



- (51) **International Patent Classification:**
G16B 20/40 (2019.01) *G16B 20/10* (2019.01)
- (21) **International Application Number:**
PCT/US2022/036384
- (22) **International Filing Date:**
07 July 2022 (07.07.2022)
- (25) **Filing Language:** English
- (26) **Publication Language:** English
- (30) **Priority Data:**
63/219,349 07 July 2021 (07.07.2021) US
- (71) **Applicant: MARS, INCORPORATED** [US/US]; 6885 Elm Street, McLean, VA 22101 (US).
- (72) **Inventors: GARRIGAN, Daniel;** 18101 SE 6th Way, Vancouver, WA 98683 (US). **HUFF, Jason;** 18101 SE 6th Way, Vancouver, WA 98683 (US). **CHODROFF FORAN, Rebecca;** 18101 SE 6th Way, Vancouver, WA 98683 (US).

KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, WS, ZA, ZM, ZW.

- (84) **Designated States** (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:

— with international search report (Art. 21(3))

- (74) **Agent: LEE, Sandra, S.;** Baker Botts LLP, 30 Rockefeller Plaza, New York, NY 10112-4498 (US).
- (81) **Designated States** (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CV, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IQ, IR, IS, IT, JM, JO, JP, KE,

- (54) **Title:** SYSTEM, METHOD, AND APPARATUS FOR PREDICTING GENETIC ANCESTRY

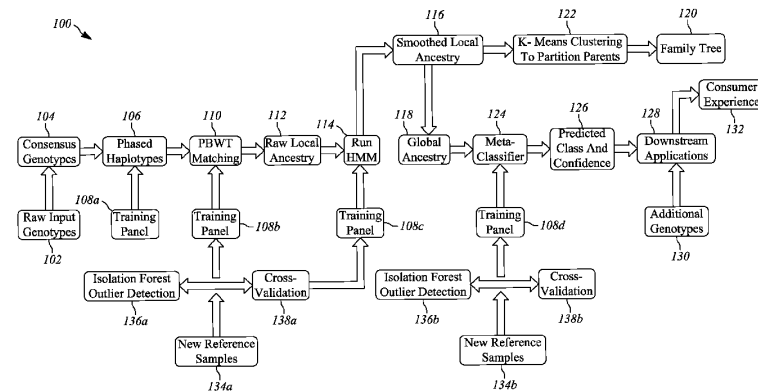


FIG. 1

- (57) **Abstract:** In one embodiment, a method includes accessing a sample of genetic material associated with a first animal, wherein the sample of genetic material comprises raw genotypes, generating phased haplotypes based on the raw genotypes, generating local assignments for genetic populations for the phased haplotypes by machine learning algorithms based on comparisons between the phased haplotypes and a reference panel comprising reference haplotypes associated with reference populations, and sending instructions to a user device for presenting an output associated with the first animal to a user, wherein the output is generated based on the local assignments for the genetic populations.

