CLAIMS

1. A method for analyzing biological samples, comprising:

identifying an analysis of biological samples in multiple regions of interest in a microfluidic device and a timeline correlated with the analysis, wherein the timeline comprises information that is temporally aligned with at least one of a workflow or a pipeline of the analysis of the biological samples;

determining one or more region-of-interest types for the multiple regions of interest, wherein the one or more region-of-interest types comprise a target-based type correlated with at least one biological sample of the biological samples or a structure-based type correlated with the microfluidic device;

determining multiple characteristics for the biological samples based at least in part upon the one or more region-of-interest types, wherein the multiple characteristics respectively correspond to an attribute, a property, or a quantifiable metric for the biological samples or the analyses; and

arranging and rendering associated data from the analysis that respectively correspond to the multiple regions of interest in a user interface for at least a portion of the biological samples based at least in part upon the multiple characteristics and the timeline.

2. The method of claim 1, wherein arranging and rendering the associated data comprises:

determining a gallery structure having a plurality of gallery sub-structures for the analysis results based at least in part upon an allocable space in the user interface for rendering the analysis results.

3. The method of claim 2, wherein arranging and rendering the analysis results comprises:

populating the analysis results into the plurality of gallery sub-structures in a gallery structure based at least in part upon a characteristic of the multiple characteristics.

4. The method of claim 3, determining the gallery structure comprising:

determining a first sequence of data correlated with a set of time points or time periods for a first biological sample obtained from a first region of interest of the multiple regions of interest from the gallery structure stored in an addressable space in a non-transitory computer accessible storage medium, wherein the first sequence of data corresponds to at least a first characteristic of the multiple characteristics; and

determining a second sequence of data correlated with the set of time points or time periods for a second biological sample obtained from a second region of interest of the multiple regions of interest from the gallery structure, wherein the second sequence of data corresponds to at least a second characteristic of the multiple characteristics; and

in response to a selection of the at least the first characteristic from the multiple characteristics with a first selection widget in the user interface,

extracting a first value of at least the first characteristic from a plurality of values for the first biological sample or for the analysis; and

extracting a second value of at least the first characteristic from the plurality of values for the second biological sample or for the analysis.

5. The method of claim 4, arranging and rendering analysis results comprising:

rendering a first interactive object and a second interactive object respectively corresponding to the first sequence of data and the second sequence of data into the gallery view, wherein

the first interactive object is representative of the first value for the first biological sample or for the analysis, and

the second interactive object is representative of the second value for the second biological sample or for the analysis.

6. The method of claim 1, further comprising:

in response to an invocation of a timeline view through a timeline view activation interactive widget in the user interface based at least in part upon the timeline, rendering the timeline view and a matching grid portion in the user interface.

7. The method of claim 6, wherein

the timeline view comprises a respective progress of multiple workflow tasks in the analysis of the biological samples, and

the respective progress graphically indicates respective temporal durations of the multiple workflow tasks.

8. The method of claim 7, further comprising:

determining whether a gallery structure exists for storing data correlated with the biological samples in the microfluidic device in response to an identification of the microfluidic device, a first sequence of data correlated with a first biological sample of the multiple regions of interest from a first region of interest, or a second sequence of data correlated with a second biological sample of the multiple regions of interest from a second region of interest represented in the user interface, wherein

the data comprises the first sequence of data correlated with the first biological sample from a first region of interest of the multiple regions of interest, or the second sequence of data correlated with the second biological sample from the second region of interest of the multiple regions of interest represented in the user interface; and

when it is determined that the gallery structure exists for the microfluidic device,

populating the matching grid portion with at least a portion of the first sequence of data or at least a portion of the associated data; and

rendering an identifier widget which, when receiving an identifier change input from the user interface, triggers an instruction that changes a first characteristic of the multiple characteristics and correlated with the first sequence of data..

9. The method of claim 1, further comprising:

associating a first region of interest of the multiple regions of interest with one or more graphical elements illustrated in a timeline view, wherein associating the first region of interest with the one or more graphical elements comprises:

rendering a first interactive object, which corresponds to a first sequence of data captured at a first time point or a first temporal period, for a first graphical

element of the one or more graphical elements in a first column in a portion of the user interface; or

rendering a first interactive object, which corresponds to a first sequence of data captured at a first time point or a first temporal period, for a first graphical element of the one or more graphical elements in a first column in a portion of the user interface and rendering a second interactive object, which corresponds to a second sequence of data captured at a second time point or a second temporal period, for a second graphical element of the one or more graphical elements, the second interactive object corresponding to a second column in the portion of the user interface..

10. The method of claim 1, wherein arranging and rendering the analysis results comprises:

determining the timeline based at least in part upon the pipeline or the workflow for the analysis of the biological samples.

11. The method of claim 10, wherein arranging and rendering the analysis results comprises:

determining a plurality of stages for the analysis based at least in part upon the timeline, wherein the plurality of stages respectively corresponds to a plurality of timepoints or time periods for the analysis of the biological samples.

12. The method of claim 11, wherein arranging and rendering the associated data comprises:

respectively determining a plurality of graphic representations for the plurality of stages based at least in part upon the plurality of timepoints or time periods.

13. The method of claim 1, further comprising rendering a data control view in the user interface, rendering the data control view comprising:

generating a microfluidic device data structure having a plurality of fields for the microfluidic device having a plurality of chambers.

14. The method of claim 13, rendering the data control view comprising:

populating first data correlated with the microfluidic device into a first field in the microfluidic device data structure, wherein the first data comprises a first identifier of the microfluidic device.

15. The method of claim 14, rendering the data control view comprising:

rendering a first interactive data control widget for the first field of the microfluidic device data structure, wherein the first interactive data control widget, when interacted upon, invokes one of multiple first candidate actions that are correlated to a timeline view or a gallery view based at least in part upon a first input received in the data control view for configuring a chamber list correlated with at least the first data and the gallery view.

16. The method of claim 14, rendering the data control view further comprising:

populating second data correlated with the microfluidic device into a second field in the microfluidic device data structure, wherein the second data comprises a tag correlated with a first biological processing on the biological samples in the microfluidic device.

17. The method of claim 16, rendering the data control view further comprising:

rendering a second interactive data control widget for the second field, wherein the second interactive data control widget invokes at least one of multiple second candidate actions in response to a second user input in the data control view for configuring one or more visualization options of the associated data.

18. The method of claim 1, further comprising rendering a filter view, wherein rendering the filter view comprises:

determining a first filter type for a first filter based at least in part upon an execution of one or more instructions triggered by an interaction with a first filter selector switch in a filter generation module.

19. The method of claim 18, rendering the filter view further comprising:

dynamically determining and displaying, in the filter view for the microfluidic device, a first total number of regions of interest for a first set of filtered regions of interest that satisfies a first dynamic constraint of the first filter applied to the multiple regions of interest.

20. The method of claim 18, rendering the filter view further comprising:

generating, at a filter generation module, a logical combination of at least a second filter of a second filter type and the first filter of the first filter type.

21. The method of claim 20, rendering the filter view further comprising:

in response to a determination of a second filter attribute, rendering a second filter configurator for filtering a plurality of chambers of the microfluidic device or the multiple regions of interest according to the second filter, wherein

the second filter configurator imposes a second dynamic constraint in response to a second filter input, and the second dynamic constraint constrains a second number of filtered regions of interest from the multiple regions of interest to be displayed in the user interface.

22. The method of claim 21, rendering the filter view further comprising:

dynamically determining and displaying, in the filter view for the microfluidic device, a second total number of filtered regions of interest that satisfies the second dynamic constraint; and

rendering a second histogram that dynamically varies in response to a second dynamic change in the second dynamic constraint from the second filter input.

23. The method of claim 1, further comprising generating a bioinformatics pipeline view, generating the bioinformatics pipeline view comprising:

determining a sequencing dataset for the biological samples in a plurality of chambers or the multiple regions of interest of the microfluidic device, wherein a biological sample comprises a sequence of nucleotides or amino acids.

24. The method of claim 23, generating the bioinformatics pipeline view further comprising:

in response to a first interaction with a first sequencing view widget in the user interface, rendering a first sequencing view in the bioinformatics pipeline view that illustrates a distribution of an attribute of the sequence of first biological samples including at least one of a sequence of nucleotides, a sequence of amino acids, or a sequence of macromolecules in the plurality of chambers or the multiple regions of interest of the microfluidic device.

25. The method of claim 24, generating the bioinformatics pipeline view further comprising:

overlaying the first sequencing view with first information that comprises one or more statistical measures of the distribution of the attribute of multiple sequences of first biological samples including the sequence of first biological

samples, wherein

the user interface comprises a total number of the multiple sequences of first biological samples, a total number of regions of interest having the sequence of first biological samples, and a respective total number of one or more sequences of first biological samples in a respective region of interest of the array of regions of interest.

26. The method of claim 1, further comprising:

rendering a multi-directional placement widget in the user interface that includes at least one view, wherein the at least one view comprises one or more of a gallery view, a timeline view, a filter view, a bioinformatics pipeline view, or a differential gene expression view; and

identifying an addition instruction for adding a separate object into the user interface based at least in part upon a first input from a user.

27. The method of claim 26, further comprising:

determining a candidate placement position from multiple candidate placement positions for the separate object based at least in part upon the first input.

28. The method of claim 27, the set of acts further comprising:

rendering a ghosting object at the candidate position in the user interface to graphically present where the separate object is to be placed in relation to the at least one view prior to placement of the separate object in the user interface.

29. The method of claim 1, wherein the multiple characteristics correspond to one or more attributes that further comprise at least one of an identifier of a region of interest in the microfluidic device, a size attribute of the biological samples, a maximum brightness attribute for the biological samples, a minimum brightness attribute for the biological samples, a first pixel count attribute in a first direction for a centroid of a first biological sample, a second pixel count attribute in a second direction for the centroid of the biological sample, a size attribute for the centroid of the biological sample, a time lapse index attribute, a device identifier for the microfluidic device, a biological sample count attribute, a verified biological sample count attribute, a biological sample type attribute, a score attribute of the plurality of regions of interest, a gate path index, an area pixel attribute, a background pixel attribute, or a median brightness attribute for the plurality of

biological samples.

30. The method of claim 1, further comprising determining a first count of the biological samples at a first time point in a region of interest in the microfluidic device.

31. The method of claim 30, further comprising:

pre-processing first image data that is captured at a first time point for a region of interest in the microfluidic device into first pre-processed image data at least by arranging the first image data into an array of first pixel information by second pixel information by pixel depth information.

32. The method of claim 31, further comprising:

determining a first count of total biological samples in the region of interest at least by recognizing the total biological samples with a convolutional neural network (CNN) having multiple processing blocks.

33. The method of claim 32, further comprising:

determining the first count of the biological samples in the region of interest based at least in part upon a first class or type of the first image data using the multiple processing blocks of the convolutional neural network (CNN).

34. The method of claim 32, wherein the multiple processing blocks comprise:

a first processing block, a second processing block, and a third processing block, the first processing block comprising a first down-sampling block that down-samples a first input to the second down-sampling block into first down-sampled image data.

35. The method of claim 34, the first processing block further comprising:

a first residual network, wherein the first residual network follows the first down-sampling block, wherein each of the first down-sampling block and the first residual network in the first processing block comprises at least one first convolutional layer, wherein

the first residual network comprises a first parallel path and a second parallel path, both of which receive a first down-sampling block output from the first down-sampling block,

the first parallel path comprises a first filter size, and

the second parallel path comprises a second filter size that is smaller than

the first filter size of the first parallel path.

36. The method of claim 32, wherein convolutional layers in the convolutional neural network have filter sizes greater than one-by-one so that no convolutional layers in the convolutional neural network have a one-by-one filter, and the convolutional neural network comprises no pooling layers.

37. A method for analyzing an image of biological samples, comprising:

receiving first image data captured at a first time point or time period for a region of interest in a microfluidic device;

pre-processing the first image data into first pre-processed image data at least by arranging the first image data into an array of first pixel information by second pixel information by pixel depth information;

determining a first class or type of the first image data at least by classifying the first image data into the first class or type with at least a machine learning model;

determining a first count of the biological samples in the region of interest based at least in part upon the first class or type at least by recognizing the biological samples with a convolutional neural network (CNN) having multiple processing blocks; and

displaying textual or graphical information correlated with the first count for the region of interest in a gallery view of a graphical user interface (GUI).

38. An article of manufacture comprising a non-transitory machine accessible storage medium storing thereupon a sequence of instructions which, when executed by a processor, causes the process to perform any of the methods of claims 1-37.

39. A system, comprising:

a processor;

a user interface coupled to the processor for processing a plurality of molecular-biological samples that comprise a first molecular-biological sample and a second molecular-biological sample in a first molecular-biological device;

a non-transitory computer accessible storage medium storing thereupon a sequence of instructions which, when executed by a processor, causes the processor to perform any of the methods of claims 1-37.