CLAIMS

1. A computer-implemented method, including:

segmenting a population of clusters of nucleotide sequences into a plurality of subpopulations of clusters of nucleotide sequences based on one or more prior bases called at one or more prior sequencing cycles of a sequencing run;

generating, for each subpopulation of clusters of nucleotide sequences in the plurality of subpopulations of clusters of nucleotide sequences, a mixture of four distributions based on intensity profiles of the clusters of nucleotide sequences within each subpopulation of clusters of nucleotide sequences, wherein the four distributions correspond to four bases adenine (A), cytosine (C), guanine (G), and thymine (T); and

at a current sequencing cycle of the sequencing run:

applying, for each subpopulation of clusters of nucleotide sequences in the plurality of subpopulations of clusters of nucleotide sequences, the mixture of four distributions to current sequenced data of each subpopulation of clusters of nucleotide sequences in the plurality of subpopulations of clusters of nucleotide sequences, wherein the current sequenced data is generated at the current sequencing cycle; and

base calling clusters of nucleotide sequences in a particular subpopulation of clusters of nucleotide sequences using a corresponding mixture of four distributions.

2. The computer-implemented method of claim 1, further including resegmenting the population of clusters of nucleotide sequences into the plurality of subpopulations at different intervals in the sequencing run.

3. The computer-implemented method of claim 2, wherein the different intervals correspond to successive sequencing cycles in the sequencing run.

4. The computer-implemented method of any one of claims 1-3, wherein the one or more prior sequencing cycles contiguously precede the current sequencing cycle, and therefore the one or more prior bases called are contiguously preceding base calls.

5. The computer-implemented method of any one of claims 1-4, wherein the one or more prior sequencing cycles non-contiguously precede the current sequencing cycle, and therefore the one or more prior bases called are non-contiguously preceding base calls.

6. The computer-implemented method of any one of claims 1-5, further including segmenting the population of clusters of nucleotide sequences into four subpopulations of clusters of nucleotide sequences based on a prior base called at a prior sequencing cycle of the sequencing run,

wherein the four subpopulations correspond to

(1) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had an A base call at the prior sequencing cycle,

(2) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had a C base call at the prior sequencing cycle,

(3) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had a G base call at the prior sequencing cycle, and

(4) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had a T base call at the prior sequencing cycle.

7. The computer-implemented method of any one of claims 1-6, further including segmenting the population of clusters of nucleotide sequences into 4^k subpopulations of clusters of nucleotide sequences based on k prior bases called at k prior sequencing cycles of the sequencing run.

8. The computer-implemented method of claim 7, further including segmenting the population of clusters of nucleotide sequences into sixteen subpopulations of clusters of nucleotide sequences based on two prior bases called at two prior sequencing cycles of the sequencing run, and

wherein the sixteen subpopulations correspond to

(1) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had AA base calls at the two prior sequencing cycles,

(2) those clusters of nucleotide sequences in the population of clusters of nucleotide

sequences that had AC base calls at the two prior sequencing cycles,

(3) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had AG base calls at the two prior sequencing cycles,

(4) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had AT base calls at the two prior sequencing cycles,

(5) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had CA base calls at the two prior sequencing cycles,

(6) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had CC base calls at the two prior sequencing cycles,

(7) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had CG base calls at the two prior sequencing cycles,

(8) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had CT base calls at the two prior sequencing cycles,

(9) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had GA base calls at the two prior sequencing cycles,

(10) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had GC base calls at the two prior sequencing cycles,

(11) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had GG base calls at the two prior sequencing cycles,

(12) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had GT base calls at the two prior sequencing cycles,

(13) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had TA base calls at the two prior sequencing cycles,

(14) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had TC base calls at the two prior sequencing cycles,

(15) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had TG base calls at the two prior sequencing cycles, and

(16) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had TT base calls at the two prior sequencing cycles.

9. The computer-implemented method of any one of claims 1-8, further including segmenting the population of clusters of nucleotide sequences into sixty-four subpopulations of clusters of nucleotide sequences based on three prior bases called at three prior sequencing cycles of the sequencing run, and

wherein the sixty-four subpopulations correspond to

(1) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had AAA base calls at the three prior sequencing cycles,

(2) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had AAC base calls at the three prior sequencing cycles,

(3) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had AAG base calls at the three prior sequencing cycles,

(4) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had AAT base calls at the three prior sequencing cycles,

(5) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had ACA base calls at the three prior sequencing cycles,

(6) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had ACC base calls at the three prior sequencing cycles,

(7) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had ACG base calls at the three prior sequencing cycles,

(8) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had ACT base calls at the three prior sequencing cycles,

(9) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had AGA base calls at the three prior sequencing cycles,

(10) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had AGC base calls at the three prior sequencing cycles,

(11) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had AGG base calls at the three prior sequencing cycles,

(12) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had AGT base calls at the three prior sequencing cycles,

(13) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had ATA base calls at the three prior sequencing cycles,

(14) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had ATC base calls at the three prior sequencing cycles,

(15) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had ATG base calls at the three prior sequencing cycles,

(16) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had ATT base calls at the three prior sequencing cycles,

(17) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had CAA base calls at the three prior sequencing cycles,

(18) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had CAC base calls at the three prior sequencing cycles,

(19) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had CAG base calls at the three prior sequencing cycles,

(20) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had CAT base calls at the three prior sequencing cycles,

(21) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had CCA base calls at the three prior sequencing cycles,

(22) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had CCC base calls at the three prior sequencing cycles,

(23) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had CCG base calls at the three prior sequencing cycles,

(24) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had CCT base calls at the three prior sequencing cycles,

(25) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had CGA base calls at the three prior sequencing cycles,

(26) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had CGC base calls at the three prior sequencing cycles,

(27) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had CGG base calls at the three prior sequencing cycles,

(28) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had CGT base calls at the three prior sequencing cycles,

(29) those clusters of nucleotide sequences in the population of clusters of nucleotide

sequences that had CTA base calls at the three prior sequencing cycles,

(30) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had CTC base calls at the three prior sequencing cycles,

(31) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had CTG base calls at the three prior sequencing cycles,

(32) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had CTT base calls at the three prior sequencing cycles,

(33) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had GAA base calls at the three prior sequencing cycles,

(34) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had GAC base calls at the three prior sequencing cycles,

(35) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had GAG base calls at the three prior sequencing cycles,

(36) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had GAT base calls at the three prior sequencing cycles,

(37) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had GCA base calls at the three prior sequencing cycles,

(38) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had GCC base calls at the three prior sequencing cycles,

(39) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had GCG base calls at the three prior sequencing cycles,

(40) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had GCT base calls at the three prior sequencing cycles,

(41) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had GGA base calls at the three prior sequencing cycles,

(42) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had GGC base calls at the three prior sequencing cycles,

(43) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had GGG base calls at the three prior sequencing cycles,

(44) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had GGT base calls at the three prior sequencing cycles,

(45) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had GTA base calls at the three prior sequencing cycles,

(46) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had GTC base calls at the three prior sequencing cycles,

(47) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had GTG base calls at the three prior sequencing cycles,

(48) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had GTT base calls at the three prior sequencing cycles,

(49) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had TAA base calls at the three prior sequencing cycles,

(50) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had TAC base calls at the three prior sequencing cycles,

(51) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had TAG base calls at the three prior sequencing cycles,

(52) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had TAT base calls at the three prior sequencing cycles,

(53) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had TCA base calls at the three prior sequencing cycles,

(54) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had TCC base calls at the three prior sequencing cycles,

(55) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had TCG base calls at the three prior sequencing cycles,

(56) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had TCT base calls at the three prior sequencing cycles,

(57) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had TGA base calls at the three prior sequencing cycles,

(58) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had TGC base calls at the three prior sequencing cycles,

(59) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had TGG base calls at the three prior sequencing cycles,

(60) those clusters of nucleotide sequences in the population of clusters of nucleotide

sequences that had TGT base calls at the three prior sequencing cycles,

(61) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had TTA base calls at the three prior sequencing cycles,

(62) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had TTC base calls at the three prior sequencing cycles,

(63) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had TTG base calls at the three prior sequencing cycles, and

(64) those clusters of nucleotide sequences in the population of clusters of nucleotide sequences that had TTT base calls at the three prior sequencing cycles.

10. A non-transitory computer readable storage medium comprising instructions that, when executed by at least one processor, cause a system to:

segment a population of clusters of nucleotide sequences into a plurality of subpopulations of clusters of nucleotide sequences based on one or more prior bases called at one or more prior sequencing cycles of a sequencing run;

generate, for each subpopulation of clusters of nucleotide sequences in the plurality of subpopulations of clusters of nucleotide sequences, a mixture of four distributions based on intensity profiles of the clusters of nucleotide sequences within each subpopulation of clusters of nucleotide sequences, wherein the four distributions correspond to four bases adenine (A), cytosine (C), guanine (G), and thymine (T); and

at a current sequencing cycle of the sequencing run:

apply, for each subpopulation of clusters of nucleotide sequences in the plurality of subpopulations of clusters of nucleotide sequences, the mixture of four distributions to current sequenced data of each subpopulation of clusters of nucleotide sequences in the plurality of subpopulations of clusters of nucleotide sequences, wherein the current sequenced data is generated at the current sequencing cycle; and

base call clusters of nucleotide sequences in a particular subpopulation of clusters of nucleotide sequences using a corresponding mixture of four distributions.

11. The non-transitory computer readable storage medium of claim 10, further comprising instructions that, when executed by the at least one processor, cause the system to segment the population of clusters of nucleotide sequences into the plurality of subpopulations based on one or more right and left flanking bases called at one or more right and left flanking sequencing cycles of the sequencing run.

12. The non-transitory computer readable storage medium of claim 11, further comprising instructions that, when executed by the at least one processor, cause the system to segment the population of clusters of nucleotide sequences into $4^{(r+l)}$ subpopulations of clusters of nucleotide sequences, where r is a number of succeeding bases called at r succeeding sequencing cycles of the sequencing run, and l is a number of prior bases called at l prior sequencing cycles of the sequencing run.

13. The non-transitory computer readable storage medium of any one of claims 10-12, further comprising instructions that, when executed by the at least one processor, cause the system to segment the population of clusters of nucleotide sequences into the plurality of subpopulations based on different signal-to-noise ratio profiles detected in sequenced data of the population of clusters of nucleotide sequences.

14. The non-transitory computer readable storage medium of claim 13, further comprising instructions that, when executed by the at least one processor, cause the system to segment the population of clusters of nucleotide sequences into p subpopulations of clusters of nucleotide sequences, where p is a number of the different signal-to-noise ratio profiles.

15. The non-transitory computer readable storage medium of any one of claims 10-14, further comprising instructions that, when executed by the at least one processor, cause the system to segment the population of clusters of nucleotide sequences into the plurality of subpopulations based on different library types from which the population of clusters of nucleotide sequences is sourced.

16. The non-transitory computer readable storage medium of claim 15, further comprising instructions that, when executed by the at least one processor, cause the system to segment the population of clusters of nucleotide sequences into the plurality of subpopulations based on different insert lengths detected for the different library types.

17. A system comprising:

at least one processor; and

at least a non-transitory computer readable storage medium comprising instructions that, when executed by the at least one processor, cause the system to:

segment a population of clusters of nucleotide sequences into a plurality of subpopulations of clusters of nucleotide sequences based on one or more prior bases called at one or more prior sequencing cycles of a sequencing run;

generate, for each subpopulation of clusters of nucleotide sequences in the plurality of subpopulations of clusters of nucleotide sequences, a mixture of four distributions based on intensity profiles of the clusters of nucleotide sequences within each subpopulation of clusters of nucleotide sequences, wherein the four distributions correspond to four bases adenine (A), cytosine (C), guanine (G), and thymine (T); and

at a current sequencing cycle of the sequencing run:

apply, for each subpopulation of clusters of nucleotide sequences in the plurality of subpopulations of clusters of nucleotide sequences, the mixture of four distributions to current sequenced data of each subpopulation of clusters of nucleotide sequences in the plurality of subpopulations of clusters of nucleotide sequences, wherein the current sequenced data is generated at the current sequencing cycle; and

base call clusters of nucleotide sequences in a particular subpopulation of clusters of nucleotide sequences using a corresponding mixture of four distributions.

18. The system of claim 17, further comprising instructions that, when executed by the at least one processor, cause the system to segment the population of clusters of nucleotide sequences into the plurality of subpopulations based on different values of variation correction coefficients determined to correct variations in sequenced data of the population of clusters of nucleotide sequences.

19. The system of claim 17 or 18, further comprising instructions that, when executed by the at least one processor, cause the system to segment the population of clusters of nucleotide sequences into the plurality of subpopulations based on different spatial configurations of the population of clusters of nucleotide sequences on a biosensor.

20. The system of claim 19, wherein the different spatial configurations include tile locations, sub-tile locations, surface locations, section locations, lane locations, lane group locations, swath locations, and/or swath group locations.