



- (51) **International Patent Classification:**
G06F 19/18 (2011.01)
- (21) **International Application Number:**
PCT/US2018/038222
- (22) **International Filing Date:**
19 June 2018 (19.06.2018)
- (25) **Filing Language:** English
- (26) **Publication Language:** English
- (30) **Priority Data:**
62/522,618 20 June 2017 (20.06.2017) US
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- (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, CZ, DE, DJ, DK, DM, DO,

DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JO, JP, KE, 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, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, 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).

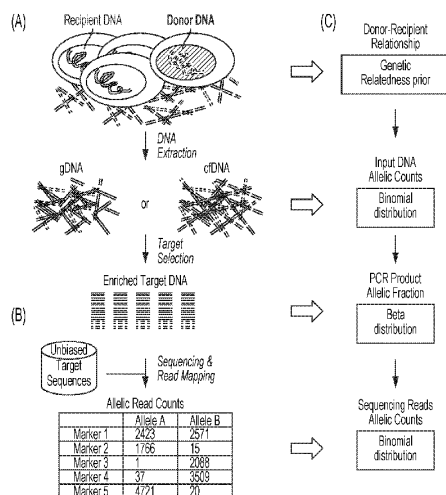
Declarations under Rule 4.17:

- as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))

Published:

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

- (54) **Title:** METHODS FOR ACCURATE COMPUTATIONAL DECOMPOSITION OF DNA MIXTURES FROM CONTRIBUTORS OF UNKNOWN GENOTYPES

**Figure 1**

- (57) **Abstract:** Computer methods and systems for quantifying a nucleic acid sample comprising nucleic acid of one or more contributors to: receive nucleic acid sequence reads obtained from the nucleic acid sample and mapped to alleles at polymorphism loci; determine, using the nucleic acid sequence reads, allele counts for each of the alleles at the polymorphism loci; use a probabilistic mixture model that applies a probabilistic mixture model to the allele counts, and that uses probability distributions to model the allele counts at the polymorphism loci; quantify, using the probabilistic mixture model, one or more fractions of nucleic acid of the one or more contributors in the nucleic acid sample; determine a probability that a specific contributor among the one or more contributors has a specific genotype; and call, based on the posterior probability, that the nucleic acid sample includes nucleic acid from the specific contributor.