

amplifying and detecting the presence and amounts of at least the first genetic element, the second genetic element and the third genetic element.

6. A computer readable medium comprising code executable by a processor, for implementing a method comprising.

entering into a digital computer, at least a plurality of first input values associated with a first genetic element, a plurality of second input values associated with a second genetic element, and a plurality of third input values associated with a third genetic element associated with a plurality of known samples, wherein each known sample includes a first input value in the plurality of first input values, a second input value in the plurality of second input values, and a third input value in the plurality of third input values;

determining a threshold value associated with the third genetic element;

separating the known samples using the threshold value into a first set of known samples and a second set of known samples;

clustering the first set of known samples in a feature space defined by the first genetic element and the second genetic element;

defining a first boundary space using the first set of known samples, wherein the first boundary space differentiates a biological status from other biological statuses; and

defining a second boundary space using the second set of known samples, wherein the second boundary space differentiates the biological status from other biological statuses.

7. A digital computer comprising the computer readable medium of claim 76, and a processor coupled to the computer readable medium.

8. A system comprising a measuring module for determining input values associated with genetic elements in samples coupled to the digital computer of claim 7.

9. A method for using an analytical model created according to the method of any of claims 1 to 5, wherein the method for using the analytical model comprises:

entering a first input value, second input value, and third input value associated with an unknown sample into the digital computer or other digital computer, wherein the first input value, the second input value and the third input value is associated with the first, second, and third genetic elements in the unknown sample; and

subjecting the samples to conditions that will expose nucleic acids in the samples; and

amplifying and detecting the presence and amounts of at least the first genetic element, the second genetic element and the third genetic element.

17. A computer readable medium comprising code executable by a processor, for implementing a method comprising:

entering, into a digital computer, at least a plurality of first input values associated with a first genetic element, a plurality of second input values associated with a second genetic element, and a plurality of third input values associated with a third genetic element;

creating one or more intermediate values using at least the plurality of first input values and at least the second input values associated with a second genetic element using the digital computer; and

creating a boundary space for the biological status using the one or more intermediate values and the plurality of third input values using the digital computer, wherein the boundary space differentiates the biological status from other biological statuses.

18. A digital computer comprising the computer readable medium of claim ~~11~~17, and a processor coupled to the computer readable medium.

19. A system comprising a measuring module for determining input values associated with genetic elements in samples coupled to the digital computer of claim 18.

20. A method for using an analytical model created according to the method of any of claims 11 to 16, wherein the method for using the analytical model comprises:

entering a first input value, second input value, and third input value associated with an unknown sample into the digital computer or other digital computer, wherein the first input value, the second input value and the third input value is associated with the first, second, and third genetic elements in the unknown sample; and

classifying the unknown sample as being associated with the biological status using the boundary space.

21. A method for determining the presence of methicillin-resistant *Staphylococcus aureus* (MRSA) in a sample, the method comprising:

35. The system of claim 33 wherein the first boundary space and the second boundary space are both elliptical boundary spaces.

36. The system of claim 35 wherein the first boundary space and the second boundary space have both undergone translations and angular displacement around an origin.

37. The system of any of claims 33 to 36 wherein the first boundary space and the second boundary space are both defined as a function of the measured amounts of mecA and femA.

38. The system of any of claims 33 to 37 wherein a cost function is used to find the optimal parameters for the first and second boundary spaces.

39. The system of claim 38 wherein the cost function is defined by the formula:

$$\text{cost} = c_1 * \text{FN\#} + c_2 * \text{FP\#}.$$

40. The system of any of claims 33 to 39 wherein the first boundary space and the second boundary space are functions defined using a neural network.

41. The system of any of claims 33 to 39 wherein the first boundary space and the second boundary space are functions defined using a genetic algorithm.

42. The system of any of claims 33 to 41 wherein the presence and amounts of at least mecA, orfX, and the Staphylococcus aureus-specific target gene sequence in the sample are detected by real-time PCR.

43. The ~~method~~system of claim 42 wherein the amounts of at least mecA, orfX, and the Staphylococcus aureus-specific target gene sequence are measured in cycles.

44. The ~~method~~system of claim 43 wherein the threshold value is approximately 45 cycles.

45. A computer-readable medium comprising:
code for a call algorithm, wherein the call algorithm uses as inputs at least the detected and measured amounts of mecA, orfX, and a Staphylococcus aureus-specific target

executed against the known samples, wherein the model creates an intermediate value from at least the Staphylococcus aureus-specific target gene sequence and mecA, wherein the call algorithm further uses a boundary space to determine the presence of MRSA, wherein the boundary space is defined using the intermediate value and SCCmec.

67. The method of claim 12 or 46, wherein SCCmec is at an orfX junction.

68. The system of claim 55, wherein SCCmec is at an orfX junction.

69. The computer readable medium of claim 64, wherein SCCmec is at an orfX junction.

70. The method of claim 12 or 46, wherein a detection of an SCCmec/orfX junction indicates the presence of SCCmec.

71. The system of claim 55, wherein a detection of an SCCmec/orfX junction indicates the presence of SCCmec.

72. The computer readable medium of claim 64, wherein a detection of an SCCmec/orfX junction indicates the presence of SCCmec.