human microbiome, the indication-specific score representing an evidence of the gene or protein being associated with the disease indication of the patient,

wherein the indication-specific score of each gene or protein is computed by first assigning numerical values to attributes indicating degrees of potential relationship to the indication and then by forming a weighted sum of the numerical values or of any monotonic transformation of the numerical values over the attributes, the attributes comprising at least one of the following list:

a) The gene or protein is a drug target,

b) The gene or protein is a biomarker or part of a biomarker,

c) The gene or protein is disease-associated,

d) The gene or protein is an oncogene or a product of an oncogene, respectively,

e) The gene or protein is a tumor suppressor,

f) The gene or protein has a cancer pathway association,

g) The gene or protein is gene ontology annotated for cancer relevant processes,

h) The gene or protein is part of a cancer-associated gene fusion,

i) The gene or protein has a tractable domain,

j) The gene or protein is embryonic lethal, and

k) The gene or protein is highly mutated in the specific indication;

retrieving a molecular profile of the patient, wherein the molecular profile is a set of molecular measurements of DNA or RNA extracted from the patient, indexed by a second set of genes or proteins, the second set of genes or proteins being equal to the first set of genes or proteins or being a subset of the first set of genes or proteins,

inferring, from the molecular profile, for each gene or protein of the first set of genes or proteins a possibly empty set of aberrations as the differences of the molecular profile to a reference profile from a control sample of the patient or from other individuals,

assigning a profile-specific score to each gene or protein of the first set of genes or proteins, the profile-specific score representing a degree of how much the function of the genes or proteins is altered by the aberrations,

wherein assigning the profile-specific score to each gene or protein of the first set of genes or proteins comprises the following steps:

computing an aberration-specific functional impact score for each aberration taking into account the direction of the impact of an aberration on the function of a gene or protein, wherein positive and negative signs of the aberration-specific functional impact score correspond to an activating and inactivating impact, respectively, and

computing a protein- or gene-specific direct functional impact score for each protein or gene by computing a weighted sum, a quantile, a median, a

generating a personalized treatment guideline for the patient by executing the method steps described in the first aspect, and

selecting the first targeted treatment from the ordered list of the targeted treatments of the personalized treatment guideline

[0013B] According to a third aspect there is provided a method for selecting patients for a clinical trial of a treatment, comprising the steps:

retrieving identifications of disease indications of a set of patients as a user's input, from an electronic health record EHR or electronic medical record EMR or from a patient database comprising medical records of a candidate set of patients,

assigning, for every patient, an indication-specific score to each gene or protein of a first set of genes or proteins, the first set of genes or proteins being part of the human microbiome, the indication-specific score representing an evidence of the gene or protein being associated with the disease indication of the patient,

wherein the indication-specific score of each gene or protein is computed by first assigning numerical values to attributes indicating degrees of potential relationship to the indication and then by forming a weighted sum of the numerical values or of any monotonic transformation of the numerical values over the attributes, the attributes comprising at least one of the following list:

a) The gene or protein is a drug target,

b) The gene or protein is a biomarker or part of a biomarker,

c) The gene or protein is disease-associated,

assigning, for every patient, a profile-specific score to each gene or protein of the first set of genes or proteins, the profile-specific score representing a degree of how much the function of the genes or proteins is altered by the aberrations,

wherein assigning the profile-specific score to each gene or protein of the first set of genes or proteins comprises the following steps:

computing an aberration-specific functional impact score for each aberration taking into account the direction of the impact of an aberration on the function of a gene or protein, wherein positive and negative signs of the aberration-specific functional impact score correspond to an activating and inactivating impact, respectively, and

computing a protein- or gene-specific direct functional impact score for each protein or gene by computing a weighted sum, a quantile, a median, a maximum or a geometric mean of the aberration-specific functional impact scores over the aberrations associated with the gene or protein, or

computing a protein- or gene-specific indirect functional impact score for each protein or gene by computing a weighted sum, a quantile, a median, a maximum or a geometric mean of the aberration-specific functional impact scores over the aberrations associated with another set of genes or proteins, the another set including the gene or protein and a set of genes or proteins that are upstream of the gene or protein according to a molecular interaction network, the molecular interaction network being a directed graph, consisting of nodes each of which represents a gene or a protein, and of edges each of which connects two nodes,

an interface for providing identifications of disease indications of patients to the system,

a module for assigning, for an identification of a disease indication of a patient, an indication-specific score to each gene or protein of the first set of genes or proteins, the indication-specific score representing an evidence of the gene or protein being associated with the disease indication of the patient,

wherein the indication-specific score of each gene or protein is computed by first assigning numerical values to attributes indicating degrees of potential relationship to the indication and then by forming a weighted sum of the numerical values or of any monotonic transformation of the numerical values over the attributes, the attributes comprising at least one of the following list:

a) The gene or protein is a drug target,

b) The gene or protein is a biomarker or part of a biomarker,

c) The gene or protein is disease-associated,

d) The gene or protein is an oncogene or a product of an oncogene, respectively,

e) The gene or protein is a tumor suppressor,

f) The gene or protein has a cancer pathway association,

g) The gene or protein is gene ontology annotated for cancer relevant processes,

CLAIMS

1. Method for generating a personalized treatment guideline for a patient, comprising the steps:

retrieving an identification of a disease indication of the patient as a user's input, from an electronic health record or electronic medical record or from a patient database comprising medical records of a candidate set of patients,

assigning an indication-specific score to each gene or protein of a first set of genes or proteins, the first set of genes or proteins being part of the human microbiome, the indication-specific score representing an evidence of the gene or protein being associated with the disease indication of the patient,

wherein the indication-specific score of each gene or protein is computed by first assigning numerical values to attributes indicating degrees of potential relationship to the indication and then by forming a weighted sum of the numerical values or of any monotonic transformation of the numerical values over the attributes, the attributes comprising at least one of the following list:

a) The gene or protein is a drug target,

b) The gene or protein is a biomarker or part of a biomarker,

c) The gene or protein is disease-associated,

d) The gene or protein is an oncogene or a product of an oncogene, respectively,

e) The gene or protein is a tumor suppressor,

f) The gene or protein has a cancer pathway association,

g) The gene or protein is gene ontology annotated for cancer relevant processes,

h) The gene or protein is part of a cancer-associated gene fusion,

i) The gene or protein has a tractable domain,

j) The gene or protein is embryonic lethal, and

k) The gene or protein is highly mutated in the specific indication;

retrieving a molecular profile of the patient, wherein the molecular profile is a set of molecular measurements of DNA or RNA extracted from the patient, indexed by a second set of genes or proteins, the second set of genes or proteins being equal to the first set of genes or proteins or being a subset of the first set of genes or proteins,

inferring, from the molecular profile, for each gene or protein of the first set of genes or proteins a possibly empty set of aberrations as the differences of the molecular profile to a reference profile from a control sample of the patient or from other individuals,

assigning a profile-specific score to each gene or protein of the first set of genes or proteins, the profile-specific score representing a degree of how much the function of the genes or proteins is altered by the aberrations,

wherein assigning the profile-specific score to each gene or protein of the first set of genes or proteins comprises the following steps:

computing an aberration-specific functional impact score for each aberration taking into account the direction of the impact of an aberration on the function of a gene or protein, wherein positive and negative signs of the aberration-specific functional impact score correspond to an activating and inactivating impact, respectively, and

computing a protein- or gene-specific direct functional impact score for each protein or gene by computing a weighted sum, a quantile, a median, a maximum or a geometric mean of the aberration-specific functional impact scores over the aberrations associated with the gene or protein, or

computing a protein- or gene-specific indirect functional impact score for each protein or gene by computing a weighted sum, a quantile, a

median, a maximum or a geometric mean of the aberration-specific functional impact scores over the aberrations associated with another set of genes or proteins, the another set including the gene or protein and a set of genes or proteins that are upstream of the gene or protein according to a molecular interaction network, the molecular interaction network being a directed graph, consisting of nodes each of which represents a gene or a protein, and of edges each of which connects two nodes,

and wherein the profile-specific score is set equal to the direct functional impact score, equal to the indirect functional impact score or equal to a weighted sum of these,

assigning a patient-specific score to each gene or protein of the first set of genes or proteins, the patient-specific score of each gene or protein being a sum, a weighted sum or a product of its indication-specific score and its profile-specific score,

retrieving a set of targeted treatments, together with associated target genes or proteins, as a user's input or by selecting treatments that are approved or under investigation for the indication of the patient or for related indications from a treatment database, the treatment database storing treatments, in particular drugs and drug combinations, together with information on the genes or proteins that are the targets of the drugs,

assigning a score to each targeted treatment from the set of targeted treatments by calculating a sum or a weighted sum over the patient-specific scores of the associated target genes or proteins, and

generating the personalized treatment guideline as an ordered list of the targeted treatments, wherein the order of the targeted treatments is determined by their score.

2. Method for selecting a treatment for a patient, comprising the steps:

generating a personalized treatment guideline for the patient by executing the method steps according to claim 1, and

selecting the first targeted treatment from the ordered list of the targeted treatments of the personalized treatment guideline.

3. Method for selecting patients for a clinical trial of a treatment, comprising the steps:

retrieving identifications of disease indications of a set of patients as a user's input, from an electronic health record EHR or electronic medical record EMR or from a patient database comprising medical records of a candidate set of patients,

assigning, for every patient, an indication-specific score to each gene or protein of a first set of genes or proteins, the first set of genes or proteins being part of the human microbiome, the indication-specific score representing an evidence of the gene or protein being associated with the disease indication of the patient,

wherein the indication-specific score of each gene or protein is computed by first assigning numerical values to attributes indicating degrees of potential relationship to the indication and then by forming a weighted sum of the numerical values or of any monotonic transformation of the numerical values over the attributes, the attributes comprising at least one of the following list:

a) The gene or protein is a drug target,

b) The gene or protein is a biomarker or part of a biomarker,

c) The gene or protein is disease-associated,

d) The gene or protein is an oncogene or a product of an oncogene, respectively,

e) The gene or protein is a tumor suppressor,

f) The gene or protein has a cancer pathway association,

g) The gene or protein is gene ontology annotated for cancer relevant processes,

h) The gene or protein is part of a cancer-associated gene fusion,

i) The gene or protein has a tractable domain,

j) The gene or protein is embryonic lethal, and

k) The gene or protein is highly mutated in the specific indication;

retrieving, for every patient, a molecular profile of the patient, wherein the molecular profile is a set of molecular measurements of DNA or RNA extracted from the patient, indexed by a second set of genes or proteins, the second set of genes or proteins being equal to the first set of genes or proteins or being a subset of the first set of genes or proteins,

inferring, from the molecular profile, for each gene or protein of the first set of genes or proteins a possibly empty set of aberrations as the differences of the molecular profile to a reference profile from a control sample of the patient or from other individuals,

assigning, for every patient, a profile-specific score to each gene or protein of the first set of genes or proteins, the profile-specific score representing a degree of how much the function of the genes or proteins is altered by the aberrations,

wherein assigning the profile-specific score to each gene or protein of the first set of genes or proteins comprises the following steps:

computing an aberration-specific functional impact score for each aberration taking into account the direction of the impact of an aberration on the function of a gene or protein, wherein positive and negative signs of the aberration-specific functional impact score correspond to an activating and inactivating impact, respectively, and

computing a protein- or gene-specific direct functional impact score for each protein or gene by computing a weighted sum, a quantile, a median, a maximum or a geometric mean of the aberration-specific functional impact scores over the aberrations associated with the gene or protein, or

computing a protein- or gene-specific indirect functional impact score for each protein or gene by computing a weighted sum, a quantile, a median, a maximum or a geometric mean of the aberration-specific functional impact scores over the aberrations associated with another

set of genes or proteins, the another set including the gene or protein and a set of genes or proteins that are upstream of the gene or protein according to a molecular interaction network, the molecular interaction network being a directed graph, consisting of nodes each of which represents a gene or a protein, and of edges each of which connects two nodes,

and wherein the profile-specific score is set equal to the direct functional impact score, equal to the indirect functional impact score or equal to a weighted sum of these,

assigning, for every patient, a patient-specific score to each gene or protein of the first set of genes or proteins, the patient-specific score of each gene or protein being a sum, a weighted sum or a product of its indication-specific score and its profile-specific score,

retrieving, for the treatment, associated target genes or proteins from a treatment database, the treatment database storing treatments, in particular drugs and drug combinations, together with information on the genes or proteins that are the targets of the drugs, which are also in the first set of genes or proteins,

assigning a score to every patient from the set of patients by calculating a sum or a weighted sum over the patient-specific scores of the associated target genes or proteins, and

generating an ordered list of the patients, wherein the order of the patients is determined by their score.

4. The method of any of the preceding claims, wherein the profile-specific score is set to zero if the gene or protein has no aberrations.

5. The method of any of the preceding claims, wherein assigning the score to a treatment or patient further takes into account a directionality of the impact of the treatment on its associated target genes or proteins by adding the profile-specific scores of target genes or proteins that are inhibited or antagonized by the treatment and by subtracting the profile-specific scores of target genes or proteins that are activated or stimulated or agonized by the treatment.

6. The method of any of the preceding claims, wherein assigning the score to a treatment or patient involves the step that patient-specific scores are further aggregated over genes or proteins downstream of their associated target genes or proteins according to the molecular interaction network by computing a weighted sum, a quantile, a median, a maximum or a geometric mean of the aberration-specific functional impact scores over the aberrations associated with another set of genes or proteins, the another set including the gene or protein and a set of genes or proteins that are downstream of the gene or protein according to the molecular interaction network.

7. System for generating a personalized treatment guideline for a patient and/or for selecting patients for a clinical trial of a treatment, comprising a processing unit with:

an interface for providing a first set of genes or proteins to the system, the first set of genes or proteins being part of the human microbiome,

an interface for providing identifications of disease indications of patients to the system,

a module for assigning, for an identification of a disease indication of a patient, an indication-specific score to each gene or protein of the first set of genes or proteins, the indication-specific score representing an evidence of the gene or protein being associated with the disease indication of the patient,

wherein the indication-specific score of each gene or protein is computed by first assigning numerical values to attributes indicating degrees of potential relationship to the indication and then by forming a weighted sum of the numerical values or of any monotonic transformation of the numerical values over the attributes, the attributes comprising at least one of the following list:

a) The gene or protein is a drug target,

b) The gene or protein is a biomarker or part of a biomarker,

c) The gene or protein is disease-associated,

d) The gene or protein is an oncogene or a product of an oncogene, respectively,

e) The gene or protein is a tumor suppressor,

f) The gene or protein has a cancer pathway association,

g) The gene or protein is gene ontology annotated for cancer relevant processes,

h) The gene or protein is part of a cancer-associated gene fusion,

i) The gene or protein has a tractable domain,

j) The gene or protein is embryonic lethal, and

k) The gene or protein is highly mutated in the specific indication;

an interface for providing molecular profiles of patients to the system, wherein a molecular profile is a set of molecular measurements of DNA or RNA extracted from a patient, indexed by a second set of genes or proteins, the second set of genes or proteins being equal to the first set of genes or proteins or being a subset of the first set of genes or proteins,

a module for assigning, for a molecular profile of a patient, a profile-specific score to each gene or protein of the first set of genes or proteins, wherein the module for assigning the profile-specific score is adapted to inferring, from the molecular profile, for each gene or protein of the first set of genes or proteins a possibly empty set of aberrations as the differences of the molecular profile to a reference profile from a control sample of the patient or from other individuals,

wherein assigning the profile-specific score to each gene or protein of the first set of genes or proteins comprises the following steps:

computing an aberration-specific functional impact score for each aberration taking into account the direction of the impact of an aberration on the function of a gene or protein, wherein positive and negative signs of the aberration-specific functional impact score correspond to an activating and inactivating impact, respectively, and

computing a protein- or gene-specific direct functional impact score for each protein or gene by computing a weighted sum, a quantile, a median, a maximum or a geometric mean of the aberration-specific functional impact scores over the aberrations associated with the gene or protein, or

computing a protein- or gene-specific indirect functional impact score for each protein or gene by computing a weighted sum, a quantile, a

median, a maximum or a geometric mean of the aberration-specific functional impact scores over the aberrations associated with another set of genes or proteins, the another set including the gene or protein and a set of genes or proteins that are upstream of the gene or protein according to a molecular interaction network, the molecular interaction network being a directed graph, consisting of nodes each of which represents a gene or a protein, and of edges each of which connects two nodes,

and wherein the profile-specific score is set equal to the direct functional impact score, equal to the indirect functional impact score or equal to a weighted sum of these,

a module for assigning a patient-specific score to each gene or protein of the first set of genes or proteins, the patient-specific score of each gene or protein being a sum, a weighted sum or a product of its indication-specific score and its profile-specific score,

an interface for providing targeted treatments, together with associated target genes or proteins, as a user's input or by selecting treatments that are approved or under investigation for the indication of the patient or for related indications from a treatment database, the treatment database storing treatments, in particular drugs and drug combinations, together with information on the genes or proteins that are the targets of the drugs, to the system, and

a module for assigning a score to patients and to treatments by calculating a sum or a weighted sum over the patient-specific scores of the associated target genes or proteins, wherein the module for assigning the score to patients and to treatments is adapted to generating ordered lists of patients or treatments, wherein the order of the patients or treatments is determined by their score.