Discussion. Repetition

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Various topics

- Exercises. Videos
- Combining Y and autosomal markers?
- Individual or joint test?
- Database searches – random matches?
- Mixtures and relatives
- Mixtures: conditioning

Exercises. Discussion

- Mixture exercises
- Relationship testing
  - Videos
    http://arken.umb.no/~theg/book/Familiasvideos.pdf

Familias videos (English and Spanish)

Thore Egeland and Manuel García Magariños
May 23, 2014

Execercise 9 Familias 3

Title: Exercise9Familias3
Description: Description Not Provided.
Duration: 0:11:26

Type	Size	Link
PC (Flash)	20.9 MB	View...
Nettbrett	17.2 MB	View...
Mobil	9.64 MB	View...
Lyd (MP3)	6.58 MB	View...

Combining autosomal and Y?

4. Two individuals, GF and GS, are submitted to the laboratory for testing. We consider the hypotheses

   H_1 : GF is the grandfather of GS.

   H_2 : The individuals GF and GS are unrelated.

   Figure 4 shows the pedigree corresponding to H_1 for the first marker (D3S1358).

   a) Enter the data manually into Familias and calculate the LR for the first marker shown in Figure 4. The allele frequencies are 14: 0.122; 15:0.258;17:0.197

   b) Calculate the LR based on all markers. Read input from the file ExS4.fam.

   c) For the discussion: Formulate a conclusion. In the CAP exercise it was stated that GF and GS share the same Y-haplotype and that the frequency of this haplotype is 0.0025. Can this information be used?

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Forensic Science International: Genetics

Article in Press

Combining autosomal and Y chromosome match probabilities using coalescent theory

Buckleton and Myers

Individual or joint test?

ADVANCED LEVEL FORM 2014

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INTERCOMPARISON PROGRAM

"ANALYSIS OF DNA POLYMORPHISMS IN BLOODSTAINS AND OTHER BIOLOGICAL SAMPLES"

ADVANCED LEVEL EXERCISE EIADN Nr 22 (2014) DEADLINE: 12-05-2014

4. Kinship paper challenge

4.1. Approach

- A pregnant woman and her husband live in Madrid. They decide to move for work to Quito leaving the two elder children in Madrid .Once in Quito, their third child, a girl, is born. Shortly after her husband dies and she decides to go back to Madrid where her fourth child, another girl, is born.
- After a quarrel due to their father's legacy , both elder children decide to challenge the paternity of their little daughters, but there is no genetic material as their father's body has been cremated.
- STR analyses of the four children and the mother are carried out in order to establish if the little girls share the same biological father with the elder children.
  Results obtained are displayed in the following table.

Table of profiles

Marker	Mother	Child 1	Child 2	Child 3	Child 4
D8S1179	10/11	10/14	10	10/14	11/14
D21S11	31.2	29/31.2	31.2/32.2	29/31.2	29/31.2

4.2_Calculate the paternity index (PI) for each of the girls for every shadowed marker (the rest of markers are only informative). Indicate the hypotheses and the population used.

Notes:

Data base searches - interpretation

Analysis of matches and partial-matches in a Danish STR data set

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Abstract: Over the recent years, the national databases of STR profiles have grown in size due to the success of forensic DNA analysis in solving crimes. The accumulation of DNA profiles implies that the probability of a random match or near match of two randomly selected DNA profiles in the database increases.

We analysed 53,295 STR profiles from individuals investigated in relation to crime case investigations at the Department of Forensic Medicine, Faculty of Health Sciences, University of Copenhagen, Denmark. Incomplete STR profiles (437 circa 0.8% of the total), 48 redundant STR profiles from monozygotic twins (0.09%), 6 redundant STR profiles of unknown cause and 1283 STR profiles from repeated testing of individuals were removed leaving 51,517 complete 10 locus STR profiles for analysis. The number corresponds to approximately 1% of the Danish population. We compared all STR profiles to each other, i.e. 1.3×10^9 comparisons.

With these large number of comparisons, it is likely to observe DNA profiles that coincide on many loci, which has concerned some commentators and raised questions about "overstating" the power of DNA evidence. We used the method of Weir [11,12] and Curran et al. [3] to compare the observed and

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Mixtures with relatives: A pedigree perspective

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