WHAT IS CLAIMED IS:

1. A method for use in diagnosing a condition based on a symptom experienced by a subject and based on a first biological sample obtained from the subject, the first biological sample including nucleic acids, the method being executed by a device, the method comprising:

based on the symptom, preselecting a first set of the nucleic acids for analysis;

capturing by the device a first plurality of the nucleic acids of the first set that are present in the first biological sample;

for each of the captured nucleic acids of the first plurality:

quantifying by the device an amount of that captured nucleic acid that is present in the first biological sample;

sequencing by the device that captured nucleic acid; and

based on the sequence of that captured nucleic acid, identifying by the device an origin of that captured nucleic acid; and

outputting by the device an indication of the quantified amount and the identified origin of at least one captured nucleic acid that is present in the first biological sample.

2. The method of claim 1, wherein preselecting the first set of the nucleic acids for analysis comprises receiving by the device a first symptom-specific cartridge comprising a first set of complementary nucleic acids configured to capture the first set of the nucleic acids for analysis.

3. The method of claim 2, further comprising, after the outputting step, removing the first symptom-specific cartridge from the device and receiving by the device a second symptom-specific cartridge comprising a second set of complementary nucleic acids.

4. The method of claim 3, wherein the first set of complementary nucleic acids is different than the second set of complementary nucleic acids.

5. The method of any one of claims 1-4, further comprising outputting by the device an indication of the quantified amount of each of the captured nucleic acids of the first plurality.

6. The method of any one of claims 1-5, wherein:

the capturing comprises separating extracellular nucleic acids in the first biological sample from intracellular nucleic acids in the first biological sample; and

the quantifying and sequencing steps are performed separately on the separated extracellular nucleic acids and on the intracellular nucleic acids.

7. The method of claim 6, further comprising outputting by the device an indication of the quantified amount of at least one of the extracellular nucleic acids and an indication of the quantified amount of at least one of the intracellular nucleic acids.

8. The method of any one of claims 1-7, wherein the identifying by the device the origin of the captured nucleic acid comprises comparing the sequence of that nucleic acid to sequences stored in a library stored in a computer-readable medium of the device.

9. The method of claim 8, wherein the library stores nucleic acid sequences for a human and for a plurality of pathogens.

10. The method of claim 9, wherein the output indicates the relative number of a pathogen per human cell.

11. The method of any one of claims 1-11, further comprising:

receiving by the device a second biological sample obtained from the subject, the second biological sample being different from the first biological sample;

capturing by the device a second plurality of the nucleic acids of the first set that are present in the second biological sample;

for each of the captured nucleic acids of the second plurality:

quantifying by the device an amount of that captured nucleic acid that is present in the second biological sample;

sequencing by the device that captured nucleic acid; and

based on the sequence of that captured nucleic acid, identifying by the device an origin of that captured nucleic acid; and

wherein the outputting by the device further includes an indication of the quantified amount and the identified origin of at least one captured nucleic acid that is present in the second biological sample.

12. The method of any one of claims 1-11, further comprising outputting by the device an indication of at least one potential diagnosis for the subject and an indication of the likelihood of the at least one potential diagnosis based on the quantified amount and the identified origin of at least one captured nucleic acid that is present in the first biological sample.

13. A device for use in diagnosing a condition based on a symptom experienced by a subject and based on a first biological sample obtained from the subject, the first biological sample including nucleic acids, the device comprising:

a first set of complementary nucleic acids configured to capture a first set of the nucleic acids, the first set of the nucleic acids being selected based on the symptom, the first set of complementary nucleic acids capturing a first plurality of the nucleic acids of the first set that are present in the first biological sample;

a nucleic acid quantifier configured to quantify an amount of each of the captured nucleic acids that is present in the first biological sample;

a nucleic acid sequencer configured to sequence each captured nucleic acid that is present in the first biological sample;

a processor coupled to the quantifier and to the sequencer and being suitably programmed to identify an origin of each captured nucleic acid based on the sequence of that captured nucleic acid; and

an output module coupled to the processor, the processor further being suitably programmed to cause the output module to output an indication of the quantified amount and the identified origin of at least one captured nucleic acid that is present in the first biological sample.

14. The device of claim 13, wherein the device comprises a receptacle configured to receive the first set of complementary nucleic acids within a first symptom-specific cartridge.

15. The device of claim 14, wherein the first symptom-specific cartridge is removable from the receptacle and replaceable with a second symptom-specific cartridge comprising a second set of complementary nucleic acids.

16. The device of claim 15, wherein the first set of complementary nucleic acids is different than the second set of complementary nucleic acids.

17. The device of any one of claims 13-16, wherein the processor further is suitably programmed to cause the output module to output an indication of the quantified amount of each of the captured nucleic acids of the first plurality.

18. The device of any one of claims 13-17, further comprising a separator configured to separate extracellular nucleic acids in the first biological sample from intracellular nucleic acids in the first biological sample; and

wherein the nucleic acid quantifier and nucleic acid sequencer separately operate on the separated extracellular nucleic acids and on the intracellular nucleic acids.

19. The device of claim 18, wherein the processor further is suitably programmed to cause the output module to output an indication of the quantified amount of at least one of the extracellular nucleic acids and an indication of the quantified amount of at least one of the intracellular nucleic acids.

20. The device of any one of claims 13-19, further comprising a computer-readable medium coupled to the processor,

wherein the processor further is suitably programmed to identify the origin of the captured nucleic acid based on comparing the sequence of that nucleic acid to sequences stored in a library stored in the computer-readable medium.

21. The device of claim 20, wherein the library stores nucleic acid sequences for a human and for a plurality of pathogens.

22. The device of claim 21, wherein the output indicates the relative number of a pathogen per human cell.

23. The device of any one of claims 13-22,

the first set of complementary nucleic acids further being configured to capture a second plurality of the nucleic acids of the first set that are present in a second biological sample obtained from the subject, the second biological sample being different from the first biological sample;

the nucleic acid quantifier further being configured to quantify an amount of each of the captured nucleic acids that is present in the second biological sample;

the nucleic acid sequencer further being configured to sequence each of the captured nucleic acids that is present in the second biological sample; and

the processor further being suitably programmed to identify an origin of each captured nucleic acid based on the sequence of the captured nucleic acid that is present in the second biological sample; and

the processor further being suitably programmed to cause the output module to output an indication of quantified amount and the identified origin of at least one captured nucleic acid that is present in the second biological sample.

24. The device of any one of claims 13-23, wherein the processor further is suitably programmed to cause the output module to output an indication of at least one potential diagnosis for the subject and an indication of the likelihood of the at least one diagnosis based on the quantified amount and the identified origin of at least one captured nucleic acid that is present in the first biological sample.

25. A database stored in a computer-readable medium, the database storing at least a plurality of symptoms, a nucleic acid sequence associated with each of the symptoms, a potential diagnosis associated with each of the symptoms, a laboratory test or a procedure for each of the symptoms, and an inferred value for each of the symptoms, the inferred value comprising a clinical inference based on a result of said laboratory test for the respective symptom.

26. A method of generating a database stored in a computer-readable medium, the method comprising:

receiving, by a device, a plurality of medical documents, each document describing at least one symptom experienced by a respective patient, a laboratory test or a procedure performed on that patient, and a diagnosis associated with the at least one symptom experienced by that patient, the diagnosis being based on a result of the laboratory test performed on that patient;

by the device, inferring values based on the symptoms, the laboratory tests, and the diagnoses described in the plurality of medical documents, each inferred value comprising a clinical inference based on a result of at least one of the laboratory tests for the respective symptom;

by the device, identifying a nucleic acid test value associated with each of the inferred values; and

by the device, generating and storing in the computer-readable medium a plurality of database entries, each database entry of the plurality comprising a symptom, a laboratory test or a procedure performed on a patient having that symptom, at least one possible diagnosis associated with that symptom, an inferred value for that diagnosis, and a nucleic acid test value for that inferred value.

27. The method of claim 26, wherein the nucleic acid test value comprises an RNA sequence or a DNA sequence.

28. The method of any one of claims 26-27, wherein the nucleic acid test values include one or more specific nucleic acid sequences, one or more groups of nucleic acid sequences, one or more quantities of nucleic acid sequences, one or more patterns of nucleic acid sequences, or one

or more contexts of nucleic acid sequences.

29. The method of claim 28, wherein the one or more contexts of nucleic acid sequences include one or more associations of nucleic acid sequences with chemical modifications, proteins, other intramolecular or extramolecular nucleic acids, or intracellular or extracellular subcompartments.

30. The method of any one of claims 26-29, wherein the plurality of medical documents comprise standard medical codes describing at least some of the symptoms, laboratory tests or procedures, and diagnoses.

31. The method of any one of claims 26-30, wherein the plurality of medical documents further include physical findings, medications, or environmental exposures.

32. A method for performing one or more nucleic acid tests based on one or more symptoms experienced by a patient, the method comprising:

receiving by a device respective identifiers of the one or more symptoms experienced by the patient;

by the device, submitting to a database a query based on the respective identifiers of each of the one or more symptoms, the database comprising a computer-readable medium storing at least a plurality of symptoms, a nucleic acid sequence associated with each of the symptoms, a potential diagnosis associated with each of the symptoms, a laboratory test or a procedure for each of the symptoms, and inferred data for each of the symptoms, the inferred value comprising a clinical inference based on a result of said laboratory test for the respective symptom;

by the device, receiving from the database a response to the query, the response comprising one or more nucleic acid tests based on the nucleic acid sequences respectively associated with the one or more symptoms identified in the query;

by the device, outputting respective representations of the one or more nucleic acid tests; and

receiving, by a receptacle of the device, a cartridge configured to perform at least one of the one or more nucleic acid tests.

33. The method of claim 32, further comprising, by the device, outputting a result of the at least one of the one or more nucleic acid tests, the result comprising a count of RNA or DNA of the subject or of a pathogen in the subject, the RNA or DNA having the nucleic acid sequence associated with at least one of the one or more symptoms identified in the query.

34. The method of any one of claims 32-33, the response to the query comprising a representation of a plurality of nucleic acid tests based on a plurality of nucleic acid sequences respectively associated with the one or more symptoms identified in the query, the cartridge being configured to perform each nucleic acid test of the plurality.

35. The method of any one of claims 32-33, further comprising receiving, by a receptacle of the device, at least one additional cartridge, the at least one additional cartridge being configured to perform at least one other of the nucleic acid tests.

36. A device for performing one or more nucleic acid tests based on one or more symptoms experienced by a patient, the device comprising:

an input module configured to receive respective identifiers of the one or more symptoms experienced by the patient;

a query module configured to submit to a database a query comprising the respective identifiers of each of the one or more symptoms, the database comprising a computer-readable medium storing at least a plurality of symptoms, a nucleic acid sequence associated with each of the symptoms, a potential diagnosis associated with each of the symptoms, a laboratory test or a procedure for each of the symptoms, and inferred data for each of the symptoms, the inferred value comprising a clinical inference based on a result of said laboratory test for the respective symptom;

the query module further being configured to receive from the database a response to the query, the response comprising one or more nucleic acid tests based on the nucleic acid sequences respectively associated with the one or more symptoms identified in the query;

an output module configured to output respective representations of the one or more nucleic acid tests; and

a receptacle configured to receive a cartridge configured to perform at least one of the

one or more nucleic acid tests.

37. The device of claim 36, wherein the output module further is configured to output a result of the at least one of the one or more nucleic acid tests, the result comprising a count of RNA or DNA of the subject or of a pathogen in the subject, the RNA or DNA having the nucleic acid sequence associated with at least one of the one or more symptoms identified in the query.

38. The device of any one of claims 36-37, the response to the query comprising a representation of plurality of nucleic acid tests based on a plurality of nucleic acid sequences respectively associated with the one or more symptoms identified in the query, the cartridge being configured to perform each nucleic acid test of the plurality.

39. The device of any one of claims 36-37, wherein the receptacle of the device further is configured to receive least one additional cartridge, the at least one additional cartridge being configured to perform at least one other of the nucleic acid tests.

40. A method for use in assessing the quality of a biological sample obtained from a subject, the biological sample including nucleic acids, the method being executed by a device, the method comprising:

quantifying by the device an amount of a first subset of the nucleic acids that are present in the biological sample, the first subset of the nucleic acids having an intracellular origin;

quantifying by the device an amount of a second subset of the nucleic acids that are present in the biological sample, the second subset of the nucleic acids having an extracellular origin;

outputting by the device an indication of the amount of the first subset of the nucleic acids; and

outputting by the device an indication of the amount of the second subset of the nucleic acids,

the relative amounts of the first and second subsets of the nucleic acids indicating the quality of the biological sample.

41. The method of claim 40, further comprising outputting by the device an indication of an expected amount of the first subset of the nucleic acids in a normal biological sample and an indication of an expected amount of the second subset of the nucleic acids in a normal biological sample.

42. A device for use in assessing the quality of a biological sample obtained from a subject, the biological sample including nucleic acids, the device comprising:

a first quantification module configured to quantify an amount of a first subset of the nucleic acids that are present in the biological sample, the first subset of the nucleic acids having an intracellular origin;

a second quantification module configured to quantify an amount of a second subset of the nucleic acids that are present in the biological sample, the second subset of the nucleic acids having an extracellular origin;

an output module configured to output an indication of the amount of the first subset of the nucleic acids and to output an indication of the amount of the second subset of the nucleic acids,

the relative amounts of the first and second subsets of the nucleic acids indicating the quality of the biological sample.

43. The device of claim 42, wherein the output module further is configured to output an indication of an expected amount of the first subset of the nucleic acids in a normal biological sample and an indication of an expected amount of the second subset of the nucleic acids in a normal biological sample.

44. The method of any one of claims 32-35, further comprising:

performing by the device the at least one of the one or more nucleic acid tests, the performing comprising:

quantifying by the device an amount of a first subset of the nucleic acids that are present in the biological sample, the first subset of the nucleic acids having a first origin;

quantifying by the device an amount of a second subset of the nucleic acids that are present in the biological sample, the second subset of the nucleic acids having a

second origin; and

determining by the device at least one possible diagnosis based on the amount of the first subset of the nucleic acids and based on the amount of the second subset of the nucleic acids;

outputting by the device an indication of the at least one possible diagnosis;

by the device, receiving an indication of at least one of: a diagnosis made by the caregiver, a result of a laboratory test or a procedure performed on the subject, a symptomatic code, a site of injury, a cellular response, a host-immune response, a contribution of a non-human organism, or an origin of cells or symptoms; and

transmitting by the device to the database the received indication for use in updating the database.

45. The method of claim 44, further comprising:

receiving by the device or by a second device respective identifiers of one or more symptoms experienced by a second patient, wherein the symptoms experienced by the second patient are the same as the symptoms experienced by the first patient;

by the device or by the second device, submitting to the updated database a second query based on the respective identifiers of each of the one or more symptoms;

by the device or by the second device, receiving from the updated database a response to the second query, the response comprising one or more updated nucleic acid tests based on the nucleic acid sequences respectively associated with the one or more symptoms identified in the second query, wherein at least one of the one or more updated nucleic acid tests is different than at least one of the one or more nucleic acid tests;

by the device or by the second device, outputting respective representations of the updated one or more nucleic acid tests; and

receiving, by the receptacle of the device or by a receptacle of the second device, a second cartridge configured to perform at least one of the updated one or more nucleic acid tests.

46. The device of any one of claims 36-39, wherein:

the cartridge comprises a first nucleic acid capture module configured to capture a first subset of the nucleic acids that are present in the biological sample, the first subset of the nucleic

acids having a first origin;

the cartridge further comprises a second nucleic acid capture module configured to capture a second subset of the nucleic acids that are present in the biological sample, the second subset of the nucleic acids having a second origin;

the device further comprises a nucleic acid quantifier configured to quantify a respective amount of each of the first and second subsets of captured nucleic acids;

the device further comprises a diagnosis module configured to determine at least one possible diagnosis based on the amount of the first subset of the nucleic acids and based on the amount of the second subset of the nucleic acids;

the output module is configured to output an indication of the at least one possible diagnosis;

the input module further is configured to receive an indication of at least one of: a diagnosis, a result of a laboratory test or a procedure performed on the subject, a symptomatic code, a site of injury, a cellular response, a host-immune response, a contribution of a non-human organism, or an origin of cells or symptoms; and

the query module further is configured to transmit by the device to the database the received indication for use in updating the database.

47. The device of claim 46, wherein:

the input module further is configured to receive respective identifiers of one or more symptoms experienced by a second patient, wherein the symptoms experienced by the second patient are the same as the symptoms experienced by the first patient;

the query module further is configured to submit to the updated database a second query based on the respective identifiers of each of the one or more symptoms;

the query module further is configured to receive from the updated database a response to the second query, the response comprising one or more updated nucleic acid tests based on the nucleic acid sequences respectively associated with the one or more symptoms identified in the second query, wherein at least one of the one or more updated nucleic acid tests is different than at least one of the one or more nucleic acid tests;

the output module further is configured to output respective representations of the updated one or more nucleic acid tests; and

the receptacle of the device further is configured to receive a second cartridge configured to perform at least one of the updated one or more nucleic acid tests.