

chance nodes represent points of uncertainty, and decision nodes or terminal nodes represent subsequent states; (c) providing a course of treatment for the subject that maximizes a probability of the subject achieving a living state at a terminal node; and (d) administering the course of treatment to the subject. In some embodiments, the method further comprises: (e) at a second time point subsequent to the initial state, obtaining information about a subject comprising at least a genetic profile of a tumor and a treatment previously or currently provided to the subject, if any, and determining an second state of the subject among a plurality of subsequent states based on the information; (f) based on the second state, providing a subsequent course of treatment for the subject that maximizes probability of the subject achieving a living state at a terminal node; and (g) administering the subsequent course of treatment to the subject. In some embodiments, the method further comprises: (e) at a second time point subsequent to the initial state, obtaining information about a subject comprising at least a genetic profile of a tumor and a treatment previously or currently provided to the subject, if any, and determining an second state of the subject among a plurality of subsequent states based on the information; (f) based on the second state, providing a subsequent course of treatment for the subject that maximizes probability of the subject achieving a living state at a terminal node; and (g) administering the subsequent course of treatment to the subject.

[0022] In one aspect, the present disclosure provides a method, comprising providing a course of treatment among a plurality of alternative treatments for a subject with cancer, wherein the subject has been characterized by a decision tree comprising a plurality of decision branches, each decision branch representing an alternative treatment among the plurality of alternative treatments, which course of treatment maximizes a probability of the subject achieving a living state at a terminal node.

[0022a] In one aspect, the present disclosure provides a computer-implemented method, comprising: (a) obtaining information about a plurality of subjects with cancer at a first time point, wherein the information comprises, for each subject of the plurality of subjects, at least a genetic profile of a tumor obtained by genotyping (i) at least 50 genes, and/or (ii) nucleic acids from a cell-free bodily fluid, and any treatment provided to the subject, and determining a first state of each of the plurality of subjects based on the information at the first time point, to produce a set of first states, wherein obtaining the information comprises sequencing cell-free deoxyribonucleic acid (cfDNA) from the plurality of subjects; (b) obtaining the information about the plurality of subjects at one or more second time points subsequent to the first time point, and determining a second state of each of the plurality of subjects at each

of the one or more second time points based on the information at a given one of the one or more second time points, to produce a set of subsequent states; and (c) using the set of first states from (a) and the set of subsequent states from (b) to generate a predictive algorithm that is configured to determine a probability that a given first state will result in a second state among a set of states at a later time point subsequent to the given first state, wherein the probability is at least in part a function of treatment choice from among a plurality of treatment choices.

[0022b] In one aspect, the present disclosure provides a non-transitory computer-readable medium comprising machine executable code that, upon execution by one or more computer processors, implements the method as described herein.

[0023] Additional aspects and advantages of the present disclosure will become readily apparent to those skilled in this art from the following detailed description, wherein only illustrative embodiments of the present disclosure are shown and described. As will be realized, the present disclosure is capable of other and different embodiments, and its several details are capable of modifications in various obvious respects, all without departing from the disclosure. Accordingly, the drawings and description are to be regarded as illustrative in nature, and not as restrictive.

INCORPORATION BY REFERENCE

[0024] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

CLAIMS

1. A computer-implemented method, comprising:
 - (a) obtaining information about a plurality of subjects with cancer at a first time point, wherein the information comprises, for each subject of the plurality of subjects, at least a genetic profile of a tumor obtained by genotyping (i) at least 50 genes, and/or (ii) nucleic acids from a cell-free bodily fluid, and any treatment provided to the subject, and determining a first state of each of the plurality of subjects based on the information at the first time point, to produce a set of first states, wherein obtaining the information comprises sequencing cell-free deoxyribonucleic acid (cfDNA) from the plurality of subjects;
 - (b) obtaining the information about the plurality of subjects at one or more second time points subsequent to the first time point, and determining a second state of each of the plurality of subjects at each of the one or more second time points based on the information at a given one of the one or more second time points, to produce a set of subsequent states; and
 - (c) using the set of first states from (a) and the set of subsequent states from (b) to generate a predictive algorithm that is configured to determine a probability that a given first state will result in a second state among a set of states at a later time point subsequent to the given first state, wherein the probability is at least in part a function of treatment choice from among a plurality of treatment choices.
2. The method of claim 1, further comprising:
 - (d) for the given first state among a set of states at an earlier time point, determining the probability that the given first state will result in the second state among the set of states at the later time point; and
 - (e) generating an electronic output indicative of the probability determined in (d).
3. The method of claim 1, wherein obtaining the information comprises performing a medical interview of each of the plurality of subjects.
4. The method of claim 1, wherein treatment was provided to the subject before the first time point.
5. The method of claim 1, further comprising generating one or more decision trees, each decision tree comprising a root node, one or more decision branches, one or more decision nodes, and one or more terminal nodes, wherein a state at the root node represents

the first time point, the one or more decision branches represent alternative treatments, and the one or more decision nodes and the one or more terminal nodes represent subsequent states.

6. The method of claim 5, wherein the one or more decision branches comprise a plurality of decision branches.
7. The method of claim 1, wherein the subsequent states comprise a viability state(s) of the subjects indicative of the subjects being alive or deceased.
8. The method of claim 7, wherein the subsequent states comprise subject survival rate.
9. The method of claim 1, wherein each of the first states comprises a common set of one or more somatic mutations.
10. The method of claim 1, wherein the information further comprises a subject profile.
11. The method of claim 1, wherein the one or more second time points comprises a plurality of subsequent time points.
12. The method of claim 11, further comprising determining the probability at a plurality of subsequent time points.
13. The method of claim 12, wherein the time points comprise at least three time points or at least four time points.
14. The method of claim 1, wherein the first time point is prior to the subject receiving the treatment and the subsequent time point is after the subject receiving the treatment.
15. The method of claim 1, wherein a second treatment choice is administered after the subsequent time point based on the subsequent state at the subsequent time point.
16. The method of claim 1, wherein the information about the plurality of subjects comprises one or more characteristics from patient profiles of the subjects, which characteristics are selected from the group consisting of: age, sex, gender, genetic profile, enzyme levels, organ function, quality of life, frequency of medical interventions, remission status, and patient outcome.

17. The method of claim 16, wherein the genetic profile comprises a genotype of a subject at one or more loci that increases cancer risk, impacts pharmacokinetics, or impacts drug sensitivity.
18. The method of claim 1, wherein the information about the plurality of subjects comprises one or more characteristics from tumor profiles of the subjects, which characteristics are selected from the group consisting of: one or more genetic variants, tissue of origin, tumor burden, tumor drug sensitivity, and tumor stage.
19. The method of claim 18, wherein the one or more characteristics are determined by assaying cell-free nucleic acid molecules from the subjects.
20. The method of claim 19, wherein the one or more genetic variants are quantified to determine a proportion of cell-free nucleic acid molecules comprising the one or more somatic mutations.
21. The method of claim 20, further comprising determining if the proportion of the one or more somatic mutations is increasing or decreasing between the first time point and the one or more subsequent time points.
22. The method of claim 20, further comprising determining if the proportion of the one or more somatic mutations is increasing or decreasing amongst a plurality of the one or more subsequent time points.
23. The method of claim 21 or 22, wherein the proportion of the one or more somatic mutations is increasing.
24. The method of claim 23, wherein the one or more somatic mutations is increasing, and further wherein the somatic mutations are associated with resistance to the treatment.
25. The method of claim 19, wherein the assaying comprises high-throughput sequencing.
26. The method of claim 1, wherein the genes are oncogenes.
27. The method of claim 26, wherein the oncogenes comprise genes listed in Figure 5.

28. A non-transitory computer-readable medium comprising machine executable code that, upon execution by one or more computer processors, implements the method of claim 1.