CLAIMS

1. A system comprising:

at least one processor;

a memory device; and

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

identify, utilizing a genotype imputation model, a haplotype reference panel for a genomic region of a genomic sample;

access, from the memory device and for a marker variant, a first allele-likelihood factor corresponding to a haplotype allele from the haplotype reference panel and a second allele-likelihood factor corresponding to the haplotype allele;

combine the first allele-likelihood factor and an adjacent-marker intermediate allele likelihood of the genomic region comprising the haplotype allele given an adjacent marker variant to generate an adjacent-marker-factor-aware allele likelihood for the marker variant and a haplotype from the haplotype reference panel;

determine, for the marker variant and the haplotype, an intermediate allele likelihood of the genomic region comprising the haplotype allele based on the adjacent-marker-factor-aware allele likelihood and the second allele-likelihood factor; and

generate, for a set of marker variants corresponding to the genomic region, allele likelihoods of the genomic region comprising haplotype alleles from the haplotype reference panel based on the intermediate allele likelihood.

2. The system of claim 1, further comprising instructions that, when executed by the at least one processor, cause the system to access, from the memory device and for the marker variant, the first allele-likelihood factor and the second allele-likelihood factor by accessing, from the memory device and for the marker variant, a first transition-aware allele-likelihood factor corresponding to the haplotype allele from the haplotype reference panel and a second transition-aware allele-likelihood factor corresponding to the haplotype allele.

3. The system of claim 2, further comprising instructions that, when executed by the at least one processor, cause the system to predetermine the first transition-aware allele-likelihood factor

and the second transition-aware allele-likelihood factor before determining one or more intermediate allele likelihoods corresponding to the marker variant as part of a pass across a haplotype matrix.

4. The system of claim 2 or 3, further comprising instructions that, when executed by the at least one processor, cause the system to:

predetermine the first transition-aware allele-likelihood factor by combining an allele-likelihood factor for the haplotype allele and a transition constant coefficient for transitioning between haplotypes from the haplotype reference panel; and

predetermine the second transition-aware allele-likelihood factor by combining the allele-likelihood factor and a transition linear coefficient for transitioning between haplotypes from the haplotype reference panel.

5. The system of claim 2, further comprising instructions that, when executed by the at least one processor, cause the system to determine the first transition-aware allele-likelihood factor by combining an allele-likelihood factor and a transition linear coefficient.

6. The system of claim 5, wherein:

the first allele-likelihood factor comprises an allele-likelihood factor for a sample reference haplotype allele or for a sample alternate haplotype allele; and

the second allele-likelihood factor comprises the allele-likelihood factor for the sample reference haplotype allele or for the sample alternate haplotype allele.

7. The system of any one of claims 1-3 and 5-6, further comprising instructions that, when executed by the at least one processor, cause the system to combine the first allele-likelihood factor and the adjacent-marker intermediate allele likelihood by multiplying a first transition-aware allele-likelihood factor and the adjacent-marker intermediate allele likelihood without further multiplication operations to determine the intermediate allele likelihood.

8. The system of any one of claims 1-3 and 5-6, further comprising a data flow engine and instructions that, when executed by the at least one processor, cause the system to:

send, from the data flow engine to respective accelerated computation engines of a cluster of accelerated computation engines, respective sets of input values comprising allele-likelihood factors, transition coefficients, and haplotype-allele values; and

determine, by the respective accelerated computation engines and based on the respective sets of input values, respective sets of intermediate allele likelihoods corresponding to respective subsets of marker variants and respective subsets of haplotypes.

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

send the respective sets of input values from the data flow engine to the respective accelerated computation engines by:

sending, from the data flow engine to a first accelerated computation engine of the cluster of accelerated computation engines, a first set of input values comprising allele-likelihood factors, transition coefficients, and haplotype-allele values;

sending, from the data flow engine to a second accelerated computation engine of the cluster of accelerated computation engines, a second set of input values comprising allele-likelihood factors, transition coefficients, and haplotype-allele values; and

determine the respective sets of intermediate allele likelihoods by:

determining, by the first accelerated computation engine and based on the first set of input values, a first set of intermediate allele likelihoods corresponding to a first subset of marker variants and a first subset of haplotypes; and

determining, by the second accelerated computation engine and based on the second set of input values, a second set of intermediate allele likelihoods corresponding to a second subset of marker variants and a second subset of haplotypes.

10. A non-transitory computer-readable medium storing instructions that, when executed by at least one processor, cause the at least one processor to:

identify, utilizing a genotype imputation model, a haplotype reference panel for a genomic region of a genomic sample;

access, from a memory device and for a marker variant, a first transition-aware allele-likelihood factor corresponding to a haplotype allele from the haplotype reference panel and a second transition-aware allele-likelihood factor corresponding to the haplotype allele;

combine, by a configurable processor, the first transition-aware allele-likelihood factor and an adjacent-marker intermediate allele likelihood of the genomic region comprising the haplotype allele given an adjacent marker variant to generate an adjacent-marker-transition-factor-aware allele likelihood for the marker variant and a haplotype from the haplotype reference panel;

determine, by the configurable processor and for the marker variant and the haplotype, an intermediate allele likelihood of the genomic region comprising the haplotype allele based on the adjacent-marker-transition-factor-aware allele likelihood and the second transition-aware allele-likelihood factor; and

generate, by the configurable processor and for a set of marker variants corresponding to the genomic region, allele likelihoods of the genomic region comprising haplotype alleles from the haplotype reference panel based on the intermediate allele likelihood.

11. The non-transitory computer-readable medium of claim 10, further comprising instructions that, when executed by the at least one processor, cause the at least one processor to predetermine the first transition-aware allele-likelihood factor and the second transition-aware allele-likelihood factor before determining one or more intermediate allele likelihoods corresponding to the marker variant.

12. The non-transitory computer-readable medium of claim 11, further comprising instructions that, when executed by the at least one processor, cause the at least one processor to:

predetermine the first transition-aware allele-likelihood factor by combining an allele-likelihood factor for the haplotype allele and a transition constant coefficient for transitioning between haplotypes from the haplotype reference panel; and

predetermine the second transition-aware allele-likelihood factor by combining the allele-likelihood factor and a transition linear coefficient for transitioning between haplotypes from the haplotype reference panel.

13. The non-transitory computer-readable medium of any one of claims 10-12, further comprising instructions that, when executed by the at least one processor, cause the at least one processor to combine the first transition-aware allele-likelihood factor and the adjacent-marker intermediate allele likelihood by multiplying the first transition-aware allele-likelihood factor and the

adjacent-marker intermediate allele likelihood without further multiplication operations to determine the intermediate allele likelihood.

14. The non-transitory computer-readable medium of any one of claims 10-12, further comprising instructions that, when executed by the at least one processor, cause the at least one processor to:

access the second transition-aware allele-likelihood factor as part of a summed-adjacent-marker transition-aware allele-likelihood factor; and

determine the intermediate allele likelihood based on the adjacent-marker-transition-factor-aware allele likelihood and the summed-adjacent-marker transition-aware allele-likelihood factor.

15. The non-transitory computer-readable medium of claim 14, further comprising instructions that, when executed by the at least one processor, cause the at least one processor to predetermine the summed-adjacent-marker transition-aware allele-likelihood factor by combining an allele-likelihood factor for the haplotype allele, a transition constant coefficient for transitioning between haplotypes from the haplotype reference panel, and summed adjacent-marker intermediate allele likelihoods for the adjacent marker variant.

16. The non-transitory computer-readable medium of claim 15, wherein the allele-likelihood factor for the haplotype allele comprises a reference allele-likelihood factor for a sample reference haplotype allele or an alternate allele-likelihood factor for a sample alternate haplotype allele.

17. A computer-implemented method comprising:

identifying, utilizing a genotype imputation model, a haplotype reference panel for a genomic region of a genomic sample;

accessing, from a memory device and for a marker variant, a first transition-aware allele-likelihood factor corresponding to a haplotype allele from the haplotype reference panel and a second transition-aware allele-likelihood factor corresponding to the haplotype allele;

combining, by a configurable processor, the first transition-aware allele-likelihood factor and an adjacent-marker intermediate allele likelihood of the genomic region comprising the haplotype allele given an adjacent marker variant to generate an adjacent-marker-transition-factor-aware allele likelihood for the marker variant and a haplotype from the haplotype reference panel;

determining, by the configurable processor and for the marker variant and the haplotype, an intermediate allele likelihood of the genomic region comprising the haplotype allele based on the adjacent-marker-transition-factor-aware allele likelihood and the second transition-aware allele-likelihood factor; and

generating, by the configurable processor and for a set of marker variants corresponding to the genomic region, allele likelihoods of the genomic region comprising haplotype alleles from the haplotype reference panel based on the intermediate allele likelihood.

18. The computer-implemented method of claim 17, wherein the genotype imputation model comprises a hidden Markov genotype imputation model.

19. The computer-implemented method of claim 17 or 18, wherein the configurable processor comprises an application-specific integrated circuit (ASIC), an application-specific standard product (ASSP), a coarse-grained reconfigurable array (CGRA), or a field programmable gate array (FPGA).

20. The computer-implemented method of any one of claims 17 or 18, wherein the memory device comprises dynamic random-access memory (DRAM), dynamic random-access memory (SRAM), or a cache memory device.