinformatics app HealthiManage, type 2 diabetics can forecast their blood glucose levels. It provides patients with relevant feedback and contrasts the measured and projected values at each glucose input reading to encourage improved disease self-management.

Oncomine

A valuable resource for cancer profiling data is Oncomine (www.oncomine.org), which allows target expression to be analysed immediately online across a wide range of cancer types, subtypes, and trials. In order to get more understanding of biology, regulation, pathways, pharmacological reactions, and patient demographics, the Oncomine database has included various gene information.

Pharmacogenomics Knoledgebase (PharmGKB)

The Pharmacogenomics Knowledgebase (PharmGKB) is a sizable database that compiles data on how genetic variation affects pharmacological response, including dosage suggestions, drug names, gene-drug connections, and genotype-phenotype associations.

The Search Tool for the Retrieval of Interacting Genes/Proteins (STRING)

The database of actual and anticipated protein interactions is known as STRING, or the Search Tool for the Retrieval of Interacting Genes/Proteins. The correlations are collected from the genetic background, high-throughput tests, co-expression, and scientific literature. There are both direct (physical) and indirect (functional) associations. STITCH, a related project.

The Search Tool for Interaction of Chemicals (STITCH)

The Search Tool for Interaction of Chemicals (STITCH) is a tool for investigating actual and anticipated chemical and protein interactions. Evidence obtained from tests, databases, and the literature links chemicals to proteins and other molecules. STRING, a sister project.[40]

PGx Annotation

Annotation in PGx the process of determining how genetic variations affect genes and diseases is known as variant annotation One can obtain annotation for PGx variants using general genetic variant annotation methods like VEP, SnpEff/SnpSift, Annovar, or Intervar. Using specialised software, such as PharmCAT, which was developed in accordance with CPIC's requirements, PGx genes could be annotated more completely. Such recommendations base prescribing recommendations on genotype/phenotype and relate genotypes to phenotypes. The most recent PGx recommendations are made by PharmVar, who is still the market leader, along with CPIC, DPWG, CPNDS, and others. Due to the scarcity of standards, such annotation strategies can only cover a very small part of PGx genes. PharmCAT can now detect just 12 recommendations out of 64 VIPs (very important pharmacogenomics) of more than 100 identified PGx genes.[41]

Put-All-Together

To locate and identify variants and haplotypes related to ADR, a variety of data analytics techniques have been developed. A pipeline analysis using WGS/WES/genotyping data on three genes—CYP2C9, CYP2C12, and HLA—has been conducted. [42]

Using the 1585 individuals' complete exome sequencing data, 39 variations were identified, and then a haplotype was determined based on U-PGx translation. Presently, the PGRN pipeline appears to be the industry standard for PGx data analysis. Several organisations, including RIKEN-Pharmacogenomics Laboratory and SEAPHARM, created their own processes for analysing pharmacogenomics data in the meantime (personal discussion). Nonetheless, effective

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haplotype identification in pharmacogenomics remains difficult, particularly for highly polymorphic areas like CYP2D6 or the HLA. There are still many unidentified PGx gene haplotypes and diplotypes. Better annotation methods must be created because it is currently difficult to annotate PGx genes that contain new alleles. The guidelines for gene-drug interactions are now still quite scarce; for instance, the CPIC database offers just 12 specific suggestions to enable enhancing drug therapy. Furthermore, due to numerous factors like age, gender, and the interactions between medication molecules, the genotype-phenotype link is frequently still unknown. It is incredibly difficult but yet very vital to create instruments to capture such ambiguity.[43]

HLA Typing

HLA typing is never easy because of the complexity and high polymorphisms of HLA regions, especially for NGS data. Utilising applications like PHLAT, Polysolver, OptiType, xHLA, or Kourami, users of NGS data can enter HLA alleles with 4-digit, 6-digit, or 8-digit codes. [44-46]

Utilizing WGS/WES data, up to 8 digits. These technologies frequently only have the ability to find known HLA alleles. Seq2HLA can be used to obtain 4-digit resolution for RNA-seq data. Despite several efforts, finding novel or class II HLA alleles is still a problem with current HLA typing techniques.[47]

Epi Info™

The tool Epi InfoTM was developed specifically for the study of epidemiology and is based on statistical applications and biology. It was created and made public by the Centres for Disease Control and Prevention (CDCs, http://www.cdc.gov/epiinfo) in Atlanta, Georgia (USA). On mobile devices running Microsoft Windows, Android, and iOS, Epi Info (beta) is available. The software gathers information from epidemiological research and enables data entry and additional analysis. T-tests, ANOVA, nonparametric statistics, cross tabulations and stratification with odds ratio, risk ratio, and risk difference estimates, logistic regression (conditional and unconditional), survival analysis (Kaplan Meier and Cox proportional hazard), and analysis of complex survey data (also from https://en.wikipedia.org/wiki/Epi Info) are all functions that can be performed by the programme. [48]

AnSWR: Analysis Software for Word-Based Records

AnSWR is an information technology-based software system that aids in the scanning, organisation, and scheduling of huge amounts of data (http://www.cdc.gov/hiv/library/software/answr/). This tool integrates qualitative and quantitative methodologies quickly and can be used for large-scale team-based analytical tasks.

AnSWR offers the following applications:

- It is advantageous to coordinate team-based qualitative data analysis from a large population.
- It manages and coordinates the use of sizable, intricate qualitative databases.
- It makes it easier to construct structured codebooks that can be further organised into hierarchical coding frameworks.
- It enhances evaluation and text coding for information collecting.
- By offering customizable reporting options with a wide range of selection criteria (files, codes, coders, and quantitative variables), this improves the integration of the massive amount of data even more.
- Because of its output formats' dependability and simplicity, both quantitative and qualitative software can easily import them. Then, it would be simple to review and include these programmes for user applications. [49]

Genetic Variant Calling

For variant calling on NGS data, the GATK best practices112 are frequently advised, together with BWAMEM113 for reading alignment. In some cases, in addition to or even in instead of BWA-MEM, additional systems, such as DeepVariant114 or Novoalign (http://novocraft.com/), can be used to improve performance. For WGS, WES, or sequencing data generated by gene panels, this is broadly relevant. The named variations frequently act as a jumping off point for subsequent investigations to investigate ADRs.[50-52]

Pharmacogenomics in COVID-19 therapy

The benefits of pharmacogenomic biomarkers are both concrete and abstract. The development of novel COVID-19 treatments has been the physical benefit, whilst the intangible benefit has been the strategic insights gained that have helped enlarge our understanding of the battle against COVID-19.

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The ACE2 gene variant is one of the several genetic variations linked to different responses to COVID-19. The SARS-CoV-2 Coronavirus has been demonstrated to enter the body through the angiotensin-converting enzyme 2 (ACE2). Angiotensin II is broken down by the ACE2 enzyme, allowing the virus to enter more easily. Recent research suggests that there may be a genetic component to the relationship between the severity of COVID-19 results and ACE gene variations.

As a result, pharmacogenomics is anticipated to offer crucial insights into therapeutic innovation for COVID-19, particularly given the likelihood of future COVID-19 waves. These revelations will be crucial in planning clinical research and will substantially facilitate the search for novel medicines. [53]

V. CONCLUSION:

In conclusion, recent trends in pharmacogenomics have shown great promise in advancing personalized medicine, enhancing drug development, and improving patient outcomes. The integration of genomic data, advanced bioinformatics tools, and innovative technologies has paved the way for more precise and individualized approaches to drug therapy. Continued advancements in these areas hold great potential for improving patient outcomes, optimizing drug development, and shaping the future of healthcare. However, further research, standardization, and ethical considerations are necessary to fully realize the potential of pharmacogenomics in clinical practice.

References

[1]. Shukla, R. (2020b). Pharmacogenomics: Overview, Applications, and Recent Developments. IntechOpen EBooks. https://doi.org/10.5772/intechopen.93737
[2]. MedlinePlus [Internet]. Bethesda (MD): National Library of Medicine (US); [updated Jun 24; cited 2020 Jul 1]. Available from: https://medlineplus.gov/.
[3]. Saunders, H., Harris, D., & Chirilă, R. M. (2020). Pharmacogenomics: introduction and use in clinical practice. Romanian Journal of Internal Medicine, 58(2), 69–74. https://doi.org/10.2478/rjim-2020-0001
[4]. https://www.genome.gov/genetics-glossary/Bioinformatics
[5]. Can, T. (2013b). Introduction to Bioinformatics. MiRNomics: MicroRNA Biology and Computational Analysis, 51–71. https://doi.org/10.1007/978-1-62703-748-8_4
[6]. Cohen N (November 2008). Pharmacogenomics and Personalized Medicine (Methods in Pharmacology and Toxicology). Totowa, NJ: Humana Press. p. 6. ISBN 978-1934115046.
[7]. https://byjus.com/biology/bioinformatics/#:~:text=Processes%20of%20Biotechnology,Application%20of%20Bioinformatics,designing%20and%20a%20lot%20more
[8]. Nida Tabassum Khan. "Clinical Bioinformatics: Linking Pharmacogenomics with Informatics". Acta Scientific Pharmaceutical Sciences.2018; 2(3) : 67-7031.Ann K Daly, Pharmacogenetics: a general review on progress to date,BritishMedicalBulletin, 2017; 124(1): 65–79
[9]. Whirl-Carrillo M., et al. "Pharmacogenomics knowledge for personalized medicine". Clinical Pharmacology and Therapeutics.2012; 92(4) : 414.
[10]. Squassina A., et al. "Realities and expectations of pharmacogenomics and personalized medicine: impact of translating genetic knowledge into clinical practice". Pharmacogenomics.2010; 11(8):1149-1167
[11]. Chakraborty, A., Mukherjee, P. C., Chakraborty, M., & Singha, D. K. (2021). An UpdatedReview onBioinformatics and Pharmacogenomics in Drug Discovery and Development Process. Asian Journal of Pharmaceutical Research and Development, 9(3), 62–65. https://doi.org/10.22270/ajprd.v9i3.942
[12]. Singh, D. B. (2019). The Impact of Pharmacogenomics in Personalized Medicine. Advances in Biochemical Engineering / Biotechnology, 369–394. https://doi.org/10.1007/10_2019_110
[13]. Chakraborty, A., Mukherjee, P. C., Chakraborty, M., & Singha, D. K. (2021). An UpdatedReview onBioinformatics and Pharmacogenomics in Drug Discovery and Development Process. Asian Journal of Pharmaceutical Research and Development, 9(3), 62–65. https://doi.org/10.22270/ajprd.v9i3.942
[14]. Mohs RC, Greig NH (2017) Drug discovery and development : Role of basic biological

International Journal of Pharmaceutical research and Applications
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research. Alzheimer's & Dementia: Translational Research & Clinical Intervention 3(4): 651-657.
[15]. Mohs RC, Greig NH (2017) Drug discovery and development : Role of basic biological research. Alzheimer's & Dementia: Translational Research & Clinical Intervention 3(4): 651-657.
[16]. Differding E (2017) The Drug Discovery and Development Industry in India- Two Decades of Proprietary Small-Molecule R & D. 12(11): 786-818.
[17]. Mohs RC, Greig NH (2017) Drug discovery and development : Role of basic biological research. Alzheimer's & Dementia: Translational Research & Clinical Interventions 3(4): 651-657.
[18]. Lihite RJ, Lahkar M, Das S, Hazarika D (2017) A study on adverse drug reactions in a tertiary care hospital of Northeast India. Alexandria Journal of Medicine 53(2): 151-156.
[19]. Priyadarshini R, Raj GM, Shewade DG (2018) Status of Pharmacogenomics Research in India During the Last Five Years. Proceedings of the Indian National Science Academy 84(1): 195-223.
[20]. Siddharthan, N., Prabu, M. R., & Sivasankari, B. (2016). Bioinformatics in Drug Discovery a Revi. International Journal of Research in Arts and Science. https://doi.org/10.9756/ijras.8099
[21]. Katara, P. Role of bioinformatics and pharmacogenomics in drug discovery and development process. Netw Model Anal Health Inform Bioinforma 2, 225–230 (2013). https://doi.org/10.1007/s13721-013-0039-5
[22]. Arindam Chakraborty,Payel Mukherjee, Manas Chakraborty, Dipak kumar Singha, An UpdatedReview onBioinformatics and Pharmacogenomics in Drug Discovery and Development Process, AsianJournal of Pharmaceutical Research and Development. 2021; 9(3):62-65.DOI: http://dx.doi.org/10.22270/ajprd.v9i3.942
[23]. Katara, P. Role of bioinformatics and pharmacogenomics in drug discovery and development process. Netw Model Anal Health Inform Bioinforma 2, 225–230 (2013). https://doi.org/10.1007/s13721-013-0039-5
[24]. https://www.pnnl.gov/explainer articles/bioinformatics#:~:text=Bioinformatics%20is%20used%20to%20analyze,evaluate%20relationships%20in%20large%20datasets.
[25]. www.ddd.mag.com
[26]. www.activemedia-guide.com/pharmaceutical_industry.htm (Industry Analysis, Pharmaceuticals Industry, source: US Business Reporter, 17/11/01).
[27]. Clinical costs skyrocket to new levels. Phil Webster, Pharma-Biotech Research Analyst (Published 09/12/04 Source: Frost and Sullivan. www.inpharm.com/External/InpH/1,2580,1-3-128917
[28]. Clinical costs skyrocket to new levels. Phil Webster, Pharma-Biotech Research Analyst (Published 09/12/04 Source: Frost and Sullivan. www.inpharm.com/ External/InpH/1,2580, 1-3-128917
[29]. Genomics Provides Crucial Tools for Breaking Bottlenecks in Drug Discovery and Development. www.healthtech.com/newsarticles/issueII_1.asp
[30]. Carneiro HA, Mylonakis E (2009) Google trends: a web-based tool for real-time surveillance of disease outbreaks. Clin Infect Dis 49(10):1557–1564
[31]. Carneiro HA, Mylonakis E (2009) Google trends: a web-based tool for real-time surveillance of disease outbreaks. Clin Infect Dis 49(10):1557–1564
[32]. Alicino C, Bragazzi NL et al (2015) Assessing Ebola-related web search behaviour: insights and implications from an analytical study of google trends-based query volumes. Infect Dis Poverty 4:54
[33]. Bragazzi NL, Bacigaluppi S et al (2016) Infodemiology of status epilepticus: a systematic validation of the google trends-based search queries. Epilepsy Behav 55:120–123
[34]. Fond G, Gaman A et al (2015) Google trends: ready for real-time suicide prevention or just a zeta-Jones effect? An exploratory study. Psychiatry Res 228(3):913–917
[35]. Pollett S, Wood N et al (2015) Validating the use of google trends to enhance pertussis surveillance in California. PLoS Curr 7
[36]. Reed DD (2015) Google search trends for tanning salons: temporal patterns indicate peakinterest in mid spring. J Am Acad Dermatol 73(6):1055–1056

International Journal of Pharmaceutical research and Applications
Volume 8, Issue 4, Jul.-Aug. 2023, pp: 396-408 www.ijprajournal.com ISSN: 2456-4494

[37]. Toosi B, Kalia S (2015) Seasonal and geographic patterns in tanning using real-time data from google trends. JAMA Dermatol 152(2):1–2
[38]. Wang HW, Chen DR et al (2015) Forecasting the incidence of dementia and dementia-related outpatient visits with google trends: evidence from Taiwan. J Med Internet Res 17(11):e264
[39]. Zou X, Zhu W et al (2015) Google flu trends--the initial application of big data in public health. Zhonghua Yu Fang Yi Xue Za Zhi 49(6):581–584
[40]. National Electronic Disease Surveillance System Working, G (2001) National Electronic Disease Surveillance System (NEDSS): a standards-based approach to connect public health and clinical medicine. J Public Health Manag Pract 7(6):43–50
[41]. https://guides.library.yale.edu/bioinformatics/pharmacogenomics
[42]. McCarthy DJ, Humburg P, Kanapin A, et al. Choice of transcripts and software has a large effect on variant annotation. Genome Med. 2014;6(3):26. doi:10.1186/gm543
[43]. van der Lee M, Allard WG, Bollen S, et al. Repurposing of diagnostic whole exome sequencing data of 1583 individuals for clinical pharmacogenetics. Clin Pharmacol Ther. 2020;107(3):617–62. doi:10.1002/cpt.1665
[44]. Srinivasan BS, Chen J, Cheng C, et al. Methods for analysis in pharmacogenomics: lessons from the Pharmacogenetics Research Network Analysis Group. Pharmacogenomics. 2009;10(2):243–251. doi:10.2217/14622416.10.2.243
[45]. Boegel S, Löwer M, Schäfer M, et al. HLA typing from RNA-Seq sequence reads. Genome Med. 2012;4(12):102. doi:10.1186/gm403
[46]. Szolek A, Schubert B, Mohr C, et al. OptiType: precision HLA typing from next-generation sequencing data. Bioinformatics (Oxford, England). 2014;30(23):3310–3316. doi:10.1093/bioinformatics/btu548
[47]. Boegel S, et al. In silico HLA typing using standard RNA-Seq sequence reads. In: Bugert P, editor. Molecular Typing of Blood Cell Antigens. New York: Springer New York; 2015:247–258
[48]. Sharma, A., Sinha, S., Johari, S., & Mazumder, B. (2018). Bioinformatics and Pharmacogenomics: Tools to Understand and Accelerate Infectious Disease Control. Genomics-Driven Healthcare, 59–69. doi:10.1007/978-981-10-7506-3_4
[49]. Sharma, A., Sinha, S., Johari, S., & Mazumder, B. (2018). Bioinformatics and Pharmacogenomics: Tools to Understand and Accelerate Infectious Disease Control. Genomics-Driven Healthcare, 59–69. doi:10.1007/978-981-10-7506-3_4
[50]. Van der Auwera GA, et al. From FastQ data to high confidence variant calls: the Genome Analysis Toolkit best practices pipeline. Curr Protoc Bioinformatics. 2013;43(1110):11.10.1–11.10.33.
[51]. Li H, Aligning sequence reads, clone sequences and assembly contigs with BWA-MEM. arXiv preprint arXiv:1303.3997, 2013.
[52]. Poplin R, Chang P-C, Alexander D, et al. A universal SNP and small-indel variant caller using deep neural networks. Nat Biotechnol. 2018;36(10):983–987. doi:10.1038/nbt.4235
[53]. https://www.pharmafocusasia.com/clinical-trials/current-trends-pharmacogenomics-clinical-trials