WHAT IS CLAIMED IS:

1. An ex vivo method for predicting a subject's diagnostic status with respect a disease or disorder, the method comprising:

(a) staining a tooth sample of the subject to produce a stained tooth sample;

(b) analyzing a fluorescence intensity spatially across the stained tooth sample, wherein the analyzing comprises generating a temporal profile of inflammation based at least in part on the fluorescence intensity, and analyzing the temporal profile of inflammation; and

(c) predicting a subject's diagnostic status with respect to the disease or disorder based at least in part on the analysis of the fluorescence intensity, wherein predicting a subject's diagnostic status with respect to the disease or disorder comprises processing the fluorescence intensity using a trained model wherein the trained model is configured to process one or more features selected from the group consisting of determination of a linear slope of the temporal profile, determination of a plurality of non-linear parameters describing curvature of the temporal profile, determination of an abrupt change in intensity of the temporal profile, determination of one or more changes in a baseline intensity of the temporal profile, determination of a change of a frequency-domain representation of the temporal profile, determination of a change of the power-spectral domain representation of the temporal profile, determination of one or more recurrence quantification analysis parameters, determination of one or more cross-recurrence quantification analysis parameters, determination of one or more joint recurrence quantification analysis parameters, determination of one or more multi-dimensional recurrence quantification analysis parameters, estimation of a Lyapunov spectra, determination of a maximum Lyapunov exponent and any combination thereof.

2. The method of claim 1, wherein the analyzing comprises obtaining a fluorescence image of the stained tooth sample, and analyzing the fluorescence intensity of the fluorescence image optionally wherein the fluorescence image of the stained tooth sample comprises using an inverted or non-inverted confocal microscope.

3. The method of claim 1, wherein staining the tooth sample comprises using a C-reactive protein immunohistochemistry stain or decalcifying the tooth sample.

4. The method of claim 1, further comprising sectioning the tooth sample.

5. The method of claim 1, wherein the disease or disorder comprises autism spectrum disorder (ASD), attention deficit/hyperactivity disorder (ADHD), amyotrophic lateral sclerosis (ALS), schizophrenia, irritable bowel disease (IBD), pediatric kidney disease, kidney transplant rejection, pediatric cancer, or any combination thereof.

6. The method of claim 1, wherein the subject is a human.

7. The method of claim 6, wherein the subject is less than 12 years old.

8. The method of claim 1, wherein at least a portion of the temporal profile of inflammation corresponds to a prenatal period of the subject.

9. The method of claim 1, wherein the trained model is selected from the group consisting of: a gradient-boosted decision tree, a neural network algorithm, a support vector machine algorithm, a decision tree algorithm, an unsupervised clustering algorithm, a supervised clustering algorithm, a regression algorithm, a gradient-boosting algorithm, and any combination thereof.

10. The method of claim 1, wherein the trained model is configured to process two or more features selected from the group consisting of determination of a linear slope of the temporal profile, determination of a plurality of non-linear parameters describing curvature of the temporal profile, determination of an abrupt change in intensity of the temporal profile, determination of one or more changes in a baseline intensity of the temporal profile, determination of a change of a frequency-domain representation of the temporal profile, determination of a change of the power-spectral domain representation of the temporal profile, determination of one or more recurrence quantification analysis parameters, determination of one or more cross-recurrence quantification analysis parameters, determination of one or more joint recurrence quantification analysis parameters, determination of one or more multi-dimensional recurrence quantification analysis parameters, estimation of a Lyapunov spectra, determination of a maximum Lyapunov exponent and any combination thereof.

11. A device comprising one or more processors, and memory storing one or more programs for execution by the one or more processors, the one or more programs comprising instructions for:

(a) sampling each respective position in a plurality of positions along a reference line on a biological sample of the subject associated with c-reactive protein of the subject, thereby obtaining a plurality of fluorescence intensity measurements, each fluorescence intensity measurement in the plurality of fluorescence intensity measurements corresponding to a different position in the plurality of positions, and each position in the plurality of positions representing a different period of growth of the biological sample of the subject associated with c-reactive protein;

(b) analyzing each fluorescence intensity across reference line on the biological sample thereby obtaining a first dataset;

(c) deriving a respective second dataset from the corresponding plurality of fluorescence intensity measurements, each respective feature in the corresponding set of features being determined by a sequential variability in c-reactive protein fluorescence intensity; and

(d) processing the features using a trained model to predict a subject's diagnostic status with respect to a disease or disorder associated with c-reactive protein, wherein the predicting the subject's diagnostic status with respect to the disease or disorder comprises processing the plurality of fluorescence intensity measurements using the trained model, wherein the trained model is configured to process one or more features selected from the group consisting of determination of a linear slope of the fluorescence intensity across the reference line, determination of a plurality of non-linear parameters describing curvature of the fluorescence intensity across the reference line, determination of an abrupt change in intensity of the fluorescence intensity across the reference line, determination of one or more changes in a baseline intensity of the fluorescence intensity across the reference line, determination of a change of a frequency-domain representation of the fluorescence intensity across the reference line, determination of a change of the power-spectral domain representation of the fluorescence intensity across the reference line, determination of one or more recurrence quantification analysis parameters, determination of one or more cross-recurrence quantification analysis parameters, determination of one or more joint recurrence quantification analysis parameters, determination of one or more multi-dimensional recurrence quantification analysis parameters,

estimation of a Lyapunov spectra, determination of a maximum Lyapunov exponent and any combination thereof.

12. The device of claim 11, wherein the plurality of fluorescence intensity measurements are measured with an inverted or non-inverted confocal microscope.

13. The device of claim 11, wherein the biological sample comprises a tooth sample.

14. The device of any claim 11, wherein the disease or disorder comprises autism spectrum disorder (ASD), attention deficit/hyperactivity disorder (ADHD), amyotrophic lateral sclerosis (ALS), schizophrenia, irritable bowel disease (IBD), pediatric kidney disease, kidney transplant rejection, pediatric cancer, or any combination thereof.

15. The device of claim 11, wherein the subject is a human.

16. The device of claim 11, wherein the analyzing (b) comprises generating a temporal profile of inflammation based at least in part on the plurality of fluorescence intensity measurements, and analyzing the temporal profile of inflammation.

17. The device of claim 11, wherein at least a portion of the temporal profile of inflammation corresponds to a prenatal period of the subject.

18. The device of claim 11, wherein the trained model is selected from the group consisting of: a gradient-boosted decision tree, a neural network algorithm, a support vector machine algorithm, a decision tree algorithm, an unsupervised clustering algorithm, a supervised clustering algorithm, a regression algorithm, a gradient-boosting algorithm, and any combination thereof.

19. The device of claim 11, wherein the trained model is configured to process two or more features selected from the group consisting of determination of a linear slope of the fluorescence intensity across the reference line, determination of a plurality of non-linear parameters describing curvature of the fluorescence intensity across the reference line, determination of an

abrupt change in intensity of the fluorescence intensity across the reference line, determination of one or more changes in a baseline intensity of the fluorescence intensity across the reference line, determination of a change of a frequency-domain representation of the fluorescence intensity across the reference line, determination of a change of the power-spectral domain representation of the fluorescence intensity across the reference line, determination of one or more recurrence quantification analysis parameters, determination of one or more cross-recurrence quantification analysis parameters, determination of one or more joint recurrence quantification analysis parameters, determination of one or more multi-dimensional recurrence quantification analysis parameters, estimation of a Lyapunov spectra, determination of a maximum Lyapunov exponent and any combination thereof.

20. A non-transitory computer readable storage medium and one or more computer programs embedded therein, the one or more computer programs comprising instructions which, when executed by a computer system, cause the computer system to perform an ex vivo method comprising:

(a) sampling each respective position in a plurality of positions along a reference line on a biological sample of the subject associated with c-reactive protein of the subject, thereby obtaining a plurality of fluorescence intensity measurements, each fluorescence intensity measurement in the plurality of fluorescence intensity measurements corresponding to a different position in the plurality of positions, and each position in the plurality of positions representing a different period of growth of the biological sample of the subject associated with c-reactive protein;

(b) analyzing each fluorescence intensity across reference line on the biological sample thereby obtaining a first dataset;

(c) deriving a respective second dataset from the corresponding plurality of fluorescence intensity measurements, each respective feature in the corresponding set of features being determined by a variation in c-reactive protein fluorescence intensity; and

(d) processing the features using a trained model to predict a subject's diagnostic status with respect to a disease or disorder associated with c-reactive protein, wherein predicting the subject's diagnostic status with respect to the disease or disorder comprises processing the plurality of fluorescence intensity measurements using the trained model, wherein the trained

model is configured to process one or more features selected from the group consisting of recurrence rates, determinism, mean diagonal length, maximum diagonal length, divergence, Shannon entropy in diagonal length, trend in recurrences, laminarity, trapping time, maximum vertical line length, Shannon entropy in vertical line lengths, mean recurrence time, Shannon entropy in recurrence times, number of the most probable recurrences, mean diagonal length (MDL), recurrence time (RT), Vmax, determinism, Lmax, determination of a linear slope of the fluorescence intensity across the reference line, determination of a plurality of non-linear parameters describing curvature of the fluorescence intensity across the reference line, determination of an abrupt change in intensity of the fluorescence intensity across the reference line, determination of one or more changes in a baseline intensity of the fluorescence intensity across the reference line, determination of a change of a frequency-domain representation of the fluorescence intensity across the reference line, determination of a change of the power-spectral domain representation of the fluorescence intensity across the reference line, determination of one or more recurrence quantification analysis parameters, determination of one or more cross-recurrence quantification analysis parameters, determination of one or more joint recurrence quantification analysis parameters, determination of one or more multi-dimensional recurrence quantification analysis parameters, estimation of a Lyapunov spectra, determination of a maximum Lyapunov exponent and any combination thereof.

21. The non-transitory computer readable storage medium of claim 20, wherein the biological sample comprises a tooth sample.

22. The non-transitory computer readable storage medium of claim 20, wherein the tooth sample is stained using a C-reactive protein immunohistochemistry stain, is sectioned, or is decalcified.

23. The non-transitory computer readable storage medium of claim 20, wherein the disease or disorder comprises autism spectrum disorder (ASD), attention deficit/hyperactivity disorder (ADHD), amyotrophic lateral sclerosis (ALS), schizophrenia, irritable bowel disease (IBD), pediatric kidney disease, kidney transplant rejection, pediatric cancer, or any combination thereof.

24. The non-transitory computer readable storage medium of claim 20, wherein the subject is a human.

25. The non-transitory computer readable storage medium of claim 20, wherein analyzing comprises generating a temporal profile of inflammation based at least in part on the plurality of fluorescence intensity measurements, and analyzing the temporal profile of inflammation.

26. The non-transitory computer readable storage medium of claim 20, wherein at least a portion of the temporal profile of inflammation corresponds to a prenatal period of the subject.

27. The non-transitory computer readable storage medium of claim 20, wherein the trained model is selected from the group consisting of: a gradient-boosted decision tree, a neural network algorithm, a support vector machine algorithm, a decision tree algorithm, an unsupervised clustering algorithm, a supervised clustering algorithm, a regression algorithm, a gradient-boosting algorithm, and any combination thereof.

28. The non-transitory computer readable storage medium of claim 20, wherein the trained model is configured to process two or more features selected from the group consisting of a determination of a linear slope of the fluorescence intensity across the reference line, determination of a plurality of non-linear parameters describing curvature of the fluorescence intensity across the reference line, determination of an abrupt change in intensity of the fluorescence intensity across the reference line, determination of one or more changes in a baseline intensity of the fluorescence intensity across the reference line, determination of a change of a frequency-domain representation of the fluorescence intensity across the reference line, determination of a change of the power-spectral domain representation of the fluorescence intensity across the reference line, determination of one or more recurrence quantification analysis parameters, determination of one or more cross-recurrence quantification analysis parameters, determination of one or more joint recurrence quantification analysis parameters, determination of one or more multi-dimensional recurrence quantification analysis parameters, estimation of a Lyapunov spectra, determination of a maximum Lyapunov exponent and any combination thereof.