

CLAIMS

What is claimed is:

1. A method comprising:

receiving, by at least one processor, at least one microenvironment image from a microscopic imaging device;

receiving, by the at least one processor, at least one engineered microenvironment feature for each microenvironment image of the at least one microenvironment image;

utilizing, by the at least one processor, at least one feature extraction machine learning model to extract at least one derived compound microenvironment feature from each microenvironment image of the at least one microenvironment image;

utilizing, by the at least one processor, at least one prognosis inference machine learning model to infer a prognosis associated with the at least one microenvironment image using the at least one engineered microenvironment feature and the at least one derived compound microenvironment feature; and

generating, by the at least one processor, a notification indicating the prognosis based on the at least one microenvironment image for display on a user computing device in communication with the at least one processor.

2. The method of claim 1, further comprising:

identifying, by the at least one processor, cellular types and subtypes of cells in the at least one microenvironment image;

determining, by the at least one processor, individual cell distances of between the cells according to the cellular types and subtypes of the cells; and

determining, by the at least one processor, an engineered microenvironment feature comprising at least one aggregate measure of cell distance to represent the individual cell distances an aggregate.

3. The method of claim 1, further comprising:

determining, by the at least one processor, locations of immune cells in the at least one microenvironment image;

determining, by the at least one processor, at least one gradient associated with changes in density of the immune cells based at least in part on the locations of the immune cells;

determining, by the at least one processor, at least one change in the at least one gradient from at least one prior gradient of at least one prior microenvironment image; and

extrapolating, by the at least one processor, an engineered microenvironment feature comprising future immune cell positions based at least in part on the at least one change in the at least one gradient.

4. The method of claim 1, further comprising:

identifying, by the at least one processor, immune cell activity of immune cells based on morphological changes associated with immune activation between the at least one microenvironment image and at least one prior microenvironment image;

determining, by the at least one processor, an efficacy score of each immune cell from at least one immune cell based on the immune cell activity; and

determining, by the at least one processor, an engineered microenvironment feature comprising an aggregate immune cell efficacy score based on a statistical aggregation of the efficacy score of each immune cell.

5. The method of claim 1, further comprising:

identifying, by the at least one processor, immune cells and vascular structures in the at least one microenvironment image; and

determining, by the at least one processor, an engineered microenvironment feature comprising a distance between the immune cells and the vascular structures.

6. The method of claim 1, wherein the at least one engineered microenvironment feature comprises at least one of:

aggregate immune cell infiltration;

immune cell sequencing;

diseased or damaged tissue;
steatosis or fatty changes;
scarring and fibrosis;
necrosis;
vascular structures;
ductal structures;
individual cell spatial characterization;
target cell and surrounding cell status;
differentiation of sub-classes of immune cells;
cell morphology;
an intersection of immune cell infiltration;
cell motility;
rates of motility of individual cells;
other structures; or
combinations thereof.

7. The method of claim 1, wherein the at least one derived compound microenvironment feature comprises at least one of:

inter-feature changes;
auto-encoder reconstruction;
convolutional neural network feature vectors;
computer vision output;
deep learning output;
time-series based prediction of features representative of a time-series of images;
data points produced by generative models;
features generated from multi-modal modelling of image data;

repeat feature reduction;
an ensemble model of weighted of features;
gradient class activation maps; and
combinations thereof.

8. The method of claim 1, further comprising:

comparing, by the at least one processor, the prognosis with a known prognosis determine a loss; and

backpropagating, by the at least one processor, the loss to the at least one prognosis inference machine learning model to update parameters of the at least one prognosis inference machine learning model.

9. The method of claim 1, further comprising determining, by the at least one processor, a correlation between patient outcomes and each engineered microenvironment feature of the at least one engineered microenvironment feature.

10. The method of claim 1, further comprising:

determining, by the at least one processor, a correlation between biological sample outcomes and each engineered microenvironment feature of the at least one engineered microenvironment feature;

utilizing, by the at least one processor, at least one toxicologic histopathology machine learning model to determine patterns of pathology to classify the correlation with groupings in chemistry based at least in part on the correlation between the biological sample outcomes to infer causality; and

generating, by the at least one processor, at least one predictive model based at least in part on the groupings to predict toxicological safety.

11. A method comprising:

receiving, by at least one processor, at least one microenvironment image captured by an imaging device and depicting a cellular microenvironment of a biological sample;

receiving, by the at least one processor, at least one structure identifier in the at least one microenvironment image via user selection to identify at least one structure in the cellular microenvironment;

determining, by the at least one processor, at least one engineered microenvironment feature for each microenvironment image of the at least one microenvironment image based at least in part on the at least one structure identifier and at least one feature computation;

utilizing, by the at least one processor, at least one feature extraction machine learning model to extract at least one derived compound microenvironment feature from each microenvironment image of the at least one microenvironment image based on trained feature extraction parameters of the at least one feature extraction machine learning model and each microenvironment image of the at least one microenvironment image;

utilizing, by the at least one processor, at least one prognosis inference machine learning model to infer a prognosis associated with the biological sample based on trained prognosis inference parameters of the at least one prognosis inference machine learning model and the at least one engineered microenvironment feature and the at least one derived compound microenvironment feature; and

generating, by the at least one processor, a notification indicating the prognosis based on the at least one microenvironment image for display on a user computing device in communication with the at least one processor.

12. The method of claim 11, wherein the at least one feature extraction machine learning model comprises at least one convolutional neural network trained to ingest the at least one microenvironment image and output a set of annotations representing the at least one derived compound microenvironment feature.

13. The method of claim 11, wherein the at least one feature extraction machine learning model comprises at least one generative adversarial network trained to ingest the at least one

microenvironment image and output a set of annotations representing the at least one derived compound microenvironment feature.

14. The method of claim 11, further comprising:

identifying, by the at least one processor, cellular types and subtypes of cells in the at least one microenvironment image;

determining, by the at least one processor, individual cell distances of between the cells according to the cellular types and subtypes of the cells; and

determining, by the at least one processor, an engineered microenvironment feature comprising at least one aggregate measure of cell distance to represent the individual cell distances an aggregate.

15. The method of claim 11, further comprising:

identifying, by the at least one processor, immune cell activity of immune cells based on morphological changes associated with immune activation between the at least one microenvironment image and at least one prior microenvironment image;

determining, by the at least one processor, an efficacy score of each immune cell from at least one immune cell based on the immune cell activity; and

determining, by the at least one processor, an engineered microenvironment feature comprising an aggregate immune cell efficacy score based on a statistical aggregation of the efficacy score of each immune cell.

16. The method of claim 11, further comprising:

identifying, by the at least one processor, immune cells and vascular structures in the at least one microenvironment image; and

determining, by the at least one processor, an engineered microenvironment feature comprising a distance between the immune cells and the vascular structures.

17. The method of claim 11, further comprising:

comparing, by the at least one processor, the prognosis with a known prognosis to determine a loss; and

backpropagating, by the at least one processor, the loss to the at least one prognosis inference machine learning model to update parameters of the at least one prognosis inference machine learning model.

18. The method of claim 11, further comprising determining, by the at least one processor, a correlation between patient outcomes and each engineered microenvironment feature of the at least one engineered microenvironment feature.

19. The method of claim 11, further comprising:

determining, by the at least one processor, a correlation between biological sample outcomes and each engineered microenvironment feature of the at least one engineered microenvironment feature;

utilizing, by the at least one processor, at least one toxicologic histopathology machine learning model to determine patterns of pathology to classify the correlation with groupings in chemistry based at least in part on the correlation between the biological sample outcomes to infer causality; and

generating, by the at least one processor, at least one predictive model based at least in part on the groupings to predict toxicological safety.

20. A non-transitory computer readable medium having software instruction stored thereon, the software instructions configured to cause at least one processor of at least one computer to perform steps to:

receive at least one microenvironment image from a microscopic imaging device;

receive at least one engineered microenvironment feature for each microenvironment image of the at least one microenvironment image;

utilize at least one feature extraction machine learning model to extract at least one derived compound microenvironment feature from each microenvironment image of the at least one microenvironment image;

utilize at least one prognosis inference machine learning model to infer a prognosis associated with the at least one microenvironment image using the at least one engineered microenvironment feature and the at least one derived compound microenvironment feature; and

generate a notification indicating the prognosis based on the at least one microenvironment image for display on a user computing device in communication with the at least one processor.