CLAIMS

1. A computer-implemented method comprising:

detecting, for a sequencing cycle, a first set of intensity values for a first signal from a first cluster of oligonucleotides and a second set of intensity values for a second signal from a second cluster of oligonucleotides;

determining a set of illumination indicators representing whether the first cluster of oligonucleotides is illuminated during the sequencing cycle based on the first set of intensity values;

determining an inter-cluster-interference metric estimating light interference from the first cluster of oligonucleotides on the second cluster of oligonucleotides based on the set of illumination indicators; and

generating, for the sequencing cycle, a modified second set of intensity values for the second signal from the second cluster of oligonucleotides by removing the inter-cluster-interference metric from the second set of intensity values.

2. The computer-implemented method of claim 1, further comprising:

determining the set of illumination indicators based further on amplitudes for the first set of intensity values and an estimated point spread function for a section of a nucleotide-sample slide comprising the first cluster of oligonucleotides; and

determining the inter-cluster-interference metric based further on the estimated point spread function.

3. The computer-implemented method of claim 2, wherein the estimated point spread function uses a location of the second cluster of oligonucleotides or a different cluster of oligonucleotides as a point and includes an area comprising the first cluster of oligonucleotides and one or more other clusters of oligonucleotides.

4. The computer-implemented method of any one of claims 1-3, wherein a first location within a nucleotide-sample slide for the first cluster of oligonucleotides is first adjacent, second adjacent, or third adjacent to a second location within the nucleotide-sample slide for the second cluster of oligonucleotides.

5. The computer-implemented method of any one of claims 1-4, further comprising:

determining, for the sequencing cycle, a nucleobase call for the first cluster of oligonucleotides based on the first set of intensity values and intensity-value boundaries for nucleobases; and

determining the set of illumination indicators based further on the nucleobase call for the first cluster of oligonucleotides.

6. The computer-implemented method of claim 5, further comprising:

determining the nucleobase call for the first cluster of oligonucleotides based on an intensity value from the first set of intensity values corresponding to a first channel and an intensity value from the first set of intensity values corresponding to a second channel; and

generating the modified second set of intensity values by subtracting values for the inter-cluster-interference metric from an intensity value from the second set of intensity values corresponding to the first channel or an intensity value from the second set of intensity values corresponding to the second channel.

7. The computer-implemented method of any one of claims 1-6, wherein determining the set of illumination indicators comprises:

determining a first illumination indicator indicating whether the first cluster of oligonucleotides is illuminated or not illuminated in a first channel during the sequencing cycle; and

determining a second illumination indicator indicating whether the second cluster of oligonucleotides is illuminated or not illuminated in a second channel during the sequencing cycle; or

determining a first continuous illumination indicator indicating a degree to which the first cluster of oligonucleotides is illuminated in the first channel during the sequencing cycle; and

determining a second continuous illumination indicator indicating a degree to which the first cluster of oligonucleotides is illuminated in the second channel during the sequencing cycle.

8. The computer-implemented method of any one of claims 1-7, further comprising determining, for the sequencing cycle and based on the modified second set of intensity values, an adjusted set of illumination indicators that represents whether the second cluster of oligonucleotides is illuminated during the sequencing cycle and that differs from an initial set of illumination indicators corresponding to the second set of intensity values.

9. The computer-implemented method of any one of claims 1-8, further comprising determining, for the sequencing cycle and based on the modified second set of intensity values, a nucleobase call for the second cluster of oligonucleotides that differs from a nucleobase corresponding to the second set of intensity values.

10. The computer-implemented method of any one of claims 1-9, further comprising:

detecting, for the sequencing cycle, a third set of intensity values for a third signal from a third cluster of oligonucleotides;

determining an additional set of illumination indicators representing whether the third cluster of oligonucleotides is illuminated during the sequencing cycle based on the third set of intensity values;

determining an additional inter-cluster-interference metric estimating light interference from the third cluster of oligonucleotides on the second cluster of oligonucleotides based on the additional set of illumination indicators; and

generating, for the sequencing cycle, the modified second set of intensity values for the second signal from the second cluster of oligonucleotides by removing the inter-cluster-interference metric and the additional inter-cluster-interference metric from the second set of intensity values.

11. The computer-implemented method of claims 1-10, further comprising:

determining the first set of intensity values for the first signal from the first cluster of oligonucleotides is within an intensity-value range;

determining the second set of intensity values for the second signal from the second cluster of oligonucleotides is not within the intensity-value range; and

based on the first set of intensity values being within the intensity-value range and the second set of intensity values not being within the intensity-value range, generating the modified second set of intensity values by removing, from the second set of intensity values, the inter-cluster-interference metric estimating light interference from the first cluster of oligonucleotides on the second cluster of oligonucleotides.

12. The computer-implemented method of claims 11, further comprising:

determining, based on the first set of intensity values, a first nucleobase call for the first cluster of oligonucleotides as part of a first subset of oligonucleotide clusters having intensity values within the intensity-value range; and

determining, based on the modified second set of intensity values, a second nucleobase call for the second cluster of oligonucleotides as part of a second subset of oligonucleotide clusters having intensity values not within the intensity-value range.

13. The computer-implemented method of any of claims 1-12, wherein:

detecting the first set of intensity values by detecting, in a single channel, a first intensity value for the first signal from a first cluster of oligonucleotides;

detecting the second set of intensity values comprises detecting, in the single channel, a second intensity value for the second signal from a second cluster of oligonucleotides; and

determining the set of illumination indicators comprises determining a single illumination indicator representing whether the first cluster of oligonucleotides is illuminated in the single channel during the sequencing cycle.

14. 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 perform a method according to any of claims 1-13.

15. A non-transitory computer-readable medium storing instructions that, when executed by at least one processor, cause a system to perform a method according to any of claims 1-13.