

CLAIMS**WHAT IS CLAIMED IS:**

1. A computer-implemented method for estimating a degree of ancestral relatedness between two individuals of a diploid population, comprising:
 - (a) receiving haplotype data for a population of test individuals, the haplotype data comprising a plurality of genetic markers shared among the population of test individuals;
 - (b) dividing the haplotype data into segments based on the plurality of genetic markers;
 - (c) for each of the population of test individuals:
 - (i) based on the plurality of genetic markers, matching segments of the haplotype data that are identical-by-descent between a first individual and a second individual among the population of test individuals, each of the matched segments having a first size that is at least a pre-determined threshold size and comprising at least a pre-determined number of genetic markers;
 - (ii) for each of the matched segments between the first individual and the second individual:
 - dividing the matched segment into a plurality of discrete genomic intervals;
 - scoring each of the plurality of discrete genomic intervals based on (i) a degree of homozygosity matching of the discrete genomic interval within the first individual or the second individual or (ii) a degree of pairwise matching of the discrete genomic interval between the first individual and the second individual, thereby generating a plurality of scores;
 - correcting the plurality of scores based on a consistency of the plurality of scores, thereby producing a plurality of corrected scores; and
 - assigning a plurality of weights to the plurality of discrete genomic intervals, based on the plurality of corrected scores of the discrete genomic intervals; and
 - (iii) calculating a weighted sum over the plurality of discrete genomic intervals of the matched segment, based on the plurality of corrected scores and the plurality of weights; and
 - (d) estimating the degree of ancestral relatedness between the first individual and the second individual based on the weighted sums of the matched segments.
2. The method of claim 1, wherein the diploid population is a mammal population.

3. The method of claim 2, wherein the mammal population is a canine population.
4. The method of claim 3, wherein the canine population is a dog population.
5. The method of claim 1, wherein the haplotype data is generated by processing genotype data of the population of test individuals using a haplotype phasing algorithm.
6. The method of claim 5, wherein the haplotype phasing algorithm comprises a reference-based haplotype phasing algorithm.
7. The method of claim 6, wherein the reference-based haplotype phasing algorithm comprises a Hidden Markov Model (HMM)-based search.
8. The method of claim 7, wherein the reference-based haplotype phasing algorithm comprises an Eagle1 algorithm, an Eagle2 algorithm, a PHASE algorithm, a fastPHASE algorithm, a BEAGLE algorithm, a Findhap algorithm, an Impute algorithm, an FImpute algorithm, an AlphaImpute algorithm, an IMPUTE2 algorithm, a MaCH algorithm, a SHAPEIT1 algorithm, a SHAPEIT2 algorithm, a SHAPEIT3 algorithm, a SHAPEIT4 algorithm, or a combination thereof.
9. The method of claim 5, wherein the haplotype phasing algorithm comprises a cohort-based haplotype phasing algorithm.
10. The method of claim 5, wherein the genotype data is obtained by assaying biological samples obtained from the population of test individuals.
11. The method of claim 10, wherein the biological samples comprise blood samples, saliva samples, swab samples, cell samples, or tissue samples.
12. The method of claim 10, wherein the assaying comprises sequencing the biological samples or derivatives thereof.

13. The method of claim 1, wherein the plurality of genetic markers comprises at least about 500, at least about 1,000, at least about 2,000, at least about 3,000, at least about 4,000, at least about 5,000, at least about 6,000, at least about 7,000, at least about 8,000, at least about 9,000, or at least about 10,000 distinct genetic markers.
14. The method of claim 1, wherein matching the segments of the haplotype data that are identical-by-descent comprises using a GERMLINE algorithm, a PLINK algorithm, a PREST algorithm, a Random Projection for IBD Detection (RaPID) algorithm, a Find IBD Shared Haplotypes Rapidly (FISHR) algorithm, a refined identical-by-descent (IBD) algorithm, a fastIBD algorithm, a KING algorithm, a HaploScore algorithm, a TRUFFLE algorithm, or a combination thereof.
15. The method of claim 1, wherein the pre-determined threshold size is about 100 kilobase pairs (kbp), about 200 kbp, about 300 kbp, about 400 kbp, about 500 kbp, about 600 kbp, about 700 kbp, about 800 kbp, about 900 kbp, or about 1,000 kbp.
16. The method of claim 1, wherein the pre-determined number of genetic markers is about 30, about 40, about 50, about 60, about 70, about 80, about 90, or about 100 distinct genetic markers.
17. The method of claim 1, further comprising dividing the matched segments such that the discrete genomic intervals of the plurality of discrete genomic intervals have an equal size.
18. The method of claim 1, further comprising dividing the matched segments such that the discrete genomic intervals of the plurality of discrete genomic intervals have a variable size.
19. The method of claim 18, wherein the variable size of a given discrete genomic interval of the plurality of discrete genomic intervals is determined based at least in part on a start position and an end position of IBD matches proximal to the given discrete genomic interval, a density of genetic markers in the given discrete genomic interval, a maximum number of markers for the given discrete genomic interval, a maximum length of the given discrete genomic interval, or a combination thereof.

20. The method of claim 1, further comprising scoring each of the plurality of discrete genomic intervals based on (i) the degree of homozygosity matching of the discrete genomic interval within the first individual or the second individual and (ii) the degree of pairwise matching of the discrete genomic interval between the first individual and the second individual, thereby generating a plurality of homozygosity matching scores and a plurality of pairwise matching scores.
21. The method of claim 20, further comprising correcting the plurality of pairwise matching scores based on a consistency of a given pairwise matching score with a corresponding homozygosity matching score, thereby producing a plurality of corrected pairwise matching scores.
22. The method of claim 20, further comprising assigning the plurality of weights to the plurality of discrete genomic intervals, based on a plurality of identity states for two alleles in two diploid individuals.
23. The method of claim 22, wherein the plurality of identity states comprises identity states selected from **Table 1**, and wherein the plurality of weights are assigned based on a plurality of contributions to relatedness r_{xy} as listed in **Table 1**.
24. The method of claim 23, wherein the degree of ancestral relatedness comprises a coefficient of relatedness.
25. The method of claim 24, further comprising calculating the weighted sum over the plurality of discrete genomic intervals of the matched segment, wherein the weighted sum is expressed by:

$$r_{xy} = \frac{\Delta 1 + \Delta 7 + (0.75 \times \Delta 3) + (0.5 \times \Delta 8)}{L}.$$
26. The method of claim 23, wherein the degree of ancestral relatedness comprises a coefficient of kinship.

27. The method of claim 26, further comprising calculating the weighted sum over the plurality of discrete genomic intervals of the matched segment, wherein the weighted sum is expressed by:
- $$k_{xy} = \frac{\Delta 1 + (0.5 \times (\Delta 3 + \Delta 7)) + (0.25 \times \Delta 8)}{L}.$$
28. The method of claim 1, wherein estimating the degree of ancestral relatedness between the first individual and the second individual comprises determining a degree of inbreeding of the first individual or the second individual.
29. The method of claim 1, wherein estimating the degree of ancestral relatedness between the first individual and the second individual comprises determining a degree of inbreeding of the first individual and the second individual.
30. The method of claim 29, further comprising determining a familial relationship between the first individual and the second individual based at least in part on the degree of inbreeding of the first individual and the second individual.
31. The method of claim 30, wherein the familial relationship is a parent-child relationship, a sibling relationship, an aunt/uncle-nephew/niece relationship, a cousin relationship, or a grandparent-grandchild relationship.
32. The method of claim 28 or 29, further comprising determining an expected degree of inbreeding of a potential offspring of the first individual and the second individual.
33. The method of claim 32, further comprising determining a recommendation indicative of whether or not to breed the first individual and the second individual together, based on the expected degree of inbreeding of the potential offspring of the first individual and the second individual.
34. The method of claim 33, further comprising determining a recommendation indicative of breeding the first individual and the second individual together, when the expected degree of inbreeding of the potential offspring of the first individual and the second individual does not exceed a pre-determined threshold degree of inbreeding.

35. The method of claim 33, further comprising determining a recommendation indicative of not breeding the first individual and the second individual together, when the expected degree of inbreeding of the potential offspring of the first individual and the second individual exceeds a pre-determined threshold degree of inbreeding.
36. The method of 34 or 35, wherein the pre-determined threshold degree of inbreeding is about 0.10, about 0.15, about 0.20, about 0.25, about 0.30, about 0.35, about 0.40, about 0.45, or about 0.50.
37. The method of claim 1, further comprising generating a social connection between a first person associated with the first individual and a second person associated with the second individual, based at least in part on the estimated degree of ancestral relatedness between the first individual and the second individual.
38. The method of claim 37, wherein the social connection is generated when the estimated degree of ancestral relatedness between the first individual and the second individual exceeds a pre-determined threshold value.
39. The method of claim 38, wherein the pre-determined threshold value is about 0.00001, about 0.0001, about 0.001, about 0.01, about 0.02, about 0.04, about 0.06, about 0.08, about 0.1, about 0.12, about 0.14, about 0.16, about 0.18, about 0.2, about 0.25, about 0.3, about 0.35, about 0.4, about 0.45, or about 0.5.
40. The method of claim 37, wherein the social connection is generated through a social media network.
41. The method of claim 37, wherein the first person is a pet owner of the first individual, and wherein the second person is a pet owner of the second individual.
42. The method of claim 1, further comprising identifying a familial relationship between the first individual and the second individual based at least in part on the degree of ancestral relatedness.

43. The method of claim 42, wherein the familial relationship is a parent-child relationship, a sibling relationship, an aunt/uncle-nephew/niece relationship, a cousin relationship, or a grandparent-grandchild relationship.
44. A computer system for estimating a degree of ancestral relatedness between two individuals of a diploid population, comprising:
- a database that is configured to store haplotype data for a population of test individuals, the haplotype data comprising a plurality of genetic markers shared among the population of test individuals; and
 - one or more computer processors operatively coupled to the database, wherein the one or more computer processors are individually or collectively programmed to:
 - (a) divide the haplotype data into segments based on the plurality of genetic markers;
 - (b) for each of the population of test individuals:
 - (i) based on the plurality of genetic markers, match segments of the haplotype data that are identical-by-descent between a first individual and a second individual among the population of test individuals, each of the matched segments having a first size that is at least a pre-determined threshold size and comprising at least a pre-determined number of genetic markers;
 - (ii) for each of the matched segments between the first individual and the second individual:
 - divide the matched segment into a plurality of discrete genomic intervals;
 - score each of the plurality of discrete genomic intervals based on (i) a degree of homozygosity matching of the discrete genomic interval within the first individual or the second individual or (ii) a degree of pairwise matching of the discrete genomic interval between the first individual and the second individual, thereby generating a plurality of scores; and
 - correct the plurality of scores based on a consistency of the plurality of scores, thereby producing a plurality of corrected scores; and
 - assign a plurality of weights to the plurality of discrete genomic intervals, based on the plurality of corrected scores of the discrete genomic intervals; and
 - (iii) calculate a weighted sum over the plurality of discrete genomic intervals of the matched segment, based on the plurality of corrected scores and the plurality of weights; and

(c) estimate the degree of ancestral relatedness between the first individual and the second individual based on the weighted sums of the matched segments.

45. The computer system of claim 44, wherein the diploid population is a mammal population.
46. The computer system of claim 45, wherein the mammal population is a canine population.
47. The computer system of claim 46, wherein the canine population is a dog population.
48. The computer system of claim 44, wherein the haplotype data is generated by processing genotype data of the population of test individuals using a haplotype phasing algorithm.
49. The computer system of claim 48, wherein the haplotype phasing algorithm comprises a reference-based haplotype phasing algorithm.
50. The computer system of claim 49, wherein the reference-based haplotype phasing algorithm comprises a Hidden Markov Model (HMM)-based search.
51. The computer system of claim 50, wherein the reference-based haplotype phasing algorithm comprises an Eagle1 algorithm, an Eagle2 algorithm, a PHASE algorithm, a fastPHASE algorithm, a BEAGLE algorithm, a Findhap algorithm, an Impute algorithm, an FImpute algorithm, an AlphaImpute algorithm, an IMPUTE2 algorithm, a MaCH algorithm, a SHAPEIT1 algorithm, a SHAPEIT2 algorithm, a SHAPEIT3 algorithm, a SHAPEIT4 algorithm, or a combination thereof.
52. The computer system of claim 48, wherein the haplotype phasing algorithm comprises a cohort-based haplotype phasing algorithm.
53. The computer system of claim 48, wherein the genotype data is obtained by assaying biological samples obtained from the population of test individuals.

54. The computer system of claim 53, wherein the biological samples comprise blood samples, saliva samples, swab samples, cell samples, or tissue samples.
55. The computer system of claim 53, wherein the assaying comprises sequencing the biological samples or derivatives thereof.
56. The computer system of claim 44, wherein the plurality of genetic markers comprises at least about 500, at least about 1,000, at least about 2,000, at least about 3,000, at least about 4,000, at least about 5,000, at least about 6,000, at least about 7,000, at least about 8,000, at least about 9,000, or at least about 10,000 distinct genetic markers.
57. The computer system of claim 44, wherein matching the segments of the haplotype data that are identical-by-descent comprises using a GERMLINE algorithm, a PLINK algorithm, a PREST algorithm, a Random Projection for IBD Detection (RaPID) algorithm, a Find IBD Shared Haplotypes Rapidly (FISHR) algorithm, a refined identical-by-descent (IBD) algorithm, a fastIBD algorithm, a KING algorithm, a HaploScore algorithm, a TRUFFLE algorithm, or a combination thereof.
58. The computer system of claim 44, wherein the pre-determined threshold size is about 100 kilobase pairs (kbp), about 200 kbp, about 300 kbp, about 400 kbp, about 500 kbp, about 600 kbp, about 700 kbp, about 800 kbp, about 900 kbp, or about 1,000 kbp.
59. The computer system of claim 44, wherein the pre-determined number of genetic markers is about 30, about 40, about 50, about 60, about 70, about 80, about 90, or about 100 distinct genetic markers.
60. The computer system of claim 44, wherein the one or more computer processors are individually or collectively programmed to further divide the matched segments such that the discrete genomic intervals of the plurality of discrete genomic intervals have an equal size.
61. The computer system of claim 44, wherein the one or more computer processors are individually or collectively programmed to further divide the matched segments such

that the discrete genomic intervals of the plurality of discrete genomic intervals have a variable size.

62. The computer system of claim 61, wherein the variable size of a given discrete genomic interval of the plurality of discrete genomic intervals is determined based at least in part on a start position and an end position of IBD matches proximal to the given discrete genomic interval, a density of genetic markers in the given discrete genomic interval, a maximum number of markers for the given discrete genomic interval, a maximum length of the given discrete genomic interval, or a combination thereof.
63. The computer system of claim 44, wherein the one or more computer processors are individually or collectively programmed to further score each of the plurality of discrete genomic intervals based on (i) the degree of homozygosity matching of the discrete genomic interval within the first individual or the second individual and (ii) the degree of pairwise matching of the discrete genomic interval between the first individual and the second individual, thereby generating a plurality of homozygosity matching scores and a plurality of pairwise matching scores.
64. The computer system of claim 63, wherein the one or more computer processors are individually or collectively programmed to further correct the plurality of pairwise matching scores based on a consistency of a given pairwise matching score with a corresponding homozygosity matching score, thereby producing a plurality of corrected pairwise matching scores.
65. The computer system of claim 63, wherein the one or more computer processors are individually or collectively programmed to further assign the plurality of weights to the plurality of discrete genomic intervals, based on a plurality of identity states for two alleles in two diploid individuals.
66. The computer system of claim 65, wherein the plurality of identity states comprises identity states selected from **Table 1**, and wherein the plurality of weights are assigned based on a plurality of contributions to relatedness r_{xy} as listed in **Table 1**.

67. The computer system of claim 66, wherein the degree of ancestral relatedness comprises a coefficient of relatedness.

68. The computer system of claim 67, wherein the one or more computer processors are individually or collectively programmed to further calculate the weighted sum over the plurality of discrete genomic intervals of the matched segment, wherein the weighted sum is expressed by:

$$r_{xy} = \frac{\Delta 1 + \Delta 7 + (0.75 \times \Delta 3) + (0.5 \times \Delta 8)}{L}$$

69. The computer system of claim 66, wherein the degree of ancestral relatedness comprises a coefficient of kinship.

70. The computer system of claim 69, wherein the one or more computer processors are individually or collectively programmed to further calculate the weighted sum over the plurality of discrete genomic intervals of the matched segment, wherein the weighted sum is expressed by:

$$k_{xy} = \frac{\Delta 1 + (0.5 \times (\Delta 3 + \Delta 7)) + (0.25 \times \Delta 8)}{L}$$

71. The computer system of claim 44, wherein estimating the degree of ancestral relatedness between the first individual and the second individual comprises determining a degree of inbreeding of the first individual or the second individual.

72. The computer system of claim 44, wherein estimating the degree of ancestral relatedness between the first individual and the second individual comprises determining a degree of inbreeding of the first individual and the second individual.

73. The computer system of claim 72, wherein the one or more computer processors are individually or collectively programmed to further determine a familial relationship between the first individual and the second individual based at least in part on the degree of inbreeding of the first individual and the second individual.

74. The computer system of claim 73, wherein the familial relationship is a parent-child relationship, a sibling relationship, an aunt/uncle-nephew/niece relationship, a cousin relationship, or a grandparent-grandchild relationship.
75. The computer system of claim 71 or 72, wherein the one or more computer processors are individually or collectively programmed to further determine an expected degree of inbreeding of a potential offspring of the first individual and the second individual.
76. The computer system of claim 75, wherein the one or more computer processors are individually or collectively programmed to further determine a recommendation indicative of whether or not to breed the first individual and the second individual together, based on the expected degree of inbreeding of the potential offspring of the first individual and the second individual.
77. The computer system of claim 76, wherein the one or more computer processors are individually or collectively programmed to further determine a recommendation indicative of breeding the first individual and the second individual together, when the expected degree of inbreeding of the potential offspring of the first individual and the second individual does not exceed a pre-determined threshold degree of inbreeding.
78. The computer system of claim 76, wherein the one or more computer processors are individually or collectively programmed to further determine a recommendation indicative of not breeding the first individual and the second individual together, when the expected degree of inbreeding of the potential offspring of the first individual and the second individual exceeds a pre-determined threshold degree of inbreeding.
79. The computer system of claim 77 or 78, wherein the pre-determined threshold degree of inbreeding is about 0.10, about 0.15, about 0.20, about 0.25, about 0.30, about 0.35, about 0.40, about 0.45, or about 0.50.
80. The computer system of claim 44, wherein the one or more computer processors are individually or collectively programmed to further generate a social connection between a first person associated with the first individual and a second person associated with the

second individual, based at least in part on the estimated degree of ancestral relatedness between the first individual and the second individual.

81. The computer system of claim 80, wherein the social connection is generated when the estimated degree of ancestral relatedness between the first individual and the second individual exceeds a pre-determined threshold value.
82. The computer system of claim 81, wherein the pre-determined threshold value is about 0.00001, about 0.0001, about 0.001, about 0.01, about 0.02, about 0.04, about 0.06, about 0.08, about 0.1, about 0.12, about 0.14, about 0.16, about 0.18, about 0.2, about 0.25, about 0.3, about 0.35, about 0.4, about 0.45, or about 0.5.
83. The computer system of claim 80, wherein the social connection is generated through a social media network.
84. The computer system of claim 80, wherein the first person is a pet owner of the first individual, and wherein the second person is a pet owner of the second individual.
85. The computer system of claim 44, wherein the one or more computer processors are individually or collectively programmed to further identify a familial relationship between the first individual and the second individual based at least in part on the degree of ancestral relatedness.
86. The computer system of claim 85, wherein the familial relationship is a parent-child relationship, a sibling relationship, an aunt/uncle-nephew/niece relationship, a cousin relationship, or a grandparent-grandchild relationship.
87. A non-transitory computer readable medium comprising machine-executable code that, upon execution by one or more computer processors, implements a method for estimating a degree of ancestral relatedness between two individuals of a diploid population, the method comprising:
 - (a) receiving haplotype data for a population of test individuals, the haplotype data comprising a plurality of genetic markers shared among the population of test individuals;
 - (b) dividing the haplotype data into segments based on the plurality of genetic markers;

(c) for each of the population of test individuals:

(i) based on the plurality of genetic markers, matching segments of the haplotype data that are identical-by-descent between a first individual and a second individual among the population of test individuals, each of the matched segments having a first size that is at least a pre-determined threshold size and comprising at least a pre-determined number of genetic markers;

(ii) for each of the matched segments between the first individual and the second individual:

dividing the matched segment into a plurality of discrete genomic intervals;

scoring each of the plurality of discrete genomic intervals based on (i) a degree of homozygosity matching of the discrete genomic interval within the first individual or the second individual or (ii) a degree of pairwise matching of the discrete genomic interval between the first individual and the second individual, thereby generating a plurality of scores;

correcting the plurality of scores based on a consistency of the plurality of scores, thereby producing a plurality of corrected scores; and

assigning a plurality of weights to the plurality of discrete genomic intervals, based on the plurality of corrected scores of the discrete genomic intervals; and

(iii) calculating a weighted sum over the plurality of discrete genomic intervals of the matched segment, based on the plurality of corrected scores and the plurality of weights; and

(d) estimating the degree of ancestral relatedness between the first individual and the second individual based on the weighted sums of the matched segments.

88. The non-transitory computer readable medium of claim 87, wherein the diploid population is a mammal population.

89. The non-transitory computer readable medium of claim 88, wherein the mammal population is a canine population.

90. The non-transitory computer readable medium of claim 89, wherein the canine population is a dog population.

91. The non-transitory computer readable medium of claim 87, wherein the haplotype data is generated by processing genotype data of the population of test individuals using a haplotype phasing algorithm.
92. The non-transitory computer readable medium of claim 91, wherein the haplotype phasing algorithm comprises a reference-based haplotype phasing algorithm.
93. The non-transitory computer readable medium of claim 92, wherein the reference-based haplotype phasing algorithm comprises a Hidden Markov Model (HMM)-based search.
94. The non-transitory computer readable medium of claim 93, wherein the reference-based haplotype phasing algorithm comprises an Eagle1 algorithm, an Eagle2 algorithm, a PHASE algorithm, a fastPHASE algorithm, a BEAGLE algorithm, a Findhap algorithm, an Impute algorithm, an FImpute algorithm, an AlphaImpute algorithm, an IMPUTE2 algorithm, a MaCH algorithm, a SHAPEIT1 algorithm, a SHAPEIT2 algorithm, a SHAPEIT3 algorithm, a SHAPEIT4 algorithm, or a combination thereof.
95. The non-transitory computer readable medium of claim 91, wherein the haplotype phasing algorithm comprises a cohort-based haplotype phasing algorithm.
96. The non-transitory computer readable medium of claim 91, wherein the genotype data is obtained by assaying biological samples obtained from the population of test individuals.
97. The non-transitory computer readable medium of claim 96, wherein the biological samples comprise blood samples, saliva samples, swab samples, cell samples, or tissue samples.
98. The non-transitory computer readable medium of claim 96, wherein the assaying comprises sequencing the biological samples or derivatives thereof.
99. The non-transitory computer readable medium of claim 87, wherein the plurality of genetic markers comprises at least about 500, at least about 1,000, at least about 2,000, at least about 3,000, at least about 4,000, at least about 5,000, at least about 6,000, at least

about 7,000, at least about 8,000, at least about 9,000, or at least about 10,000 distinct genetic markers.

100. The non-transitory computer readable medium of claim 87, wherein matching the segments of the haplotype data that are identical-by-descent comprises using a GERMLINE algorithm, a PLINK algorithm, a PREST algorithm, a Random Projection for IBD Detection (RaPID) algorithm, a Find IBD Shared Haplotypes Rapidly (FISHR) algorithm, a refined identical-by-descent (IBD) algorithm, a fastIBD algorithm, a KING algorithm, a HaploScore algorithm, a TRUFFLE algorithm, or a combination thereof.
101. The non-transitory computer readable medium of claim 87, wherein the pre-determined threshold size is about 100 kilobase pairs (kbp), about 200 kbp, about 300 kbp, about 400 kbp, about 500 kbp, about 600 kbp, about 700 kbp, about 800 kbp, about 900 kbp, or about 1,000 kbp.
102. The non-transitory computer readable medium of claim 87, wherein the pre-determined number of genetic markers is about 30, about 40, about 50, about 60, about 70, about 80, about 90, or about 100 distinct genetic markers.
103. The non-transitory computer readable medium of claim 87, wherein the method further comprises dividing the matched segments such that the discrete genomic intervals of the plurality of discrete genomic intervals have an equal size.
104. The non-transitory computer readable medium of claim 87, wherein the method further comprises dividing the matched segments such that the discrete genomic intervals of the plurality of discrete genomic intervals have a variable size.
105. The non-transitory computer readable medium of claim 104, wherein the variable size of a given discrete genomic interval of the plurality of discrete genomic intervals is determined based at least in part on a start position and an end position of IBD matches proximal to the given discrete genomic interval, a density of genetic markers in the given discrete genomic interval, a maximum number of markers for the given discrete genomic interval, a maximum length of the given discrete genomic interval, or a combination thereof.

106. The non-transitory computer readable medium of claim 87, wherein the method further comprises scoring each of the plurality of discrete genomic intervals based on (i) the degree of homozygosity matching of the discrete genomic interval within the first individual or the second individual and (ii) the degree of pairwise matching of the discrete genomic interval between the first individual and the second individual, thereby generating a plurality of homozygosity matching scores and a plurality of pairwise matching scores.
107. The non-transitory computer readable medium of claim 106, wherein the method further comprises correcting the plurality of pairwise matching scores based on a consistency of a given pairwise matching score with a corresponding homozygosity matching score, thereby producing a plurality of corrected pairwise matching scores.
108. The non-transitory computer readable medium of claim 106, wherein the method further comprises assigning the plurality of weights to the plurality of discrete genomic intervals, based on a plurality of identity states for two alleles in two diploid individuals.
109. The non-transitory computer readable medium of claim 108, wherein the plurality of identity states comprises identity states selected from **Table 1**, and wherein the plurality of weights are assigned based on a plurality of contributions to relatedness r_{xy} as listed in **Table 1**.
110. The non-transitory computer readable medium of claim 109, wherein the degree of ancestral relatedness comprises a coefficient of relatedness.
111. The non-transitory computer readable medium of claim 110, wherein the method further comprises calculating the weighted sum over the plurality of discrete genomic intervals of the matched segment, wherein the weighted sum is expressed by:
- $$r_{xy} = \frac{\Delta 1 + \Delta 7 + (0.75 \times \Delta 3) + (0.5 \times \Delta 8)}{L}.$$
112. The non-transitory computer readable medium of claim 109, wherein the degree of ancestral relatedness comprises a coefficient of kinship.

113. The non-transitory computer readable medium of claim 112, wherein the method further comprises calculating the weighted sum over the plurality of discrete genomic intervals of the matched segment, wherein the weighted sum is expressed by:

$$k_{xy} = \frac{\Delta 1 + (0.5 \times (\Delta 3 + \Delta 7)) + (0.25 \times \Delta 8)}{L}.$$

114. The non-transitory computer readable medium of claim 87, wherein estimating the degree of ancestral relatedness between the first individual and the second individual comprises determining a degree of inbreeding of the first individual or the second individual.
115. The non-transitory computer readable medium of claim 87, wherein estimating the degree of ancestral relatedness between the first individual and the second individual comprises determining a degree of inbreeding of the first individual and the second individual.
116. The non-transitory computer readable medium of claim 115, wherein the method further comprises determining a familial relationship between the first individual and the second individual based at least in part on the degree of inbreeding of the first individual and the second individual.
117. The non-transitory computer readable medium of claim 116, wherein the familial relationship is a parent-child relationship, a sibling relationship, an aunt/uncle-nephew/niece relationship, a cousin relationship, or a grandparent-grandchild relationship.
118. The non-transitory computer readable medium of claim 114 or 115, wherein the method further comprises determining an expected degree of inbreeding of a potential offspring of the first individual and the second individual.
119. The non-transitory computer readable medium of claim 118, wherein the method further comprises determining a recommendation indicative of whether or not to breed the first

individual and the second individual together, based on the expected degree of inbreeding of the potential offspring of the first individual and the second individual.

120. The non-transitory computer readable medium of claim 119, wherein the method further comprises determining a recommendation indicative of breeding the first individual and the second individual together, when the expected degree of inbreeding of the potential offspring of the first individual and the second individual does not exceed a pre-determined threshold degree of inbreeding.
121. The non-transitory computer readable medium of claim 119, wherein the method further comprises determining a recommendation indicative of not breeding the first individual and the second individual together, when the expected degree of inbreeding of the potential offspring of the first individual and the second individual exceeds a pre-determined threshold degree of inbreeding.
122. The non-transitory computer readable medium of claim 120 or 121, wherein the pre-determined threshold degree of inbreeding is about 0.10, about 0.15, about 0.20, about 0.25, about 0.30, about 0.35, about 0.40, about 0.45, or about 0.50.
123. The non-transitory computer readable medium of claim 87, wherein the method further comprises generating a social connection between a first person associated with the first individual and a second person associated with the second individual, based at least in part on the estimated degree of ancestral relatedness between the first individual and the second individual.
124. The non-transitory computer readable medium of claim 123, wherein the social connection is generated when the estimated degree of ancestral relatedness between the first individual and the second individual exceeds a pre-determined threshold value.
125. The non-transitory computer readable medium of claim 124, wherein the pre-determined threshold value is about 0.00001, about 0.0001, about 0.001, about 0.01, about 0.02, about 0.04, about 0.06, about 0.08, about 0.1, about 0.12, about 0.14, about 0.16, about 0.18, about 0.2, about 0.25, about 0.3, about 0.35, about 0.4, about 0.45, or about 0.5.

126. The non-transitory computer readable medium of claim 123, wherein the social connection is generated through a social media network.
127. The non-transitory computer readable medium of claim 123, wherein the first person is a pet owner of the first individual, and wherein the second person is a pet owner of the second individual.
128. The non-transitory computer readable medium of claim 87, wherein the method further comprises identifying a familial relationship between the first individual and the second individual based at least in part on the degree of ancestral relatedness.
129. The non-transitory computer readable medium of claim 128, wherein the familial relationship is a parent-child relationship, a sibling relationship, an aunt/uncle-nephew/niece relationship, a cousin relationship, or a grandparent-grandchild relationship.