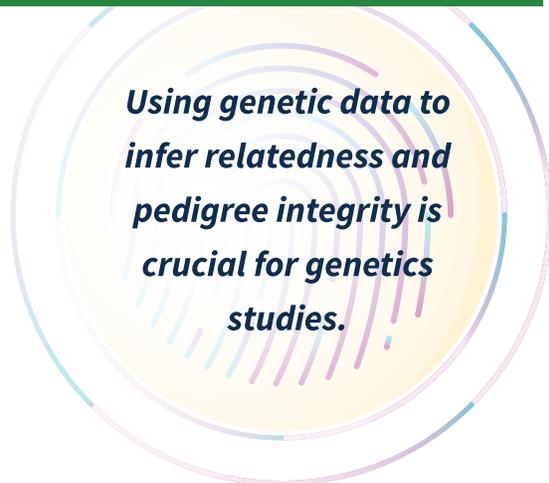


What can GRAF do for you?

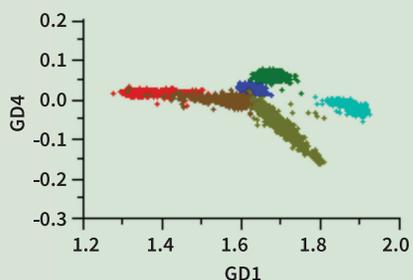
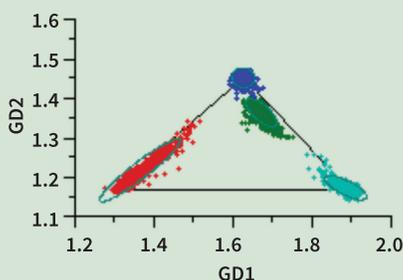
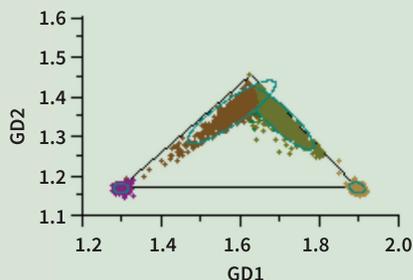
- Free software to quickly find relationships using Single-Nucleotide Polymorphism (SNP) genotype data.
- Validate data in Genome-Wide Association Studies (GWAS).
- Detect closely related samples even when the sets of genotyped markers differ and the DNA strand orientations are unknown.
- Uses All Genotype Mismatch Rate (AGMR) and Homozygous Genotype Mismatch Rate (HGMR) statistical metrics.



How do we compare to other tools?



	GRAF	King 2.0	Principal Components Analysis (PCA)
Process data sets with million samples?	✓	✓	✗
Work with multiple data sets across genotyping methods?	✓	✗	✗
Can plot results to compare genetic relatedness/ancestry against self-reported ones?	✓	✗	✗
Data comparable across genotyping methods?	✓	✗	✗
Work with subjects having high genotype missing rates?	✓	✗	✗
Fast computational speed with large data sets	✓	✓	✗

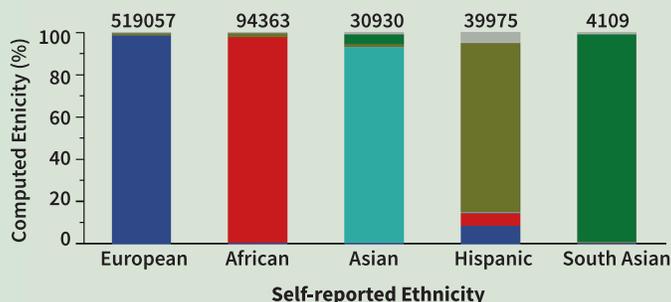


- European
- West African
- Chinese/Japanese
- African American
- Puerto Rican/Dominican
- Mexican/Latino
- Asian
- South Asian

GRAF Plot

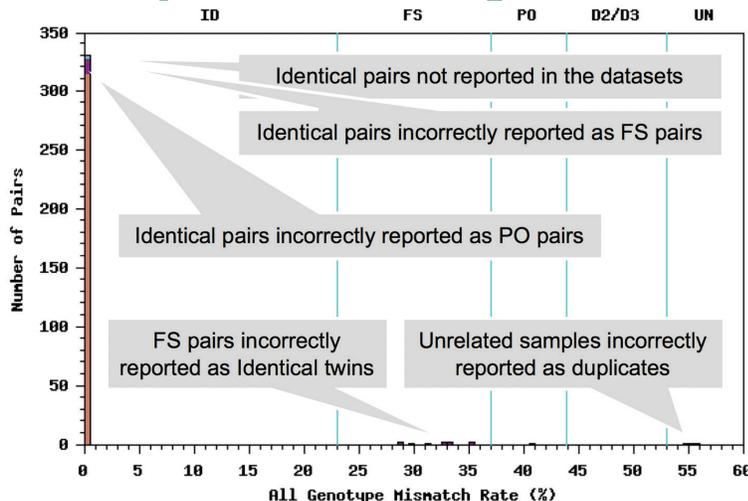
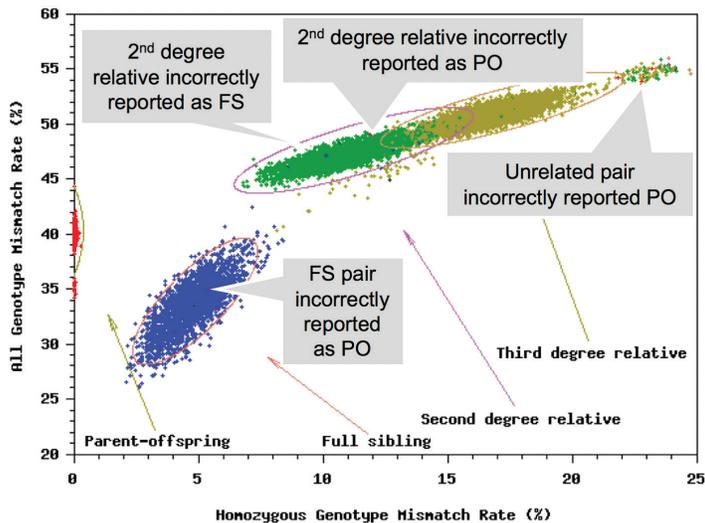
10,000 pre-selected, autosomal biallelic SNPs with high minor allele frequencies to accurately infer subject ancestry in a population

Prediction accuracies of GRAF-pop for continental populations





GRAF to identify identical and closely related samples

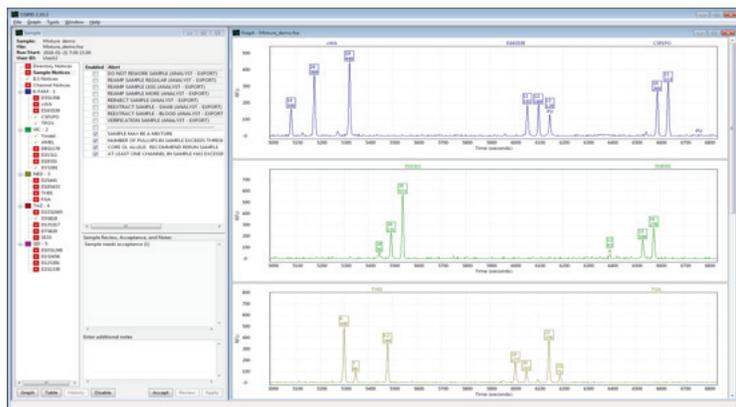


Note: colored bars represent related subjects derived from the pedigree

DP MT PO FS D2 D3 UN

GRAF can be used to find identical pairs (duplicate samples or identical twins) that are not reported or incorrectly reported in the submitted datasets

GRAF finds closely related subjects not reported or incorrectly reported in the pedigree file



OSIRIS for human identification

OSIRIS was created out of a collaboration with the Kinship and DNA Analysis Panel (KADAP) by the U.S. Department of Justice, state, local and federal forensic laboratories, and National Institute of Standards and technology (NIST), to assist the New York City Office of the Medical Examiner (OCME) and New York State Police (NYSPP) DNA laboratories in the difficult and unprecedented legal and humanitarian challenges the World Trade Center victim identification.

OSIRIS at a glance

- ▲ Fast STR analysis – over 11,000 samples per hour.
- ▲ Used in over 39,000 analyses last year
- ▲ MHL analyzed 5000 transplant samples last year
- ▲ Increased efficiency saved MHL 3-4 weeks of analyst time
- ▲ Reduces editing of profiles by as much as 95%
- ▲ Sensitive – detect as little as 1% of minor profile in a mixture

