CLAIMS

1. A system comprising:

at least one processor; and

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

detect a signal from labeled nucleotide bases within a section of a nucleotide-sample slide;

determine, for the section of the nucleotide-sample slide, a scaling factor and a noise level corresponding to the signal based on intensity values for the signal;

generate a signal-to-noise-ratio metric for the section of the nucleotide-sample slide based on the scaling factor and the noise level; and

generate, utilizing a base-call-quality model, a quality metric estimating an error of a nucleotide-base call corresponding to the signal based on the signal-to-noise-ratio metric.

2. The system of claim 1, further comprising instructions that, when executed by the at least one processor, cause the system to determine, for the section of the nucleotide-sample slide, the noise level corresponding to the signal based on the intensity values for the signal by:

determining, for the section of the nucleotide-sample slide, corrected intensity values for the signal; and

determining the noise level corresponding to the signal based on the corrected intensity values for the signal.

3. The system of claim 2, further comprising instructions that, when executed by the at least one processor, cause the system to determine, for the section of the nucleotide-sample slide, the corrected intensity values for the signal by determining the corrected intensity values based on the intensity values for the signal, the scaling factor corresponding to the signal, and correction offset factors corresponding to the signal.

4. The system of claim 2, further comprising instructions that, when executed by the at least one processor, cause the system to determine the noise level corresponding to the signal based on the corrected intensity values for the signal by:

determining centroid intensity values for the nucleotide-base call corresponding to the signal; and

determining distances between the centroid intensity values and the corrected intensity values for the signal.

5. The system of any one of claims 1-4, further comprising instructions that, when executed by the at least one processor, cause the system to:

determine, for the section of the nucleotide-sample slide, an average noise level for one or more previous sequencing cycles; and

determine, for the section for the nucleotide-sample slide, the noise level corresponding to the signal by determining the noise level for a current sequencing cycle based on the average noise level for the one or more previous sequencing cycles.

6. The system of any one of claims 1-5, further comprising instructions that, when executed by the at least one processor, cause the system to determine, for the section of the nucleotide-sample slide, the scaling factor corresponding to the signal based on the intensity values for the signal by:

determining a relationship between a measured intensity for the labeled nucleotide bases and variation correction coefficients comprising the scaling factor;

determining an error function based on the relationship between the measured intensity and the variation correction coefficients; and

determining the scaling factor by generating a partial derivative of the error function with respect to the scaling factor.

7. The system of any one of claims 1-6, further comprising instructions that, when executed by the at least one processor, cause the system to generate the signal-to-noise-ratio metric for the section of the nucleotide-sample slide by generating the signal-to-noise-ratio metric for a well of a patterned flow cell or a subsection of a non-patterned flow cell.

8. The system of any one of claims 1-7, further comprising instructions that, when executed by the at least one processor, cause the system to generate the quality metric estimating the error of the nucleotide-base call corresponding to the signal based on the signal-to-noise-ratio metric by generating a Phred quality score estimating an accuracy of the nucleotide-base call corresponding to the signal based on the signal-to-noise-ratio metric.

9. The system of any one of claims 1-8, further comprising instructions that, when executed by the at least one processor, cause the system to:

determine a chastity value for the section of the nucleotide-sample slide based on distances between the intensity values for signal and intensity values of a nearest centroid and between the intensity values for the signal and intensity values for at least one additional centroid; and

generate, utilizing the base-call-quality model, the quality metric based on the signal-to-noise-ratio metric and the chastity value.

10. The system of any one of claims 1-9, further comprising instructions that, when executed by the at least one processor, cause the system to:

determine, for the section of the nucleotide-sample slide, a plurality of noise levels for a plurality of previous sequencing cycles;

determine a weighted average noise level for the plurality of previous sequencing cycles by applying weighted values to the plurality of noise levels based on sequencing-cycle recency; and

determine, for the section for the nucleotide-sample slide, the noise level corresponding to the signal by determining the noise level for a current sequencing cycle based on the weighted average noise level for the plurality of previous sequencing cycles.

11. A non-transitory computer-readable medium storing instructions thereon that, when executed by at least one processor, cause a computing device to:

detect a signal from labeled nucleotide bases within a section of a nucleotide-sample slide;

determine, for the section of the nucleotide-sample slide, a scaling factor and a noise level corresponding to the signal based on intensity values for the signal;

generate a signal-to-noise-ratio metric for the section of the nucleotide-sample slide based on the scaling factor and the noise level; and

based on comparing the signal-to-noise-ratio metric to a signal-to-noise-ratio threshold, include or exclude a nucleotide-base call corresponding to the signal within or from nucleotide-base-call data.

12. The non-transitory computer-readable medium of claim 11, further comprising instructions that, when executed by the at least one processor, cause the computing device to exclude subsequent nucleotide-base calls corresponding to subsequent signals detected from subsequent labeled nucleotide bases added to a cluster of oligonucleotides within the section of the nucleotide-sample slide based on determining that the signal-to-noise-ratio metric is lower than the signal-to-noise-ratio threshold.

13. The non-transitory computer-readable medium of claim 11 or 12, further comprising instructions that, when executed by the at least one processor, cause the computing device to generate the signal-to-noise-ratio metric by equating the scaling factor to the signal to determine a ratio of the scaling factor to the noise level.

14. The non-transitory computer-readable medium of any one of claims 11-13, further comprising instructions that, when executed by the at least one processor, cause the computing device to:

detect the signal by detecting the signal from the labeled nucleotide bases incorporated into a growing oligonucleotide at a genomic position later determined in alignment with a reference genome; and

generate the signal-to-noise-ratio metric for the nucleotide-base call at the genomic position corresponding to the signal.

15. A method comprising:

detecting signals from labeled nucleotide bases within sections of at least one nucleotide-sample slide;

generating signal-to-noise-ratio metrics for the sections of the at least one nucleotide-sample slide based on the signals and noise levels corresponding to the signals;

determining signal-to-noise-ratio ranges for the signal-to-noise-ratio metrics; and

generating, for each signal-to-noise-ratio range of the signal-to-noise-ratio ranges, intensity-value boundaries for differentiating signals corresponding to different nucleotide bases according to one or more base-call-distribution models.

16. The method of claim 15, wherein generating, for each signal-to-noise-ratio range of the signal-to-noise-ratio ranges, the intensity-value boundaries for differentiating the signals corresponding to the different nucleotide bases according to the one or more base-call-distribution models comprises:

generating, for a first signal-to-noise-ratio range, a first set of intensity-value boundaries corresponding to the different nucleotide bases according to a first base-call-distribution model; and

generating, for a second signal-to-noise-ratio range, a second set of intensity-value boundaries corresponding to the different nucleotide bases according to a second base-call-distribution model, the second set of intensity-value boundaries differing from the first set of intensity-value boundaries.

17. The method of claim 16, further comprising:

detecting a first signal corresponding to a first signal-to-noise-ratio metric within the first signal-to-noise-ratio range and having a set of intensity values outside of the first set of intensity-value boundaries and outside the second set of intensity-value boundaries;

detecting a second signal corresponding to a second signal-to-noise-ratio metric within the second signal-to-noise-ratio range and having the set of intensity values;

generating a first nucleotide-base call for the first signal based on the first set of intensity-value boundaries for the first base-call-distribution model; and

generating a second nucleotide-base call for the second signal based on the second set of intensity-value boundaries for the second base-call-distribution model.

18. The method of any one of claims 15-17, further comprising:

detecting a signal from a subset of labeled nucleotide bases from a cluster of oligonucleotides within a section of a nucleotide-sample slide;

generating a signal-to-noise-ratio metric, within a signal-to-noise-ratio range, for the section of the nucleotide-sample slide based on the signal; and

determining a nucleotide-base call corresponding to the signal based on a set of intensity-value boundaries of the intensity-value boundaries corresponding to the signal-to-noise-ratio range.

19. The method of claim 18, further comprising:

detecting an additional signal from an additional subset of labeled nucleotide bases from an additional cluster of oligonucleotides within an additional section of the nucleotide-sample slide;

generating an additional signal-to-noise-ratio metric, within an additional signal-to-noise-ratio range, for the additional section of the nucleotide-sample slide based on the additional signal, wherein the additional signal-to-noise-ratio range differs from the signal-to-noise-ratio range; and

determining an additional nucleotide-base call corresponding to the additional signal based on an additional set of intensity-value boundaries of the intensity-value boundaries corresponding to the additional signal-to-noise-ratio range.

20. The method of any one of claims 15-19, wherein generating the intensity-value boundaries for differentiating the signals corresponding to the different nucleotide bases according to the one or more base-call-distribution models comprises generating the intensity-value boundaries according to on one or more Gaussian distribution models for each signal-to-noise-ratio range of the signal-to-noise-ratio ranges.