Kinship and Relatedness

ML-Relate

Basics
Download: http://www.montana.edu/kalinowski/ML-Relate/ML-Relate_Home.htm
Operating system: Windows 98 or higher
File format: GENEPOP
Data type: codominant data (microsatellites, SNPs, allozymes)

Background
ML-Relate estimates relatedness (r) via the downhill simplex routine and can also estimate relationships. Null microsatellite alleles may be accommodated.

Instructions
1. Open file
    a. <File>→<Open>
    b. Select GENEPOP file

   Your data should appear in the window
2. Confirm data
    a. <Summary>→*one of four options*
        i. <Sample sizes>
           Total number of alleles sampled per population per locus
        ii. <Number of alleles>
           Number of different alleles per locus
        iii. <Allele frequencies OBSERVED>
           Frequency of each allele
        iv. <Expected heterozygosity>
           Nei's (1978) unbiased estimate of expected heterozygosity
3. Test for null alleles
    a. <Nulls>→<Hardy-Weinberg test for excess homozygotes>
    b. Enter number of randomizations

   Returns a P value for heterozygote deficiency of each locus
4. Designate null alleles
    a. <Nulls>→<Specify which loci have null alleles>
    b. Check the boxes corresponding to the loci with null alleles
5. Retest allele frequencies with the null alleles
    a. <Nulls>→<Estimate allele frequencies with NULL allele PRESENT>

   Note that now the loci designated as containing null alleles contain an extra null allele
6. Estimate relatedness
    a. <Relatedness>→*one of three output options*
        i. Matrix
        ii. List
        iii. Two specific individuals

   This will provide the estimates of r

7. Estimate relationship
    a. <Relationship>→<Estimate relationship>→*one of three output options*
        i. Matrix
        ii. List
            Will also provide the log-likelihood for each of the relationship possibilities
            Excluded relationships are designated 9999
        iii. Two specific individuals

    This will provide the relationship with the highest probability between each individual in the population

    U = unrelated
    HS = half sibling
    FS = full sibling
    PO = parent offspring
8. Confidence sets
    a. <Relationship>→<Confidence sets>
    b. Enter number of randomizations

    Returns a list of all relationships that are consistent with the data
9. Specific hypothesis testing
    a. <Relatinoship>→<Specific hypothesis test>
    b. Select the two individuals you would like to test
    c. Select the putative relationship
    d. Select the alternative relationship
    e. <OK>
    f. Enter number of randomizations

    Returns the P value for the relationship hypothesis (if p is small, the putative relationship fits the data better than the alternative)

References

Blouin MS (2003) DNA-based methods for pedigree reconstruction and kinship analysis

Milligan BG (2003). Maximum-likelihood estimation of relatedness. *Genetics* **163:** 1153-1167.

Wagner AP, S Creel, ST Kalinowski (2005) Estimating relatedness and relationships using microsatellite loci with null alleles. *Heredity*, (Accepted pending revision**).**

Weir BS, AD Anderson, AB Helper (2006) Genetic relatedness analysis: modern data and new challenges. *Nature Review Genetics* **7**: 771-780.