

CLAIMS

1. An electronic system for determining the sequence of a nucleic acid comprising at least two bound primers bound to the same strand of the nucleic acid sequence, where each of the bound primers comprises a labeled nucleotide base, and wherein the system comprises a processor configured to perform a method comprising:

obtaining signal data corresponding to at least one labeled nucleotide base incorporated at each of the at least two bound primers;

determining from said signal data the identity of the nucleotide bases; and
allocating said identity of the nucleotide bases to an extension read.

2. The system of claim 1, further comprising a signal processor configured to process the signal data.

3. The system of claim 1, wherein the processor is configured to perform a method of determining the identity of the nucleotide bases by one or more of signal deconvolution, signal refinement and signal selection.

4. The system of claim 1, wherein the processor is configured to perform a method of obtaining signal data by obtaining one or more images.

5. The system of claim 4, wherein the processor is configured to perform a method of obtaining signal data by obtaining color signal data corresponding to a plurality of nucleotide analogues incorporated at the primers.

6. The system of claim 5, wherein each color signal corresponds to a different nucleotide analogue or combination of nucleotide analogues.

7. The system of claim 1, wherein the processor is configured to perform a method of determining the identity of the nucleotide bases by analyzing a signal intensity profile corresponding to unique labels detected at each primer.

8. The system of claim 1, wherein the processor is configured to perform a method of allocating the identity of the nucleotide bases by performing a preliminary base call followed by a final base call for each of the labeled nucleotide bases.

9. The system of claim 8, wherein the processor is configured to perform the final base call by comparing the preliminary base call with a reference genome.

10. An electronic system configured to hold a flow cell comprising a support having a plurality of bound polynucleotides, wherein the electronic system comprises a processor configured to perform a method comprising:

activating a first fluidic component to hybridize a plurality of first and second primers to the plurality of bound polynucleotides, wherein at least a first and second primer hybridize to the same strand of each polynucleotide;

activating a second fluidic component to extend the first and second primers hybridized to the same strand of each polynucleotide with a labeled nucleotide base that generates a signal;

obtaining signal data corresponding to at least one nucleotide base incorporated at each of the extended first and second primers;

determining from the signal data the identity of the nucleotide bases; and allocating the identity of the nucleotide bases to an extension read of the first and second primers.

11. The system of claim 10, wherein the processor is configured to perform a method of obtaining signal data by obtaining one or more images.

12. The system of claim 10, wherein the processor is configured to perform a method of obtaining signal data by obtaining color signal data corresponding to a plurality of nucleotide analogues incorporated at the primers.

13. The system of claim 12, wherein each color signal corresponds to a different nucleotide analogue or combination of nucleotide analogues.

14. The system of claim 10, wherein the processor is configured to perform a method of determining the identity of the nucleotide bases by one or more of signal deconvolution, signal refinement and signal selection.

15. The system of claim 10, wherein the processor is configured to perform a method of determining the identity of the nucleotide bases by analyzing a signal intensity profile corresponding to unique labels detected at each primer.

16. The system of claim 10, wherein the plurality of first and second primers comprise blocked and unblocked primers to chemically differentiate between each extension read of the first and second primers.

17. The system of claim 10, further comprising using bioinformatics information to allocate the nucleotide bases to each extension read.

18. The system of claim 10, wherein the processor is configured to perform a method of allocating the identity of the nucleotide bases by performing a preliminary base call followed by a final base call for each of the labeled nucleotide bases.

19. The system of claim 18, wherein the processor is configured to perform the final base call by comparing the preliminary base call data with a reference genome.

20. An electronic system for determining the sequence of a nucleic acid comprising at least two bound primers bound to the same strand of the nucleic acid sequence, where each of the bound primers comprises a labeled nucleotide base, and wherein the system comprises:

a flow cell comprising a nucleic acid bound by two primers, wherein a first primer comprises a first labeled nucleotide base and the second primer comprises a second labeled nucleotide base;

an image capture system that captures images of the first and second labeled nucleotide bases on the bound primers; and

a signal processor that obtains signal data from the image capture system corresponding to the first and second labeled nucleotide bases and identifies the labeled nucleotide bases by calculating an intensity histogram of the signal data from the first and second labeled nucleotide bases.

21. The system of claim 20, wherein the signal processor is configured to perform a method of determining the identity of the nucleotide bases by one or more of signal deconvolution, signal refinement and signal selection.

22. The system of claim 20, wherein the signal processor is configured to perform a method of obtaining signal data by obtaining one or more images.

23. The system of claim 22, wherein the signal processor is configured to perform a method of obtaining signal data by obtaining color signal data corresponding to a plurality of nucleotide analogues incorporated at the primers.

24. The system of claim 23, wherein each color signal corresponds to a different nucleotide analogue or combination of nucleotide analogues.

25. The system of claim 20, wherein the signal processor is configured to perform a method of determining the identity of the nucleotide bases by analyzing a signal intensity profile corresponding to unique labels detected at each primer.

26. The system of claim 20, wherein the signal processor is configured to perform a method of allocating the identity of the nucleotide bases by performing a preliminary base call followed by a final base call for each of the labeled nucleotide bases.

27. The system of claim 26, wherein the signal processor is configured to perform the final base call by comparing the preliminary base call with a reference genome.

28. An electronic system configured to hold a flow cell comprising a support having a plurality of bound polynucleotides, wherein the electronic system comprises:

- a flow cell comprising a plurality of bound polynucleotides;

- fluidic components in fluid connection to the flow cell through one or more fluidic lines; an image capture system; and

- a signal processor configured to perform a method comprising:

- activating a first fluidic component to hybridize a plurality of first and second primers to the plurality of bound polynucleotides, wherein at least a first and second primer hybridize to the same strand of each polynucleotide;

- activating a second fluidic component to extend the first and second primers hybridized to the same strand of each polynucleotide with a labeled nucleotide base that generates a signal;

- obtaining signal data from the image capture system corresponding to at least one nucleotide base incorporated at each of the extended first and second primers;

- determining from the signal data the identity of the nucleotide bases; and allocating the identity of the nucleotide bases to an extension read of the first and second primers.

29. The system of claim 28, wherein the signal processor is configured to perform a method of obtaining signal data by obtaining one or more images from the image capture system.

30. The system of claim 28, wherein the signal processor is configured to perform a method of obtaining signal data by obtaining color signal data corresponding to a plurality of nucleotide analogues incorporated at the primers.

31. The system of claim 30, wherein each color signal corresponds to a different nucleotide analogue or combination of nucleotide analogues.

32. The system of claim 28, wherein the signal processor is configured to perform a method of determining the identity of the nucleotide bases by one or more of signal deconvolution, signal refinement and signal selection.

33. The system of claim 28, wherein the signal processor is configured to perform a method of determining the identity of the nucleotide bases by analyzing a signal intensity profile corresponding to unique labels detected at each primer.

34. The system of claim 28, wherein the plurality of first and second primers comprise blocked and unblocked primers to chemically differentiate between each extension read of the first and second primers.

35. The system of claim 28, further comprising using bioinformatics information to allocate the nucleotide bases to each extension read.

36. The system of claim 28, wherein the signal processor is configured to perform a method of allocating the identity of the nucleotide bases by performing a preliminary base call followed by a final base call for each of the labeled nucleotide bases.

37. The system of claim 36, wherein the signal_processor is configured to perform the final base call by comparing the preliminary base call data with a reference genome.

38. A kit for determining the sequence of a nucleic acid comprising at least two bound primers bound to the same strand of the nucleic acid sequence, where each of the bound primers comprises a labeled nucleotide base.