WHAT IS CLAIMED IS:

1. A method of nucleic acid detection, comprising steps of:

(a) contacting a primed template nucleic acid with a polymerase and a first mixture of nucleotides under conditions for stabilizing a ternary complex at a nucleotide position in the template, wherein the first mixture comprises a nucleotide cognate of a first base type and a nucleotide cognate of a second base type;

(b) contacting the primed template nucleic acid with a polymerase and a second mixture of nucleotides under conditions for stabilizing a ternary complex at the nucleotide position in the template, wherein the second mixture comprises a nucleotide cognate of the first base type and a nucleotide cognate of a third base type;

(c) examining products of steps (a) and (b) for signals produced by a ternary complex that comprises the primed template nucleic acid, a polymerase and a next correct nucleotide, wherein signals acquired for the product of step (a) are ambiguous for the first and second base type, and wherein signals acquired for the product of step (b) are ambiguous for the first and third base type;

(d) disambiguating signals acquired in step (c) to identify a base type that binds the next correct nucleotide.

2. The method of claim 1, wherein the primed template nucleic acid is not in contact with a nucleotide cognate of a fourth base type during step (c).

3. The method of claim 2, wherein (i) the first base type is correlated with presence of signals for the product of step (a) and presence of signals for the product of step (b),

(ii) the second base type is correlated with presence of signals for the product of step (a) and absence of signals for the product of step (b), and

(iii) the third base type is correlated with absence of signals for the product of step (a) and presence of signals for the product of step (b).

4. The method of claim 3, wherein the first mixture lacks nucleotide cognates of the third and fourth base types, and wherein the second mixture lacks nucleotide cognates of the second and fourth base types.

5. The method of claim 4, wherein (iv) the fourth base type is correlated with absence of signals for the product of step (a) and absence of signals for the product of step (b).

6. The method of claim 1, wherein the signals acquired in step (c) are produced by exogenous labels attached to polymerases.

7. The method of claim 1, further comprising (e) adding a reversibly terminated, next correct nucleotide to the primer of the primed template nucleic acid after step (c), thereby producing an extended, reversibly terminated primer;

further comprising repeating steps (a) through (c) for the primed template nucleic acid that comprises the extended, reversibly terminated primer;

further comprising (f) removing the reversible terminator moiety from the extended, reversibly terminated primer after steps (a) through (c) are repeated.

8. The method of claim 7, wherein step (e) is carried out prior to step (d).

9. The method of claim 1, wherein the steps are carried out for a plurality of primed template nucleic acids having different sequences.

10. The method of claim 1, further comprising

(i) contacting the primed template nucleic acid with a polymerase and a third mixture of nucleotides under conditions for stabilizing a ternary complex at the nucleotide position in the template, wherein the third mixture comprises a nucleotide cognate of the second base type and a nucleotide cognate of a fourth base type;

(ii) contacting the primed template nucleic acid with a polymerase and a fourth mixture of nucleotides under conditions for stabilizing a ternary complex at the nucleotide position in the template, wherein the fourth mixture comprises a nucleotide cognate of the third base type and a nucleotide cognate of the fourth base type; and

(iii) examining products of steps (i) and (ii) for signals produced by a ternary complex that comprises the primed template nucleic acid, a polymerase and a next correct nucleotide, wherein signals acquired for the product of step (i) are ambiguous for the second and fourth base type, and wherein signals acquired for the product of step (ii) are ambiguous for the third and fourth base type.

11. A method of nucleic acid detection, comprising:

(a) sequentially contacting a primed template nucleic acid with first and second mixtures under ternary complex stabilizing conditions, wherein each of the mixtures comprises a polymerase and nucleotide cognates for at least two of four different base types in the primed template nucleic acid, wherein the mixtures differ by at least one type of nucleotide cognate;

(b) examining the first and second mixtures, or products thereof, separately to detect ternary complexes; and

(c) identifying the next correct nucleotide for the primed template nucleic acid molecule, wherein the next correct nucleotide is identified as a cognate of one of the four different base types if ternary complex is detected in the two mixtures.

12. The method of claim 11, wherein the first mixture comprises a labeled nucleotide cognate of a first base type and a labeled nucleotide cognate of a second base type, and wherein the first mixture comprises a non-labeled nucleotide cognate of a third or fourth base types.

13. The method of claim 12, wherein the second mixture comprises a labeled nucleotide cognate of the first base type and a labeled nucleotide cognate of the third base type, wherein the second mixture comprises a non-labeled nucleotide cognate of the second or fourth base types.

14. A method of determining a nucleic acid sequence, comprising:

(a) contacting a primed template nucleic acid with a series of mixtures for forming ternary complexes, wherein each of the mixtures comprises a polymerase and nucleotide cognates for at least two different base types suspected of being present at the next template position of the template nucleic acid;

(b) monitoring the next template position for ternary complexes formed by the series of mixtures, wherein a signal state indicates presence or absence of ternary complex formed at the next template position by each individual mixture, thereby determining a series of signal states that encodes a base call for the next template position; and

(c) decoding the series of signal states to distinguish a correct base call for the next template position from an error in the base call.

15. The method of claim 14, wherein the series of signal states comprises an error correcting code.

16. The method of claim 15, wherein the series of mixtures consists of three mixtures and the series of signal states is represented by three digits, each digit representing a signal state obtained from a mixture.

17 The method of claim 16, wherein each of the signal states is represented by a binary digit, and wherein the error correcting code comprises a repetition code;

further comprising correcting the invalid base call by a majority vote between the three digits.

18. The method of claim 14, wherein the series of mixtures consists of four mixtures and the series of signal states is represented by four digits, each digit representing a signal state obtained from a mixture.

19. The method of claim 18, wherein each of the signal states is represented by a ternary digit, wherein the error correcting code comprises a Hamming code, and wherein the Hamming distance between valid base calls is three;

further comprising correcting the invalid base call to a valid base call having a code with the closest Hamming distance to the code for the invalid base call.

20. The method of claim 14, wherein the series of mixtures consists of five mixtures and the series of signal states is represented by five digits, each digit representing a signal state obtained from a mixture.

21. The method of claim 20, wherein each of the signal states is represented by a binary digit, wherein the error correcting code comprises a Hamming code, and wherein each valid base call differs from other valid base calls by three digits;

further comprising correcting the invalid base call to a valid base call having a code with the closest Hamming distance to the code for the invalid base call.

22. The method of claim 14, wherein the decoding of the series of signal states identifies the base call as being an invalid base call;

further comprising correcting the invalid base call to make a valid base call for the next template position.

23. The method of claim 14, wherein the series of signal states comprises a repetition code, Hamming code, linear code or parity code.

24. The method of claim 14, wherein each of the signal states is represented by a binary digit;

wherein the binary digit comprises (i) symbols for presence and absence of a signal; (ii) symbols for signals emitted at two different wavelengths; (iii) symbols for signals having two different intensities; or (iv) symbols for signals resulting from excitation at two different wavelengths.

25. The method of claim 14, wherein each of the signal states is represented by a ternary digit;

wherein the ternary digit comprises (i) symbols for signals emitted at three different wavelengths; (ii) symbols for signals having three different intensities; or (iii) symbols for signals resulting from excitation at three different wavelengths.

26. The method of claim 14, wherein each of the mixtures comprises nucleotide cognates for at least two and no more than three of four different base types suspected of being in the primed template nucleic acid.

27. The method of claim 14, wherein the mixtures differ by the presence or absence of at least one type of nucleotide cognate.

28. The method of claim 14, wherein the mixtures differ by the number or type of label attached to at least one type of nucleotide cognate.

29. The method of claim 14, further comprising:

(d) adding a next correct nucleotide to the primer of the primed template nucleic acid after step (b), thereby producing an extended primer;

further comprising repeating steps (a) through (d) for the primed template nucleic acid that comprises the extended primer.

30. The method of claim 29, wherein the next correct nucleotide that is added to the primer is a reversibly terminated nucleotide;

further comprising repeating steps (a) through (d) for the primed template nucleic acid that comprises the extended, reversibly terminated primer;

further comprising (e) removing the reversible terminator moiety from the extended, reversibly terminated primer after steps (a) through (d) are repeated.