

## WHAT IS CLAIMED IS

1. 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, wherein the first genetic element comprises *mecA*, the second genetic element comprises a *Staphylococcus aureus*-specific target gene sequence and the third genetic element comprises *OrfX*, and wherein the biological status comprises an MRSA status.
2. The method of claim 1 wherein the second genetic element comprises *femA*.
3. The method of claim 1 or 2 wherein the first boundary space and the second boundary space are defined by first and second ellipses, respectively.
4. The method of any of claims 1 to 3 wherein the first, second and third values are Ct values.
5. The method of any of claims 1 to 4 further comprising, prior to entering:  
subjecting the known samples to conditions that will expose nucleic acids in the known 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.

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,

wherein the first genetic element comprises *mecA*, the second genetic element comprises a *Staphylococcus aureus*-specific target gene sequence and the third genetic element comprises *OrfX*, and wherein the biological status comprises an MRSA status.

7. A digital computer comprising the computer readable medium of claim 6, 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

classifying the unknown sample as being associated with the biological status using the first boundary space or the second boundary space using the digital computer or other digital computer.

10. The method of claim 9 wherein the biological status comprises a MRSA status.

11. A method of creating an analytical model, which differentiates a biological status from other biological statuses, the 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,  
wherein the first genetic element comprises *mecA*, the second genetic element comprises a *Staphylococcus aureus*-specific target gene sequence and the third genetic element comprises *SCCmec*, and wherein the biological status comprises an MRSA status.

12. The method of claim 11 wherein the second genetic element comprises *femA*.

13. The method of claim 11 or 12 wherein the boundary space is defined by an ellipse.

14. The method of claim 13 wherein a cost function is used to optimize the ellipse.

15. The method of any of claims 11 to 14 wherein the first, second and third values are Ct values.

16. The method of any of claims 11 to 15 further comprising, prior to entering:

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,

wherein the first genetic element comprises *mecA*, the second genetic element comprises a *Staphylococcus aureus*-specific target gene sequence and the third genetic element comprises *SCCmec*, and wherein the biological status comprises an MRSA status.

18. A digital computer comprising the computer readable medium of claim 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, or 13 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:

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 11 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 11 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.

WHAT IS CLAIMED IS:

1. 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.
2. The method of claim 1 wherein the first genetic element comprises *mecA*, the second genetic element comprises *femA*, and the third genetic element comprises *OrfX*, and wherein the biological status comprises an MRSA status.
3. The method of claim 1 or 2 wherein the first boundary space and the second boundary space are defined by first and second ellipses, respectively.
4. The method of any of claims 1 to 3 wherein the first, second and third values are Ct values.
5. The method of any of claims 1 to 4 further comprising, prior to entering:  
subjecting the known samples to conditions that will expose nucleic acids in the known 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.

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 6, 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

classifying the unknown sample as being associated with the biological status using the first boundary space or the second boundary space using the digital computer or other digital computer.

10. The method of claim 9 wherein the biological status comprises a MRSA status.

11. A method of creating an analytical model, which differentiates a biological status from other biological statuses, the 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.

12. The method of claim 11 wherein the first genetic element comprises *mecA*, the second genetic element comprises *femA*, and the third genetic element comprises *SCCmec*, and wherein the biological status comprises an MRSA status.

13. The method of claim 11 or 12 wherein the boundary space is defined by an ellipse.

14. The method of claim 13 wherein a cost function is used to optimize the ellipse.

15. The method of any of claims 11 to 14 wherein the first, second and third values are Ct values.

16. The method of any of claims 11 to 15 further comprising, prior to entering:

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 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:

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.