INDIVIDUAL AND COHORT PHARMACOLOGICAL PHENOTYPE PREDICTION PLATFORM

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to and the benefit of the filing date of (1) provisional U.S. Application Serial No. 62/505,422, filed on May 12, 2017, entitled "Individual and Cohort Pharmacological Phenotype Prediction Platform," and (2) provisional U.S. Application Serial No. 62/633,355, filed on February 21, 2018, entitled "Individual and Cohort Pharmacological Phenotype Prediction Platform," the entire disclosures of each of which is hereby expressly incorporated by reference herein.

FIELD OF THE INVENTION

[0002] The present application relates to pharmacological patient phenotypes and, more specifically, to a method and system for utilizing machine learning and statistical techniques to predict drug response phenotypes for patients, and stratified cohorts of patients, based on their biological, ancestry, demographic, clinical, sociological, and environmental characteristics.

BACKGROUND

[0003] Today, drug response for some patients may be predicted based on a patient's coding genome. Specific genetic traits may be mapped to a particular response to a drug and a drug may be selected for a patient based on the patient's predicted response.

[0004] However, noncoding genomic variants account for the vast majority of genetic differences for traits such as drug response, adverse drug response, and disease risk in patients. The convergence of epigenomic regulation research and genome wide association studies (GWAS) has also shown that epigenomic alterations may be indicators of disease risk, drug response, and adverse drug response in both human and animals, in a broad set of medical specialties and pharmacological research settings. Moreover, disease-related phenotype variation may be dictated by differences in chromatin state which had previously been attributed to genetic differences.

[0005] Current systems do not utilize chromatin state, genomic regulatory elements, epigenomics, proteomics, metabolomics, or transcriptomics to predict pharmacological phenotypes for patients. Current systems also do not factor in environmental and sociological

characteristics that may alter genetic traits for determining the pharmacological phenotypes. Additionally, such systems do not utilize machine learning techniques to train the systems to adapt to changes in biological characteristics and/or pharmacological phenotypes corresponding to the biological characteristics over time.

[0006] Accordingly, there is a need for a system that accurately predicts pharmacological phenotypes including pharmacological response, disease risk, substance abuse or other pharmacological phenotypes based on panomic characteristics including genomics, epigenomics, chromatin state, proteomics, metabolomics, transcriptomics, etc., and sociological and environmental characteristics of a patient in near real-time.

SUMMARY

[0006a] According to a first aspect of the present invention, there is provided a computer-implemented method for identifying pharmacological phenotypes using statistical modeling and machine learning techniques, the method executed by one or more processors programmed to perform the method, the method comprising:

obtaining, at one or more processors, a set of training data including for each of a plurality of first patients:

panomic data indicative of biological characteristics of the first patient, including one or more of: chromosomic data, transcriptomic data, proteomic data, or metabolomic data,

sociomic data indicative of risk factors associated with adverse cultural, childhood, acute or chronic traumatic events, or chronic stress resulting from adverse conditions,

environmental data indicative of experiences of the first patient collected at a plurality of instances over a time period, including exposures encountered by the first patient, and

phenomic data indicative of at least one of: a response to one or more drugs, whether the first patient experiences substance abuse, or one or more chronic diseases of the first patient;

generating, by the one or more processors, a statistical model for determining pharmacological phenotypes based on the set of training data;

receiving, at the one or more processors, a set of panomic data, and sociomic and environmental data for a second patient collected over a period of time;

applying, by the one or more processors, the panomic data, and the sociomic and environmental data for the second patient to the statistical model to determine one or more pharmacological phenotypes for the second patient; and

providing, by the one or more processors, the one or more pharmacological phenotypes for the second patient for display to a health care provider, wherein the health care provider recommends a course of treatment to the second patient according to the pharmacological phenotypes.

[0006b] According to a second aspect of the present invention, there is provided a computing device for identifying pharmacological phenotypes using statistical modeling and machine learning techniques, the computing device comprising:

a communication network,

one or more processors; and

a non-transitory computer-readable memory coupled to the one or more processors and storing thereon instructions that, when executed by the one or more processors, cause the computing device to:

obtain a set of training data including for each of a plurality of first patients:

panomic data indicative of biological characteristics of the first patient, including one or more of: chromosomic data, transcriptomic data, proteomic data, or metabolomic data,

sociomic and environmental data indicative of experiences of the first patient collected at a plurality of instances over a time period, including exposures encountered by the first patient, and

phenomic data indicative of at least one of: a response to one or more drugs, whether the first patient experiences substance abuse, or one or more chronic diseases of the first patient;

generate a statistical model for determining pharmacological phenotypes s based on the set of training data;

receive a set of panomic data, and sociomic and environmental data for a second patient collected over a period of time;

apply the panomic data and the sociomic and environmental data for the second patient to the statistical model to determine one or more pharmacological phenotypes for the second patient; and

provide, via the communication network, the one or more pharmacological phenotypes for the second patient for display to a health care provider, wherein the health care provider recommends a course of treatment to the second patient according to the pharmacological phenotypes.

[0006c] According to a third aspect of the present invention, there is provided a method for treating a patient comprising:

obtaining panomic data from a biological sample of a patient;

comparing the panomic data for the patient to one or more genes or SNPs within a warfarin response pathway;

determining a dosage of warfarin for administering to the patient based on the comparison; and

administering the determined dosage of warfarin to the patient.

[0007] To predict pharmacological phenotypes for a patient, a pharmacological phenotype prediction system may be trained using various machine learning techniques. More specifically, the pharmacological phenotype prediction system may be trained to analyze a patient's panomic, sociological, and environmental data to predict the patient's response to various drugs, a likelihood of substance abuse for the patient, a risk of various illnesses, or any other pharmacological phenotype for the patient. The pharmacological phenotype prediction system may be trained by obtaining panomic, sociological, and environmental data (also referred to

herein as “training data”) for a group of patients (also referred to herein as “training patients”).

[0008] In some embodiments, the sociological and environmental data for a patient may be obtained at several points in time to capture a detailed account of the patient’s experiences. For each of the training patients, the pharmacological phenotype prediction system may obtain pharmacological phenotypes for the patient as training data, such as whether the patient suffers from substance abuse problems, the patient’s chronic illnesses, the patient’s responses to various drugs prescribed to the patient, etc. The training data may be analyzed using the various machine learning techniques to generate a statistical model which may be used to predict a patient’s response to various drugs, a likelihood of substance abuse for the patient, a risk of various illnesses, or any other pharmacological phenotype for the patient. For example, the statistical model may be a neural network generated based on a combination of a network analysis of gene regulatory networks and environmental impacts on gene expression.