What is Claimed is:

1. A configurable handheld biological analyzer for identification of biological products based on Raman spectroscopy using ensemble artificial intelligence (AI), the configurable handheld biological analyzer comprising:

a first housing adapted for handheld manipulation;

a first scanner carried by the first housing;

a first processor communicatively coupled to the first scanner; and

a first computer memory communicatively coupled to the first processor,

wherein the first computer memory is configured to load a biological ensemble classification model configuration, the biological ensemble classification model configuration comprising a biological classification ensemble model comprising an unsupervised model and a supervised model,

wherein the unsupervised model is trained with Raman-based spectra training data to configure the unsupervised model to output a first indicator of one or more biological product types,

wherein the supervised model is trained with Raman-based spectra training data to configure the supervised model to output a second indicator of the one or more biological product types,

wherein the biological classification ensemble model configuration further comprises one or more spectral preprocessing algorithms, the first processor configured to execute the one or more spectral preprocessing algorithms to reduce a spectral variance of a first Raman-based spectra dataset when the first Raman-based spectra dataset is received by the first processor, and

wherein the biological classification ensemble model is configured to execute on the first processor, the first processor configured to (1) receive a first Raman-based spectra dataset defining a first biological product sample as scanned by the first scanner, and (2) identify, with the biological classification ensemble model, a biological product type of the one or more biological product types based on the first Raman-based spectra dataset.

2. The configurable handheld biological analyzer of claim 1, wherein the biological ensemble classification model configuration is electronically transferrable to a second configurable handheld biological analyzer, the second configurable handheld biological analyzer comprising:

a second housing adapted for handheld manipulation;

a second scanner coupled to the second housing;

a second processor communicatively coupled to the second scanner; and

a second computer memory communicatively coupled to the second processor,

wherein the second computer memory is configured to load the biological classification ensemble model configuration, the biological classification ensemble model configuration comprising the biological classification ensemble model, wherein the biological classification ensemble model is configured to execute on the second processor, the second processor configured to (1) receive a second Raman-based spectra dataset defining a second biological product sample as scanned by the second scanner, and (2) identify, with the biological classification ensemble model, the biological product type based on the second Raman-based spectra dataset,

wherein the second biological product sample is a new sample of the biological product type.

3. The configurable handheld biological analyzer of claim 1, wherein the spectral variance is an analyzer-to-analyzer spectral variance between the first Raman-based spectra dataset and one or more other Raman-based spectra

datasets of one or more corresponding other handheld biological analyzers, each of the one or more other Raman-based spectra datasets representative of the biological product type, and

wherein the one or more spectral preprocessing algorithms are configured to mitigate the analyzer-to-analyzer spectral variance between the first Raman-based spectra dataset and the one or more other Raman-based spectra datasets.

4. The configurable handheld biological analyzer of claim 3, wherein the one or more spectral preprocessing algorithms comprises:

applying a derivative transformation to the first Raman-based spectra dataset to generate a modified Raman-based spectra dataset,

aligning the modified Raman-based spectra dataset across a Raman shift axis, and

normalizing the modified Raman-based spectra dataset across a Raman intensity axis.

5. The configurable handheld biological analyzer of claim 4, wherein the modified Raman-based spectra dataset is centered.

6. The configurable handheld biological analyzer of claim 4, wherein the derivative transformation is applied to consecutive groups of 5 to 15 Raman intensity values across the Raman shift axis.

7. The configurable handheld biological analyzer of claim 5, wherein corresponding derivatives of the consecutive groups of 5 to 15 Raman intensity values are determined across the Raman shift axis.

8. The configurable handheld biological analyzer of any one of claims 1-7, wherein the unsupervised model is configured to detect variability associated with identifying the one or more biological product types.

9. The configurable handheld biological analyzer of claim 8, wherein the variability comprises instrument variability or sample lot-to-lot variability.

10. The configurable handheld biological analyzer of any one of claims 1-9, wherein the biological classification ensemble model identifies the biological product type upon determination that the first indicator passes a first pass-fail based threshold value and that the second indicator passes a second pass-fail based threshold value.

11. The configurable handheld biological analyzer of any one of claims 1-9, wherein the first indicator as output by the unsupervised model is based on whether the one or more biological product types satisfies a threshold value.

12. The configurable handheld biological analyzer of claim 11, wherein the unsupervised model outputs a pass-fail determination based on the threshold value.

13. The configurable handheld biological analyzer of claim 11 or 12, wherein the threshold value is based on one or more of: a reduced Q-residual error, a Hotelling's T-squared value, a Mahalanobis distance value, or specific range values for principal component scores.

14. The configurable handheld biological analyzer of any one of claims 1-13, wherein a first biological product type of the one or more biological product types and a second biological product type of the one or more biological product types have similar Raman-based spectra.

15. The configurable handheld biological analyzer of any one of claim 1-14, wherein the second indicator as output by the supervised model is based on whether the one or more biological product types satisfies a biological product type prediction threshold value.

16. The configurable handheld biological analyzer of claim 15, wherein the supervised model outputs a pass-fail determination based on the biological product type prediction threshold value.

17. The configurable handheld biological analyzer of any one of claims 1-16, wherein the computer memory is configured to load a new biological classification ensemble model, the new biological ensemble classification model comprising an updated unsupervised model and/or an updated supervised model.

18. The configurable handheld biological analyzer of any one of claims 1-17, wherein the biological classification ensemble model configuration is implemented in an extensible markup language (XML) format.

19. The configurable handheld biological analyzer of any one of claims 1-18, wherein the biological product type is of a therapeutic product.

20. The configurable handheld biological analyzer of any one of claims 1-19, wherein the biological product type is identified by the biological classification ensemble model during manufacture of a biological product having the biological product type.

21. The configurable handheld biological analyzer of any one of claims 1-20, wherein the supervised model of the biological classification ensemble model is configured to distinguish the first biological product sample having the biological product type from a different biological product sample having a different biological product type.

22. The configurable handheld biological analyzer of claim 21 wherein the biological product type and the different biological product type each have distinct localized features within a similar Raman spectra range.

23. The configurable handheld biological analyzer of any one of claims 1-22, wherein the biological classification ensemble model is generated by a remote processor being remote to the configurable handheld biological analyzer.

24. The configurable handheld biological analyzer of any one of claims 1-23, wherein the unsupervised model is configured based on: a principal component analysis (PCA), a Euclidean distance or correlation; a neighbor-based algorithm, a K-means algorithm, Quality Threshold (QT) algorithm, a Centroid algorithm, a Ward algorithm, or a Fuzzy C-Means clustering algorithm.

25. The configurable handheld biological analyzer of claim 24, wherein the unsupervised model is a PCA model, and wherein the PCA model comprises a reduced set of principal components.

26. The configurable handheld biological analyzer of any one of claims 1-25, wherein the supervised model is trained using a partial least squares discriminant analysis (PLSDA), a linear discriminant analysis (LDA), a K-nearest neighbor (KNN) algorithm, a soft independent modeling using class analogy (SIMCA), or a logistic regression discriminant analysis (LREGDA) algorithm.

27. The configurable handheld biological analyzer of claim 26, wherein the supervised model is a PLSDA model, and wherein the PLSDA model comprises a reduced set of latent variables.

28. The configurable handheld biological analyzer of any one of claims 1-27, wherein the unsupervised model is configured based on a principal component analysis (PCA) and the supervised model is configured on a partial least squares discriminant analysis (PLSDA).

29. The configurable handheld biological analyzer of any one of claims 1-28, wherein the one or more spectral preprocessing algorithms are executed to modify at least one of: (a) training data as used to train one or both of the supervised model or the unsupervised model; or (b) production data as used to produce an output from one or both of the supervised model or the unsupervised model.

30. A biological analytics method for identification of biological products based on Raman spectroscopy using ensemble artificial intelligence (AI), the biological analytics method comprising:

loading, into a first computer memory of a first configurable handheld biological analyzer having a first processor and a first scanner, a biological ensemble classification model configuration, the biological ensemble classification model configuration comprising a biological classification ensemble model comprising an unsupervised model and a supervised model,

wherein the unsupervised model is trained with Raman-based spectra training data to configure the unsupervised model to output a first indicator of one or more biological product types, and

wherein the supervised model is trained with Raman-based spectra training data to configure the supervised model to output a second indicator of the one or more biological product types;

receiving, at the first processor, a first Raman-based spectra dataset defining a first biological product sample as scanned by the first scanner;

executing, by the first processor, one or more spectral preprocessing algorithms as specified by the biological ensemble classification model configuration, to reduce a spectral variance of the first Raman-based spectra dataset; and

identifying, with the biological classification ensemble model, a biological product type based on the first Raman-based spectra dataset.

31. The biological analytics method of claim 30 further comprising:

transferring the biological ensemble classification model configuration to a second configurable handheld biological analyzer;

loading, into a second computer memory, the biological classification ensemble model configuration, the biological classification ensemble model configuration comprising the biological classification ensemble model;

receiving, by a second processor of the second configurable handheld biological analyzer, a second Raman-based spectra dataset defining a second biological product sample as scanned by the second scanner; and

identifying, by the second processor implementing the biological classification ensemble model, the biological product type based on the second Raman-based spectra dataset,

wherein the second biological product sample is a new sample of the biological product type.

32. The biological analytics method of claim 30, wherein the spectral variance is an analyzer-to-analyzer spectral variance between the first Raman-based spectra dataset and one or more other Raman-based spectra datasets of one or more corresponding other handheld biological analyzers, each of the one or more other Raman-based spectra datasets representative of the biological product type, and

wherein the one or more spectral preprocessing algorithms are configured to mitigate the analyzer-to-analyzer spectral variance between the first Raman-based spectra dataset and the one or more other Raman-based spectra datasets.

33. The biological analytics method of claim 32, wherein the one or more spectral preprocessing algorithms comprises:

applying a derivative transformation to the first Raman-based spectra dataset to generate a modified Raman-based spectra dataset,

aligning the modified Raman-based spectra dataset across a Raman shift axis, and

normalizing the modified Raman-based spectra dataset across a Raman intensity axis.

34. The biological analytics method of claim 33, wherein the modified Raman-based spectra dataset is centered.

35. The biological analytics method of claim 33, wherein the derivative transformation is applied to consecutive groups of 5 to 15 Raman intensity values across the Raman shift axis.

36. The biological analytics method of claim 34, wherein corresponding derivatives of the consecutive groups of 5 to 15 Raman intensity values are determined across the Raman shift axis.

37. The biological analytics method of any one of claims 30-36, wherein the unsupervised model is configured to detect variability associated with identifying the one or more biological product types.

38. The biological analytics method of claim 37, wherein the variability comprises instrument variability or sample lot-to-lot variability.

39. The biological analytics method of any one of claims 30-38, wherein the biological classification ensemble model identifies the biological product type upon determination that the first indicator passes a first pass-fail based threshold value and that the second indicator passes a second pass-fail based threshold value.

40. The biological analytics method of any one of claims 30-38, wherein the first indicator as output by the unsupervised model is based on whether the one or more biological product types satisfies a threshold value.

41. The biological analytics method of claim 40, wherein the unsupervised model outputs a pass-fail determination based on the threshold value.

42. The biological analytics method of claim 40 or 41, wherein the threshold value is based on one or more of: a reduced Q-residual error, a Hotelling's T-squared value, a Mahalanobis distance value, or specific range values for principal component scores.

43. The biological analytics method of any one of claims 30-42, wherein a first biological product type of the one or more biological product types and a second biological product type of the one or more biological product types have similar Raman-based spectra.

44. The biological analytics method of any one of claim 30-43, wherein the second indicator as output by the supervised model is based on whether the one or more biological product types satisfies a biological product type prediction threshold value.

45. The biological analytics method of claim 44, wherein the supervised model outputs a pass-fail determination based on the biological product type prediction threshold value.

46. The biological analytics method of any one of claims 30-45, wherein the computer memory is configured to load a new biological classification ensemble model, the new biological ensemble classification model comprising an updated unsupervised model and/or an updated supervised model.

47. The biological analytics method of any one of claims 30-46, wherein the biological classification ensemble model configuration is implemented in an extensible markup language (XML) format.

48. The biological analytics method of any one of claims 30-47, wherein the biological product type is of a therapeutic product.

49. The biological analytics method of any one of claims 30-48, wherein the biological product type is identified by the biological classification ensemble model during manufacture of a biological product having the biological product type.

50. The biological analytics method of any one of claims 30-49, wherein the supervised model of the biological classification ensemble model is configured to distinguish the first biological product sample having the biological product type from a different biological product sample having a different biological product type.

51. The biological analytics method of claim 50, wherein the biological product type and the different biological product type each have distinct localized features within a similar Raman spectra range.

52. The biological analytics method of any one of claims 30-51, wherein the biological classification ensemble model is generated by a remote processor being remote to the configurable handheld biological analyzer.

53. The biological analytics method of any one of claims 30-52, wherein the unsupervised model is configured based on: a principal component analysis (PCA), a Euclidean distance or correlation; a neighbor-based algorithm, a K-means algorithm, Quality Threshold (QT) algorithm, a Centroid algorithm, a Ward algorithm, or a Fuzzy C-Means clustering algorithm.

54. The biological analytics method of claim 53, wherein the unsupervised model is a PCA model, and wherein the PCA model comprises a reduced set of principal components.

55. The biological analytics method of any one of claims 30-54, wherein the supervised model is trained using a partial least squares discriminant analysis (PLSDA), a linear discriminant analysis (LDA), a K-nearest neighbor (KNN) algorithm, a soft independent modeling using class analogy (SIMCA), or a logistic regression discriminant analysis (LREGDA) algorithm.

56. The biological analytics method of claim 55, wherein the supervised model is a PLSDA model, and wherein the PLSDA model comprises a reduced set of latent variables.

57. The biological analytics method of any one of claims 30-56, wherein the unsupervised model is configured based on a principal component analysis (PCA) and the supervised model is configured on a partial least squares discriminant analysis (PLSDA).

58. The biological analytics method of any one of claims 30-57, wherein the one or more spectral preprocessing algorithms are executed to modify at least one of: (a) training data as used to train one or both of the supervised model or the unsupervised model; or (b) production data as used to produce an output from one or both of the supervised model or the unsupervised model.

59. A tangible, non-transitory computer-readable medium storing instructions for identification of biological products based on Raman spectroscopy using ensemble artificial intelligence (AI), that when executed by one or more processors of a configurable handheld biological analyzer cause the one or more processors of the configurable handheld biological analyzer to: load, into a first computer memory of a first configurable handheld biological analyzer having a first processor and a first scanner, a biological ensemble classification model configuration, the biological ensemble classification model configuration comprising a biological classification ensemble model comprising an unsupervised model and a supervised model,

wherein the unsupervised model is trained with Raman-based spectra training data to configure the unsupervised model to output a first indicator of one or more biological product types, and

wherein the supervised model is trained with Raman-based spectra training data to configure the supervised model to output a second indicator of the one or more biological product types;

receive, at the first processor, a first Raman-based spectra dataset defining a first biological product sample as scanned by the first scanner;

execute, by the first processor, one or more spectral preprocessing algorithms as specified by the biological ensemble classification model configuration, to reduce a spectral variance of the first Raman-based spectra dataset; and

identify, with the biological classification ensemble model, a biological product type based on the first Raman-based spectra dataset.