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Challenges in Combining Pharmacogenomics with Electronic Health Records in the Field of Biomedical Data Science and Informatics

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ABSTRACT

The discipline of biological data science and informatics has considerable obstacles in integrating pharmacogenomics with electronic health records (EHRs). Pharmacogenomics is the study of how genetic variations affect drug responses. To do this, it combines information from molecular science, pharmacology, and clinical medicine. Addressing genetic variability among populations, developing data interchange standards, merging disparate information, mining scientific literature, and comprehending how structural variations and quality articulation impact drug absorption are some of the major hurdles. Furthermore, given that genetic information is unique to each individual, securing sensitive patient data is essential. The intricacy of integrating genetic data into clinical practice is highlighted by the fact that, although some healthcare systems have successfully integrated pharmacogenomic decision support systems, or clinical decision support (CDS), into EHRs, these initiatives typically rely on institutional infrastructure and custom-fabricated rules. In order to improve tailored medicine, effective CDS devices incorporate latent and active cautions that direct physicians in drug prescription based on a patient's genetic profile. Still, there are a lot of issues with EHR analytics, such as the need for standardized, repeatable procedures to impede research reproducibility and the difficulty of phenotyping and data pre-processing. These problems include the need for interdisciplinary cooperation, advanced computation sharing, and methodical procedures in order to fully address pharmacogenomics in healthcare.

Keywords: Challenges, Combining Pharmacogenomics, Electronic Health Records, Biomedical Data Science, Informatics, Clinical Decision Support

INTRODUCTION

The study of pharmacogenomicsthe search for the characteristics that influence a person's response to medicationhas great promise for developing personalized treatment. Healthcare providers can tailor medications to each patient, improving therapeutic outcomes and reducing adverse drug responses, by incorporating genetic information into clinical practice. However, realizing this promise necessitates the constant integration of pharmacogenomic data with Electronic Health Records (EHRs), a task fraught with numerous difficulties in the biomedical informatics and data science fields.

The intricacy of genomic data is a major obstacle to pharmacogenomics' integration with EHRs. Unlike traditional clinical data, which is limited to particular parameters like cholesterol or circulatory strain, genetic data is dynamic, wide-ranging, and very specific. Within EHR systems, this poses problems with translation, capacity, and usability. Large-scale genetic datasets should be handled by EHRs, often necessitating complex computations and cutting-edge computational capabilities, in order to provide healthcare professionals with actionable experiences. In addition, the integration process demands the establishment of precise and standardized methods to ensure the reliability and correctness of the genetic data that is used.

The lack of communication between pharmacogenomic databases and current EHR systems is another issue. Different EHR systems are usually used by healthcare facilities, and the lack of common data architecture makes it more difficult to share pharmacogenomic information between phases. In order to facilitate seamless communication between healthcare providers and systems, standardization is needed for both the collection and translation of pharmacogenomic data within the EHR. To do this, more inclusive data organizations, APIs, and tools that can handle the subtleties of genetic data while ensuring data integrity and consistency must be developed.

Security and data privacy are further important issues. Genetic data is extremely sensitive since it reveals deeply personal experiences on an individual's health, family history, and susceptibility to specific diseases. Concerns about

who can access this data and how it is safeguarded arise when it is integrated into EHRs. Secure systems for storing and exchanging pharmacogenomic data should be promoted by biomedical data science to ensure adherence to stringent administrative requirements, such as the Health Insurance Portability and Accountability Act (HIPAA) in the United States. It is still a difficult task to strike a balance between patient privacy protection and healthcare supplier accessibility.

Similarly, to enable healthcare providers to take proactive steps using pharmacogenomic data, clinical decision support systems (CDSS) has to be streamlined. EHR systems ought to be designed to interpret complicated genetic data and provide physicians with concise, fact-based advice. In any case, the ability to apply this data successfully is often limited by the absence of comprehensive training and preparation among healthcare professionals in pharmacogenomics. Clinicians may find it challenging to integrate genetic information into their decision-making process if they lack appropriate training in genomics, which could lead to an underutilization of data that is readily available.

Infrastructure and financial limitations are major roadblocks. It is expensive and resource-intensive to establish systems that integrate pharmacogenomic data with EHRs; healthcare associations must invest in new staff, programming, and infrastructure. Smaller healthcare institutions might not have the means to implement these systems, particularly in developing areas, which would worsen disparities in access to personalized medication.

REVIEW OF LITERATURE

Gammal et al. (2016)discusses the relationship between UGT1A1 genotypes and the appropriate dosage of atazanavir, an antiretroviral drug used to treat HIV, for the Clinical Pharmacogenetics Implementation Consortium (CPIC). A person's risk of developing hyperbilirubinemia while taking atazanavir can be influenced by variations in UGT1A1 quality, as this enzyme plays a crucial role in the glucuronidation and digestion of bilirubin. The regulation highlights the importance of personalized treatment by suggesting particular dosage adjustments based on UGT1A1 genotypes.

For example, individuals carrying the UGT1A1*28/*28 genotype have a higher risk of having elevated bilirubin levels and may need to undergo elective therapies. The goal of this pharmacogenetic strategy is to maintain therapeutic efficacy while lowering drug toxicity in order to enhance patient outcomes. The research emphasizes how clinically valuable genetic testing is for enhancing therapy personalization and minimizing side effects in prescription practices.

Hicks et al. (2015)concentrate on the impact of CYP2D6 and CYP2C19 genotypes on selective serotonin reuptake inhibitor (SSRI) dosage. SSRIs are commonly used to treat depression and anxiety disorders. Key enzymes involved in the digestion of certain SSRIs, such as sertraline, citalopram, and paroxetine, are CYP2D6 and CYP2C19. These substances have four different types of metabolizers: poor, midway, broad (typical), and extremely rapid metabolizers.

Genetic polymorphisms in these compounds can cause variations in drug digestion. The guideline provides detailed advice on adjusting SSRI dosages based on a patient's genotype. Due to their slower medicine clearance, unfortunate metabolizers, for example, would need smaller portions, whilst extremely speedy metabolizers might need larger quantities or optional treatments. The rule aims to improve therapeutic efficacy, lower the risk of side effects, and prevent subpar treatment reactions by incorporating pharmacogenetic data into clinical decision-making, especially for patients with unique metabolic profiles.

Iqbal et al. (2016)examine the reproducibility and transparency of research methods critically in biomedical writing, bringing up issues with the reliability of dispersed discoveries. The authors examine important elements that are causing the reproducibility dilemma, including inadequate data sharing, selective announcing, and a lack of scientific depth. They support the adoption of open science methods, such as preregistration of research protocols, open access to raw data, and openness in statistical analysis. The focus also emphasizes the significance of initiatives aimed at advancing the credibility of research, such as the unavoidable adoption of the FAIR (Findable, Accessible, Interoperable, Reusable) data management principles. The authors argue that by increasing openness and comprehensiveness in biomedical research, scientific findings will become more reliable and useful, ultimately improving public health outcomes. The paper also discusses the role that journals, funding organizations, and establishments have in promoting laws that promote accountability and reproducibility in research.

Johnson and Weitzel (2016)examine how pharmacogenomics functions within the broader context of precision medicine, emphasizing the potential for changing medication therapy. They talk about the ways that pharmacogenomics can be advanced, including as integrating genetic testing into conventional clinical care, developing uniform regulations, and training healthcare providers. The authors argue that comprehending the benefits of pharmacogenomics—which enable more individualized medications that improve efficacy and reduce adverse drug reactions—will require clinical application. They highlight particular fields like psychiatry and oncology, where patient

differences in treatment response are substantial, where pharmacogenomics can be broadly advantageous. The infrastructure—such as clinical decision support tools that employ genetic data and electronic health records—that is anticipated to support pharmacogenomics is also discussed in the paper. Johnson and Weitzel emphasize the importance of working together with scientists, physicians, legislators, and educators to increase the use of pharmacogenomics in precision medicine and, ultimately, achieve long-term results through tailored treatment approaches.

Leckband et al. (2013)emphasize the relationship between HLA-B genotypes and the risk of severe side effects from carbamazepine, a drug that is frequently used to treat bipolar disorder and epilepsy. Before administering carbamazepine, the Clinical Pharmacogenetics Implementation Consortium (CPIC) guidelines advise testing for the HLA-B15:02 allele, particularly in populations where this variant is more prevalent, such as individuals of Asian origin. Toxic epidermal necrolysis (TEN) and Stevens-Johnson syndrome (SJS) are two severe cutaneous adverse reactions (SCARs) that are strongly linked to the existence of HLA-B15:02. The guideline advises against using carbamazepine in individuals with the HLA-B*15:02 genotype due to the significant risk associated with these dangerous responses. By integrating genetic information into prescribing practices, these regulations address a crucial step in lowering drug-related harm through pharmacogenetic testing, thereby promoting the safer use of carbamazepine and promoting tranquil wellbeing.

Muir et al. (2014)provide CPIC guidelines for the use of IFNL3 (now renamed IL28B) genotyping in conjunction with Stake interferon-alpha-based treatment plans for long-term hepatitis C infection. In individuals with hepatitis C virus (HCV) genotype 1, treatment outcomes range markedly based on genetic variation, and the IFNL3 genotype is a major predictor of treatment response in this population. According to the rule, patients with the more favourable TT or TC genotypes may see lower reaction rates and greater treatment disappointment, but those with the positive IFNL3 CC genotype will almost always respond better to interferon-based therapies. Clinicians can make better treatment decisions with the use of this pharmacogenetic knowledge, especially when contemplating the use of more proven interferon-based therapies or when direct-acting antiviral specialists are unavailable. The integration of IFNL3 genotyping into clinical practice improves the ability to forecast treatment results and provides a more individualized method of managing HCV infections, leading to more informed treatment decisions and improved long-term results.

Challenges for Biomedical Informatics In Pharmacogenomics

All of the challenges facing biomedical informatics in the study of pharmacogenomics flow directly from the previous conversation. Since pharmacogenomics is still relatively young, the current buzz stems, in part, from the amazing opportunity for contributions that currently exists. One of the key topics in pharmacogenomics is that the important informatics competency encompasses data from clinical medicine (drugs, diseases, side effects), pharmacology (pharmacokinetics and pharmacodynamics), and molecular science (sequences, structures, pathways). This way, it tackles another wave of informatics problem whereby fundamental biology and clinical data has to be merged and analyzed. Even though bioinformatics was previously limited to problems related to molecular science (sequence and structure analysis), applications are now becoming more closely associated with the aspects of clinical informatics that center on the association of clinical data, especially for research objectives. There are nine main areas where biomedical informatics in pharmacogenomics faces challenges:

Representing the Diversity of Pharmacogenomic Data:

One area of focus in pharmacogenomics is the implications of genetic variations for patient responses to medications. The variability in characteristics responsible for medication absorption, transportation, and targeting gives rise to the diversity of pharmacogenomic data. Since genetic variations can differ greatly between ethnic groups, addressing this data requires gathering information from a variety of populations. Researchers should make sure that the information gathered represents a wide range of genetic origins, lifestyles, and natural opportunities in order to work on personalized medicine and the effectiveness of medications across diverse populations.

Developing Standards for Data Exchange:

As pharmacogenomic research involves massive datasets from multiple sources and fields, standardizing data interchange protocols is essential. Standards ensure that information gathered in one location can be interpreted and used by researchers in another. By regulating data organization, communication, and storage, these standards ensure system compatibility and interoperability. Their ability to facilitate seamless data coordination from various sources makes them essential for pharmacogenomics advancement and collaborative research.

Integrating Data from Multiple Data Resources:

Integrating several types of data, such as genetic, clinical, medication response, and ecological aspects, is essential to pharmacogenomic research. This combination provides a thorough understanding of the factors that affect drug response. Either way, integrating this kind of diverse data is hard and needs sophisticated computing tools to correct

patterns and ensure precision. Efficient integration enables scientists to compile robust information for identifying biomarkers, forecasting medication effectiveness, and developing personalized therapies.

Mining Literature for Knowledge:
literature mining is the process of gleaning useful information from vast amounts of scientific literature by applying computational tools. This helps in pharmacogenomics to identify novel genetic variants, comprehend drug interactions, and reveal previously unknown relationships. Writing mining, through process robotization, ensures that vital information in the rapidly evolving field of pharmacogenomics is not overlooked, helps keep up with the latest developments, and speeds up discovery.

Using Expression Data to Understand Regulation:
Understanding which qualities regulate medication response depends on knowing which qualities are active in particular tissues or situations, which is revealed by quality articulation data. Within pharmacogenomics, dissecting quality articulation designs identifies the molecular processes governing a patient's response to medicine. By identifying quality targets and comprehending the ways in which different qualities interact to affect drug efficaciousness and digestion, this information can shed light on the development of drugs and personalized treatment approaches.

Understanding the Structural Basis for Variability:
Genetic variation often results from variations in the structural characteristics of traits, such as larger structural variants or single nucleotide polymorphisms (SNPs). These genetic alterations may have an impact on how drugs work with their intended targets, are used, and are transported throughout the body. Comprehending the structural basis for these variations enables researchers to more precisely anticipate drug responses and customize medications based on individuals' genetic makeup, so improving treatment security and efficacy.

Using Comparative Genomics:
Comparing the genomes of different animals or individuals allows comparative genomics to identify conserved or unique elements. It helps scientists identify genetic variations in pharmacogenomics that may affect drug responses in different species or populations. Scientists can more easily comprehend how these genetic characteristics contribute to changeability in medication reactivity by focusing on similarities and differences in properties related to drug digestion, transport, or targets. This approach can guide the development of novel therapeutics and customized therapies.

Managing Laboratory Information:
Effective administration of laboratory information is essential because pharmacogenomic research generates enormous amounts of data, ranging from genetic sequences to tranquilize reaction testing. Laboratory information management systems, or LIMS, assist with organizing, storing, and monitoring data; they ensure that the data is traceable and easily available. Proper management ensures that laboratory procedures and outcomes are routinely and securely recorded, which promotes administrative compliance, data examination, and collaboration.

Protecting Sensitive Patient Information:
Privacy considerations are significant because pharmacogenomics often involves sensitive genetic and clinical data. Maintaining confidentiality and making sure that legal and ethical requirements are met are both dependent on protecting patient information. Individual data is protected by the use of sophisticated encryption methods, data anonymization, and stringent access limits. It is a fine line to walk when it comes to maintaining public confidence and enabling the use of genetic data in healthcare without jeopardizing security. Protecting patient privacy while enabling research is essential.

Integrating Pharmacogenomics Into The Ehr With CDS: Model Practices
Pharmacogenomic data is increasingly being integrated into the EHR with CDS by health care organizations. Pharmacogenomic deployments to date have comprised of bespoke rules developed by the real organizations, in contrast to other types of CDS where merchants contribute databases that shape the foundation of the CDS.

These underlying pharmacogenomic CDS models demonstrate how useful it is to set up processes for: 1) interpreting pharmacogenomic data into a predicted aggregate and clinical recommendation; and 2) addressing these data separately in the EHR to enable the introduction of pharmacogenomic information as both latent and active information. Additionally, through seller-neutral implementation tools, such as test CDS language and descriptions of the clinical work process, CPIC provides model practices through its informatics working group.

Informative remarks or demonstrating how to use the medicine request screen are two ways to deliver pharmacogenomic information subtly. Pharmacogenomic insights were integrated into the EHR since static notes might

provide useful information such as a summary of test results. In some situations, where it is challenging to distribute an aggregate (as in cases of CYP2D6 allele duplications), these notes are especially helpful.

Another well-founded method for introducing pharmacogenetic information is the use of active or interruptive CDS alerts. When it comes to practical application, there are two basic types of interruptive alarms that pharmacogenomics should consider.

Prescribers are advised not to arrange a medicine influenced by pharmacogenomic variety if the corresponding genotype test is not available in the EHR due to pre-testing (no genotype results available at the time of prescribing). If a patient has a high-risk aggregate, the alarm might inform the practitioner of the possible risks involved with giving the medication. In addition, it can provide recommended elective specialists to use in place of high-risk medications and allow the genotyping test to be ordered directly from the ready window. When a patient is prescribed a medication that should be modified due to the patient's genetic makeup, post-test (high-risk genotype) alerts fire.

In addition to providing a list of optional medications, this type of alarm helps the doctor understand any possible problems that might arise if the patient were to take the prescription as prescribed. The EHR can be enhanced by integrating these two types of active decision support CDS to make it easier to prescribe the right drug at the right starting dose for each patient based on their unique genetic profile. This can limit side effects, advance pharmacotherapy, and ensure that genotype-directed treatment is used when it is available for each tolerant patient.

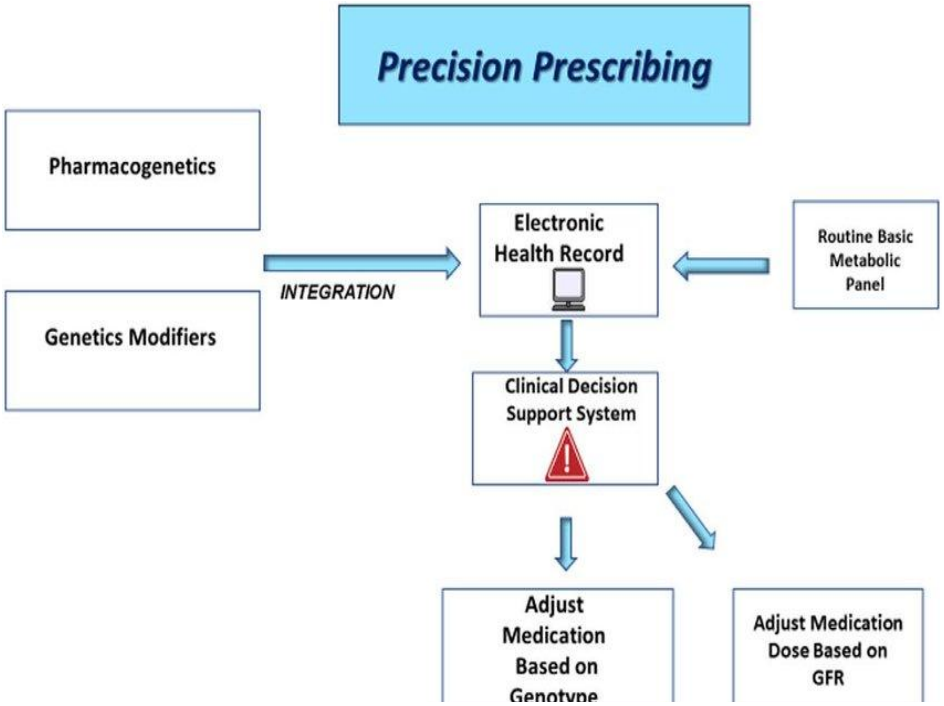

Figure 1: The utilization of available actionable data can be facilitated by the integration of clinical decision support (CDS) technologies with electronic health records (EHRs).

A methodical approach of gathering social event data, evaluating it, interpreting it into clinically meaningful CDS terminology, and obtaining the required approvals to implement the CDS can be quite beneficial. It is imperative to cultivate a methodical approach with established protocols. Most model implementations to date have made advantage of the established institutional framework for CDS organization and medication usage. The Pharmacy and Therapeutics (P&T) committee of the health-framework has frequently been used for auditing CDS recommendations, wherein measures or elective therapies that supplement current financial policies and pharmacotherapy are identified. P and T oversight can be done directly or by forming a subcommittee with a pharmacogenomics-specific focus. Furthermore, the best resources for implementing pharmacogenomic CDS inside clinical work procedures are health framework informatics coordination committees.

Electronic Health Record Analytical Challenges

EHR data can be broadly categorized into four categories: binary, semi-structured, unstructured, and structured. Despite the many advantages that EHR data provide, there are still several obstacles that researchers must overcome (Fig. 2).

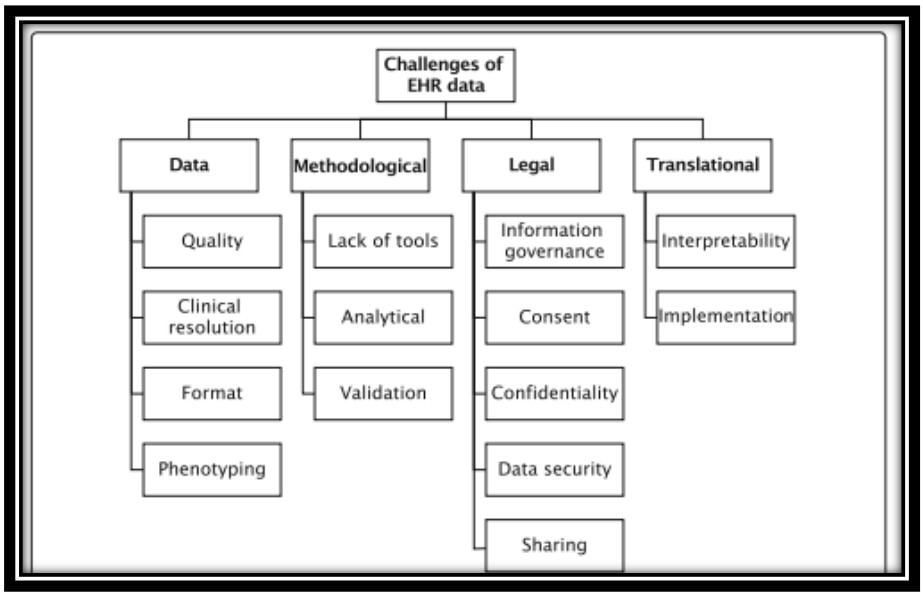

Figure 2: Big health data for biomedical research presents analytical issues in the methodological, ethical, analytical, and translational domains

Accurately extracting phenotypic data—a process called phenotyping—for use in observational and interventional research is a crucial use-case of EHR data. In any case, the process of prototyping is difficult and time-consuming because raw EHR data need to be heavily pre-processed in order to be transformed into research-ready data for statistical analysis. Different sources have different diagnostic granularity, data quality, and context and purpose for data collection.

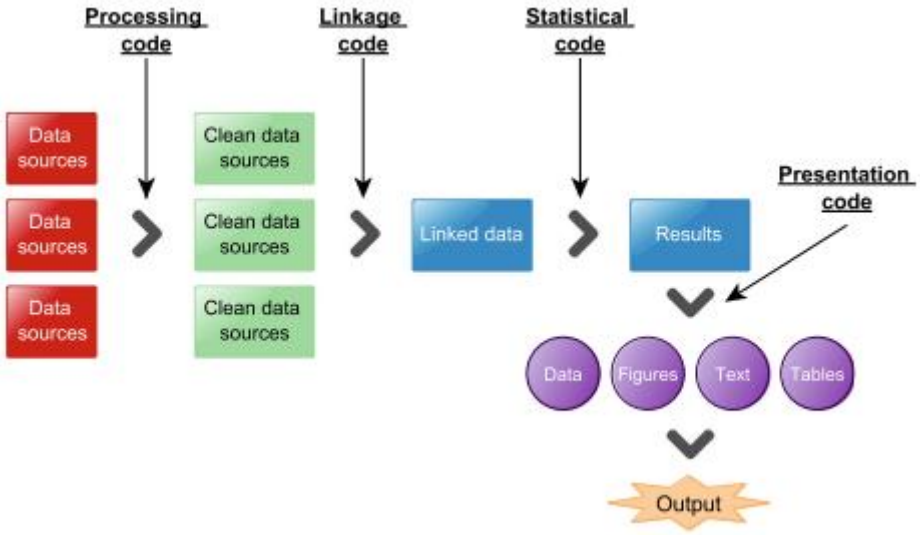

Figure 3: A typical generic EHR analytical pipeline can be divided into a number of more manageable, discrete steps that are frequently carried out iteratively: First, pre-processed, connected, and statistically analyzeable datasets are created from raw EHR data. The data are statistically analyzed, and the results are presented and shared in the form of tables, figures, narratives, and data in scientific output.

Pre-processing of EHR data, however, isn't done in a systematic or repeatable manner, and as a result, findings from studies that focus on using EHR data may suffer from poor repeatability. When phenotyping computations are provided in research journals, they are sometimes presented as a monolithic list of diagnostic terms or as a focus on openings, covariates, and clinical outcomes, but they usually exclude important implementation details. In phenotyping calculations, for example, a term's status as the primary driver of confirmation should be considered when calculating diagnostic terms in clinic treatment; nevertheless, manuscripts often fail to make this important distinction. Researchers repeat common data controls (Fig. 3) on EHR datasets indefinitely, but programmatic code and data are not shared in a systematic way. Surveying the strength, generalizability, and accuracy of these calculations requires a substantial amount of labor due to the absence of clear methods for sharing and cross-approving calculations. Cross-referencing

explanations of data generated by related technologies, for example, are standard practice in genomics, but they are not widely adopted or used in biomedical research using electronic health record (EHR) data.

CONCLUSION

Pharmacogenomics and electronic health records (EHRs) integration offers a promising avenue for personalized medicine, but it also comes with a number of obstacles that call for concerted efforts in biomedical informatics. The complexities of pharmacogenomic data, which include genetic variability among populations and the need for secure patient data, necessitate the development of robust standards for data interchange, sophisticated computing tools for data integration, and effective laboratory and clinical data management. Clinical decision support systems (CDS) have demonstrated the viability of using pharmacogenomics to guide medication treatment; however, scaling these efforts to unlimited clinical implementation remains challenging due to differences in data processing, privacy issues, and the lack of repeatable methods for decomposing EHR data. To address these issues, interdisciplinary cooperation, the establishment of standardized work procedures, and a dedication to ensuring data security and ethical compliance are necessary. Overcoming these challenges will ultimately enable pharmacogenomics to reach its full potential in improving healthcare outcomes by providing more individualized and precise medicines based on an individual's genetic profile.

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