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 indicating genetic variants, and one or more treatment provided to the subject prior to the first time point, 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 respective 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 and the predictive algorithm corresponds to a decision tree that includes:

a root node corresponding to the first state and indicating a genetic variant included in one or more genetic profiles of one or more tumors,

one or more branches emanating from the root node and leading to one or more intermediate nodes, wherein a first portion of the intermediate nodes correspond to a treatment of the one or more treatments and a second portion of the intermediate nodes correspond to an additional genetic variant indicating resistance to the treatment, and

a terminal node indicating an outcome of the treatment with respect to a subject, wherein the terminal node and one or more intermediate nodes correspond to one or more subsequent states of the set of subsequent states.

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, wherein:

a state at the root node represents the first time point,

the first portion of the one or more intermediate nodes include one or more chance nodes, individual chance nodes of the one or more chance nodes indicating a probability of at least one subsequent state; and

the second portion of the one or more intermediate nodes include one or more decision nodes that 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 a first treatment included in the one or more treatments and the subsequent time point is after the subject received the first treatment.

15. The method of claim 1, wherein a second treatment of the one or more treatments is to be 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 genetic profile comprises at least one oncogene.

27. The method of claim 26, wherein the at least one oncogene is 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.