Protecting Kinship Privacy in Genomic Databases

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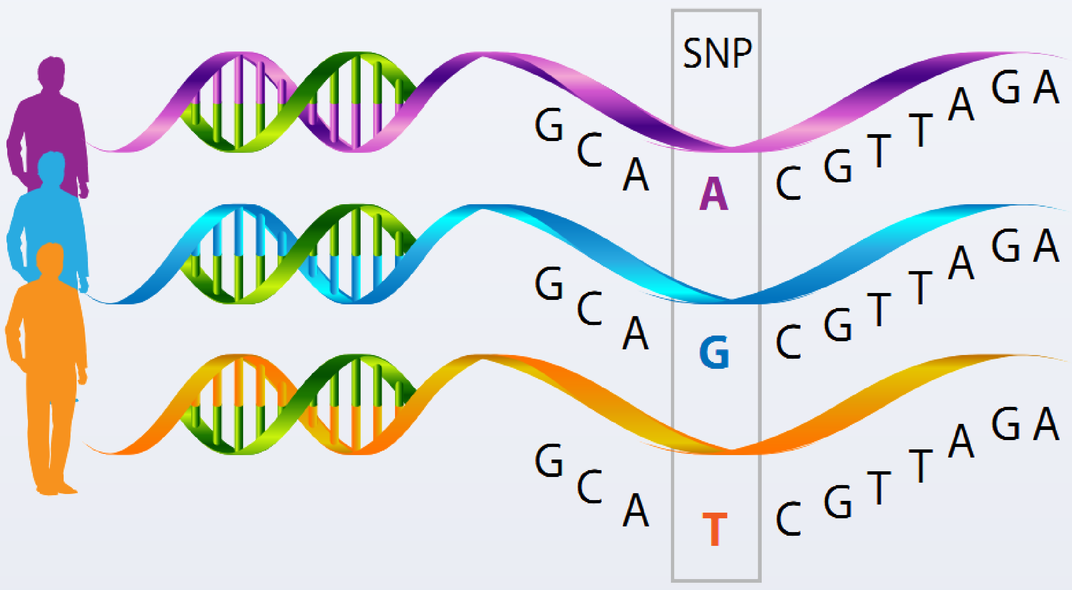
FROM SNPs TO GENOMIC DATABASES



What Makes You Different?

- The human genome sequence is **99.6%** identical in all people.
- SNP (**Single Nucleotide Polymorphism**) is DNA sequence variation occuring when a single nucleotide differs between two or more genomes.
- SNPs make up **0.4%** of the genome.

What is Kinship?

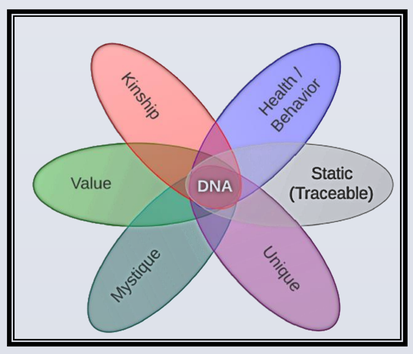
Relationship	Kinship Coefficient
Individual-self	1/2
Siblings	1/4
Parent-offspring	1/4
Grandparent-grandchild	1/8
Uncle/aunt-nephew/niece	1/8
First Cousins	1/16
Half-siblings	1/8

What is KING Coefficient?

$$\phi_{ij} = \frac{2n_{11} - 4(n_{02} + n_{20}) - n_{*1} + n_{1*}}{4n_{1*}}.$$

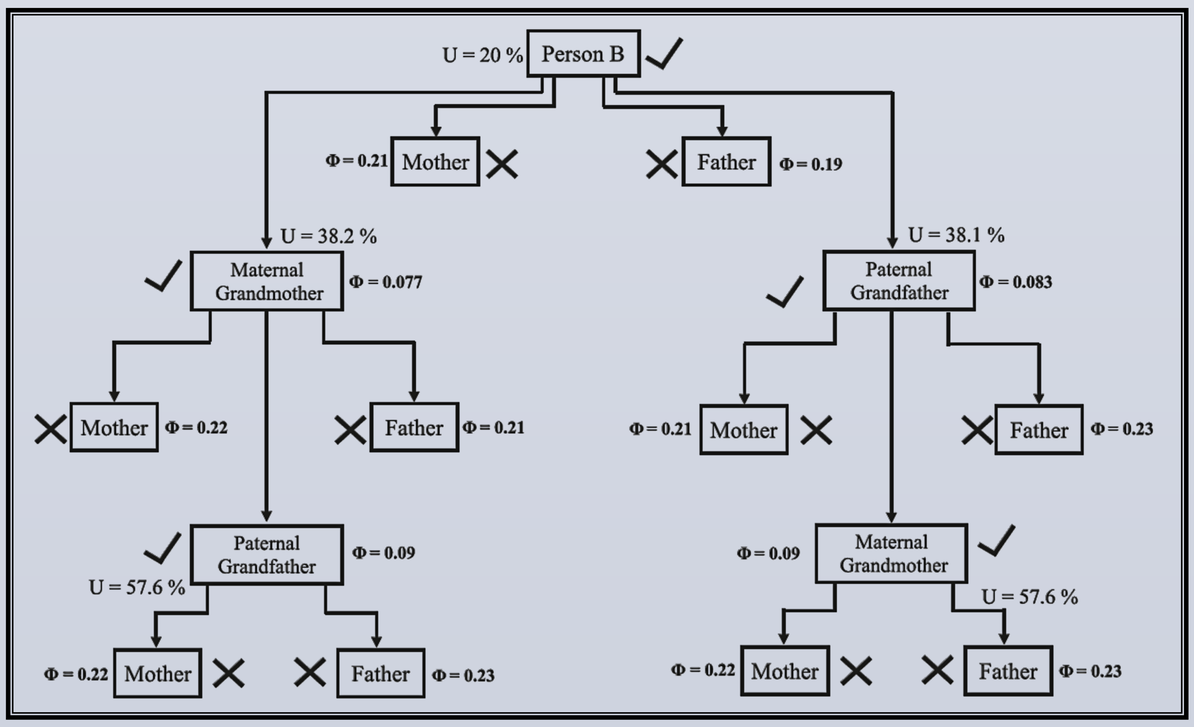
Here, n_{11} is the number of genomic positions that are heterozygous in both individuals, n_{02} is the number of SNPs where the first individual (i) is homozygous dominant and the second individual (j) is homozygous recessive. n_{20} denotes the positions where j is homozygous dominant and i is homozygous recessive. n_{1*} and n_{*1} are the number of SNPs that are heterozygous for individual i and for individual j, respectively.

Genomic Data has:



PURPOSE AND MOTIVATION

- A researcher found out that he had a half-sibling from genomic database:
  - «With genetic testing, I gave my parents the gift of divorce»
- The law enforcement recently tracked (and identified) the Golden State Killer
  - (by using a relative's genomic data in a database)
- Real-life examples led us build a privacy-protection system for **genomic databases**.



METHODOLOGY AND CALCULATIONS

We have a .gds file that contains a matrix of 262178 SNP positions belonging to 1412 people

	Individual 1	Individual 2	Individual 3	Individual n
SNP Position 1	1	0	1	2
SNP Position 2	2	1	1	0
SNP Position 3	0	0	2	1
SNP Position 4	2	1	0	1
SNP Position 5	1	0	2	2
SNP Position 6	0	2	2	1
SNP Position m	1	0	0	0

And this is how we convert the organic bases into 0, 1, 2 whilst creating this .gds file:

SNP Position	Alleles in one Individual	Alleles in the Reference Genome	How Many of the Alleles Changed?
788822	AG	AG	0
788825	GC	CC	1
788829	AA	GG	2

❑ **We focused on the correlation between the missing SNP position and all other SNP positions in the database.**

❑ **We considered the result of the SNP position with the highest correlation coefficient. Max{0,1,2} has been taken and injected into the masked .vcf file of the individual.**

$$r = \frac{\sum_{i=1}^{n}(x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_{i=1}^{n}(x_i - \bar{x})^2}\sqrt{\sum_{i=1}^{n}(y_i - \bar{y})^2}}$$

CONCLUSION

❖ **Since we have the fully revealed file of the firstly added individual,**
❖ **Since we unmasked the masked individual by the calculated values**

❖ **We calculated KING before & after and compared, trying to see whether the kinship has been revealed.**

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