

What is claimed:

1. A method for determining the presence of microorganisms in a subject comprising:
 - (a) sequencing nucleic acids present in a biological sample obtained from the subject to obtain a plurality of nucleic acid sequence reads;
 - (b) comparing sequence reads obtained in step (a) with one or more databases comprising the genetic information from a control subject of the same species and the genetic information from a plurality of microorganisms to determine whether or not a compared sequence read maps to a species comprised within the one or more databases; and
 - (c) determining over time the number of compared sequence reads mapping to a particular microorganism and the number of compared sequence reads mapping to a species.
2. A method for determining the presence of microorganisms in a subject comprising:
 - (a) comparing sequence reads with one or more databases comprising the genetic information from a control subject of the same species and the genetic information from a plurality of microorganisms to determine whether or not a compared sequence read maps to a species comprised within the one or more databases, wherein the sequence reads are obtained by sequencing nucleic acids present in a biological sample obtained from the subject; and
 - (b) determining over time the number of compared sequence reads mapping to a particular microorganism and the number of compared sequence reads mapping to a species.
3. The method according to claim 1 or 2, wherein the method further comprises computing a significance score for the probability of finding in the subject a compared sequence read mapping to the particular microorganism based on the number of compared sequence reads mapping to the particular microorganism and the number of compared sequence reads mapping to a species.
4. A method for determining the presence of microorganisms in a subject comprising:

a step of computing over time a significance score for the probability of finding in the subject a sequence read mapping to a particular microorganism based on the number of sequence reads mapping to the particular microorganism and the number of sequence reads mapping to a species,

wherein the sequence reads mapping to the particular microorganism and the sequence reads mapping to a species are obtained by comparing sequence reads with one or more databases comprising the genetic information from a control subject of the same species and the genetic information from a plurality of microorganisms to determine whether or not a compared sequence read maps to a species comprised within the one or more databases, and wherein the sequence reads are generated by sequencing nucleic acids present in a biological sample obtained from the subject.

5. A method for determining the presence of microorganisms in a subject comprising:

(a) step of determining over time the number of sequence reads mapping to a particular microorganism and the number of sequence reads mapping to a species, wherein the sequence reads are obtained by comparing sequence reads with one or more databases comprising the genetic information from a control subject of the same species and the genetic information from a plurality of microorganisms to determine whether or not a sequence read maps to a species comprised within the one or more databases, and wherein the sequence reads are generated by sequencing nucleic acids present in a biological sample obtained from the subject; and

(b) computing a significance score for the probability of finding in the subject a sequence read mapping to the particular microorganism based on the number of sequence reads mapping to the particular microorganism and the number of sequence reads mapping to a species.

6. The method according to any one of claims 3 to 5, wherein when the significance score for the particular microorganism meets or exceeds a threshold value, the particular microorganism is determined to be present in the subject.

7. The method according to any one of claims 3 to 5, wherein when the significance score for the particular microorganism meets or exceeds a threshold value, the particular microorganism is determined to be relevant for causing a disease in the subject.

8. The method according to claim 7, wherein when the significance score for the particular microorganism exceeds a threshold value with few sequence reads, the disease due to the presence of the microorganism is considered to be severe.

9. A method for determining the presence of a disease state in a subject comprising:

(a) sequencing nucleic acids present in a biological sample obtained from the subject to obtain a plurality of nucleic acid sequence reads;

(b) comparing sequence reads obtained in step (a) with one or more databases comprising the genetic information from a control subject of the same species to determine whether or not a compared sequence read maps to the control subject; and

(c) determining over time the number of compared sequence reads mapping and not mapping to the control subject.

10. The method according to claim 9, wherein the method further comprises computing a significance score for the probability of finding in the subject a compared sequence read not mapping to the control subject based on the number of compared sequence reads not mapping to the control subject and the number of compared sequence reads mapping to the control subject.

11. A method for determining the presence of a disease state in a subject comprising:

a step of computing over time a significance score for the probability of finding in the subject a sequence read not mapping to the control subject based on the number of sequence reads not mapping to the control subject and the number of sequence reads mapping to the control subject,

wherein the sequence reads mapping to the control subject and the sequence reads not mapping to the control subject are obtained by comparing sequence reads with one or more databases comprising the genetic information from a control subject of the same species to determine whether or not a compared sequence read maps to the control subject, and wherein the sequence reads are generated by sequencing nucleic acids present in a biological sample obtained from the subject.

12. The method according to claim 10 or 11, wherein when the significance score meets or exceeds a threshold value, the disease state is determined to be present in the subject.

13. The method according to any one of claims 9 to 12, wherein the disease state is cancer.

14. The method according to any one of claims 9 to 12, wherein the disease state is an infection caused by a microorganism.

15. The method according to any one of the preceding claims, wherein when the particular microorganism or the disease state is determined to be present in the subject, the method further comprises administering to the subject a pharmaceutically-active compound known to treat a disease caused by the particular microorganism or the disease state.

16. A method for diagnosing an infectious disease caused by microorganisms in a subject comprising:

(a) sequencing nucleic acids present in a biological sample obtained from the subject to obtain a plurality of nucleic acid sequence reads;

(b) comparing sequence reads obtained in step (a) with one or more databases comprising the genetic information from a control subject of the same species and the genetic information from a plurality of microorganisms to determine whether or not a compared sequence read maps to a species comprised within the one or more databases;

(c) determining over time the number of compared sequence reads mapping to a particular microorganism and the number of compared sequence reads mapping to a species; and

(d) computing a significance score for the probability of finding in the subject a compared sequence read mapping to the particular microorganism based on the number of compared sequence reads mapping to the particular microorganism and the number of compared sequence reads mapping to a species,

wherein when the significance score for the particular microorganism meets or exceeds a threshold value, the particular microorganism is determined to be causing the infectious disease.

17. A computer-readable storage medium storing program code comprising instructions which when executed by a processor carry out the method according to any one of claims 1 to 16.

18. A computer system comprising a processor configured to carry out the method according to any one of claims 1 to 16.

19. Use of a compound that inhibits the growth of a microorganism whose significance score meets or exceeds a threshold value in the manufacture of a medicament for treating a disease or infection, wherein the significance score is calculated according to any one of claims 3 to 8.