

Claims

We Claim:

1. A system for evaluating an antibiotics-treatable condition in relation to a user, the system comprising:

- a handling system operable to collect containers comprising nucleic acid material from a set of users, the handling system comprising a sequencer system operable to determine microorganism sequences from the nucleic acid material;
- a microbiome characterization system operable to:
 - determine microbiome pharmacogenomics data and at least one of microbiome composition data and microbiome functional diversity data based on the microorganism sequences,
 - collect supplementary data associated with the antibiotics-treatable condition for the set of users, and
 - generate a characterization model associated with the antibiotics-treatable condition based on the supplementary data and features extracted from the microbiome pharmacogenomics data and the at least one of the microbiome composition data and the microbiome functional diversity data; and
- a treatment system operable to:
 - characterize the user in relation to the antibiotics-associated condition based upon processing at least one of a microbiome pharmacogenomics data, a microbiome composition data, and a microbiome functional diversity data derived from a nucleic acid sample from the user with the characterization model, and
 - provide a treatment recommendation to the user for the antibiotics-treatable condition based on characterizing user nucleic acid material with the characterization model in relation to the antibiotics-treatable condition,

wherein the microbiome pharmacogenomics data includes presence or absence or the quantity of genes associated with antibiotic resistance or susceptibility of the set of users,

wherein the features comprise microbiome pharmacogenomics features associated with at least one of a codon mutation, an exon deletion, a substitution, a gene rearrangement, and a translocation for a taxon associated with the antibiotics-treatable condition, and

wherein the supplementary dataset is informative of the antibiotics-associated condition for the set of subject, the supplementary dataset is at least one of survey-derived data, contextual data derived from sensor or user device and medical data.

2. The system of Claim 1, wherein the handling system is operable to determine the microorganism sequences based on amplifying nucleic acid material from the nucleic acid material using a primer for a nucleic acid sequence associated with the antibiotics-treatable condition.
3. The system of Claim 1, wherein the handling system is operable to collect a user container comprising the user nucleic acid material, wherein the treatment system is operable to promote the treatment based on characterizing the sampled user nucleic acid material, and wherein the treatment is operable to modulate a user microbiome composition for improving a state of the antibiotics-treatable condition.
4. The system of Claim 1, wherein the microbiome pharmacogenomics features are associated with at least one of microbial strain mutability, microbial strain resistance to antibiotics, and microbial strain co-dependent behavior.
5. The system of Claim 1, wherein the microbiome pharmacogenomics features are associated with a relative abundance of microbial pharmacogenomics markers in relation to the antibiotics-treatable condition.
6. The system of Claim 1, wherein the features comprise a nucleotide-associated functional feature associated with at least one of resistance and metabolization of a biologically active molecule, including at least one of the following: structural RNAs, regulatory RNAs, messenger RNAs, proteins and peptides.
7. The system of Claim 1, wherein the antibiotics-treatable condition comprises at least one of a urinary tract infection and a sexually transmitted disease, and wherein the microbiome characterization system is operable to transform the supplementary data and the features extracted from the microbiome pharmacogenomics data and the at least one of the microbiome composition data and the microbiome functional diversity data into the characterization model for the at least one of the urinary tract infection and the sexually transmitted disease.
8. The system of Claim 7, wherein the antibiotics-treatable condition comprises a gonorrhea-associated condition, and wherein the features comprise a microbiome pharmacogenomics feature extracted from the microbiome pharmacogenomics data and associated with a mosaic penA allele.

9. The system of Claim 8, wherein the treatment system is operable to evaluate an efficacy of a cephalosporin treatment based on the microbiome pharmacogenomics feature.

10. The system of Claim 1, further comprising an interface operable to improve display of antibiotics-related information associated with the antibiotics-treatable condition and derived based on a comparison between a user microbiome pharmacogenomics profile for the user relative to a user group sharing a demographic characteristic.

11. A method for evaluating an antibiotics-associated condition in relation to a first user, the method comprising:

- determining microbiome pharmacogenomics data based on microorganism sequences derived from biological samples from a set of subjects;
- receiving a supplementary dataset informative of the antibiotics-associated condition for the set of subjects;
- determining a first set of microbiome pharmacogenomics features based on the microbiome pharmacogenomics data and the supplementary dataset;
- generating a characterization model associated with the antibiotics-associated condition based on the first set of microbiome pharmacogenomics features;
- determining a characterization for the first user in relation to the antibiotics-associated condition based upon processing at least one of a microbiome pharmacogenomics data, a microbiome composition data, and a microbiome functional diversity data derived from a nucleic acid sample from the first user with the characterization model; and
- providing a therapy recommendation to the first user based on the characterization, wherein the therapy recommendation is associated with the antibiotics-associated condition,

wherein the microbiome pharmacogenomics data includes presence or absence or the quantity of genes associated with antibiotic resistance or susceptibility of the set of users,

wherein the microbiome pharmacogenomics features associated with at least one of a codon mutation, an exon deletion, a substitution, a gene rearrangement, and a translocation for a taxon associated with the antibiotics-treatable condition, and

wherein the supplementary dataset is informative of the antibiotics-associated condition for the set of subject, the supplementary dataset is at least one of survey-derived data, contextual data derived from sensor or user device and medical data.

12. The method of Claim 11, wherein determining the microbiome pharmacogenomics data comprises:

- determining the microorganism sequences based on amplifying nucleic acid material from the biological samples;
- determining alignments of the microorganism sequences to a reference nucleic acid sequence set associated with the antibiotics-associated condition; and
- determining the microbiome pharmacogenomics data based on the alignments.

13. The method of Claim 12, wherein amplifying the nucleic acid material comprises performing, with a bridge amplification substrate of a next generation sequencing platform, multiplex amplification with the nucleic acid material, and wherein determining the microbiome pharmacogenomics data comprises determining the microbiome pharmacogenomics data at a computing system operable to communicate with the next generation sequencing platform.

14. The method of Claim 11, further comprising obtaining a microbiome pharmacogenomics feature-selection rule associated with a correlation between the first set of microbiome pharmacogenomics features and antibiotic efficacy in relation to the antibiotic-associated condition, wherein determining the first set of microbiome pharmacogenomics features comprises determining the first set of microbiome pharmacogenomics features based on evaluating the microbiome pharmacogenomics data against the microbiome pharmacogenomics feature-selection rule.

15. The method of Claim 11, wherein the first set of microbiome pharmacogenomics features comprises a nucleotide-associated functional feature associated with at least one of resistance and metabolism of a biologically active molecule.

16. The method of Claim 11, further comprising:

- receiving a post -therapy biological sample from the first user;
- determining an updated set of microbiome pharmacogenomics features based on the post-therapy biological sample;

- determining an updated characterization for the first user in relation to the antibiotics- associated condition based on the characterization model and the updated set of microbiome pharmacogenomics features; and

- providing a first updated therapy recommendation to the first user based on the updated characterization.

17. The method of Claim 16, further comprising:

- generating an updated antibiotic therapy model based on the updated characterization for the first user; and

- providing an antibiotic therapy recommendation to a second user based on the updated antibiotic therapy model.

18. The method of Claim 17, further comprising: determining a second set of microbiome pharmacogenomics features for the second user based on a second user biological sample, wherein promoting the antibiotic therapy based on the updated antibiotic therapy model comprises determining the antibiotic therapy based on processing the second set of microbiome pharmacogenomics features with a decision tree model.

19. The method of Claim 11,

- wherein generating the characterization model comprises generating the characterization model based on a microbiome feature set comprising the first set of microbiome pharmacogenomics features and at least one of a microbiome composition diversity feature and a microbiome functional diversity feature, and

- wherein determining the characterization for the first user comprises determining the characterization for the first user based on a user microbiome feature set comprising a user microbiome pharmacogenomics feature and at least one of a user microbiome composition diversity feature and a user microbiome functional diversity feature.

20. The method of Claim 19, wherein the antibiotics-associated condition comprises a gonorrhea-associated condition, wherein the microbiome composition diversity feature comprises a composition feature for a taxon associated with the gonorrhea-associated condition, and wherein the first set of microbiome pharmacogenomics features comprises a point mutation feature set for genes associated with the taxon.

21. The method of Claim 20, wherein the point mutation feature set is associated with point mutations in at least one of a gyrA gene and aparC gene for the taxon.