

The Weight of Evidence

Likelihood Ratios in Forensic Statistics

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Scope of the workshop

This workshop is not intended to provide an exhaustive introduction to forensic statistics.

Its aim is to:

- ▶ introduce some fundamental ideas for evaluating forensic evidence;
- ▶ illustrate them through selected examples and real cases;
- ▶ highlight the role of assumptions, propositions and statistical models;
- ▶ provide insights and questions for further reflection.

Main goal

The aim is not to cover every topic, but to provide a starting point and encourage further curiosity about forensic statistics.

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Introduction

- ▶ A trial starts with uncertainty
- ▶ As the trial progresses, new information becomes available
- ▶ Our uncertainty therefore changes throughout the trial: it may decrease, but it does not necessarily decrease in a steady way
- ▶ The hope is that, by the end of the trial, the remaining uncertainty will be small enough to support a decision.
- ▶ This changing uncertainty lies at the heart of legal reasoning.

Evidence is used to assess how plausible the competing explanations appear.

The role of probability and statistics

- ▶ Probability gives us a language for representing uncertainty.
- ▶ Statistics gives us methods for learning from data and for assessing how evidence should change that uncertainty.
- ▶ Neither probability nor statistics decides whether a defendant is guilty.
- ▶ Their role is to make the reasoning about uncertain evidence more explicit, more coherent, and open to criticism.
- ▶ This leads to the central question of this workshop:

How should we measure the change produced by one or more piece of forensic evidence?

The likelihood ratio

The likelihood ratio provides one possible answer

- ▶ How probable the observed evidence would be under one proposition compared with another.
- ▶ It measures the direction and the strength of the change produced by the evidence, while keeping the scientific assessment separate from the final legal decision.
- ▶ The likelihood ratio framework is valid for all kind of scientific evidence.

Let see it more in details:

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An example

- ▶ A bloodstain is found at a crime scene.
- ▶ Blood type matches the defendant's blood type.
- ▶ Only 1% of the relevant population has this type.

How should we interpret this match?

A prosecutor might argue as follows: “The probability of observing this blood type if someone else left the stain is only 0.01. Therefore, the probability that someone else left the stain is 0.01. We can therefore be 99% certain that the defendant was the source.

This might sound plausible **but it's wrong**.

An example

- ▶ A bloodstain is found at a crime scene.
- ▶ blood type matches the defendant's blood type
- ▶ one per cent of the relevant population has this type.

How should we interpret this match?

The defence may also reason incorrectly:

“In a population of 10 millions persons, there are a hundred of thousands of people with this blood type. Therefore, the probability that the defendant left the stain is only one in a hundred thousand.”

An example

The two arguments reach opposite conclusions, but make a similar mistake. Both attempts to move directly from the rarity of the evidence to the probability of a hypothesis.

The problem is that they ask the forensic evidence to answer a question that it cannot answer by itself: **“What is the probability that the defendant left the stain?”**

The likelihood ratio paradigm begins with a different and more limited question:

“How probable are these findings under each of the competing explanations?”

This example shows that we need a disciplined way to interpret scientific findings.

The likelihood ratio: the three principles of interpretation

The three principles of forensic evidence interpretation were explicitly formulated by Evett et al. (2000), building on the case assessment and interpretation framework introduced by Cook et al. (1998b).

- ▶ **I principle: interpretation must take place within a framework of circumstances.**

Scientific findings cannot be interpreted in isolation. We need to know what question the expert has been asked, how the evidence was collected, and which background information is being treated as given.

- ▶ **II principle: interpretation requires at least two competing propositions.**

The evidence cannot support a proposition in absolute terms. It can only support one proposition relative to another. Changing the alternative proposition may change the value of the evidence

- ▶ **III principle: the expert must consider the probability of the findings given each proposition**

The relevant questions are therefore: $\Pr(E \mid H_p, I)$ and $\Pr(E \mid H_d, I)$. The expert should not reverse these probabilities and directly assess $\Pr(H_p \mid E, I)$.

The likelihood ratio framework

These three principles give us the structure of the evaluation. They mention

- ▶ The evidence E ,
- ▶ The framework of circumstances I
- ▶ The two competing propositions, H_p and H_d .

How should we combine the two conditional probabilities?

Bayes' theorem, in odds form provides the answer:

$$\frac{\Pr(H_p | E, I)}{\Pr(H_d | E, I)} = \frac{\Pr(E | H_p, I)}{\Pr(E | H_d, I)} \times \frac{\Pr(H_p | I)}{\Pr(H_d | I)}$$

$$\text{posterior odds} = \text{LR} \times \text{prior odds}$$

The likelihood ratio framework

$$\frac{\Pr(H_p | E, I)}{\Pr(H_d | E, I)} = \frac{\Pr(E | H_p, I)}{\Pr(E | H_d, I)} \times \frac{\Pr(H_p | I)}{\Pr(H_d | I)}$$

The LR measures how the evidence changes the relative odds of the two propositions.

- ▶ If $LR > 1$, the evidence supports H_p rather than H_d .
- ▶ If $LR < 1$, it supports H_d rather than H_p .
- ▶ If $LR = 1$, the evidence does not discriminate between them.

An LR of 100 means that the findings are one hundred times more probable under H_p than under H_d .

An LR of 0.01 expresses the same strength in the opposite direction.

The likelihood ratio framework

The likelihood ratio is therefore not an arbitrary convention: it follows naturally when we combine the three principles of forensic interpretation with Bayesian updating.

This also gives us a useful distinction between two questions:

The scientist asks: “How probable are the findings under each proposition?”

The court must ultimately ask: “How plausible are the propositions after considering all the evidence?”

From LR to Weight of Evidence

The likelihood ratio can span many orders of magnitude:

It is often convenient to express it on a logarithmic scale, the so-called *weight of evidence* (Good, 1950):

$$W = \log_{10}(LR).$$

- ▶ $W > 0$: the evidence supports H_p over H_d ;
- ▶ $W = 0$: the evidence does not discriminate between them;
- ▶ $W < 0$: the evidence supports H_d over H_p .

LR	$\log_{10}(LR)$	Interpretation
1,000	3	Supports H_p
1	0	Neutral
0.01	-2	Supports H_d

A key advantage is additivity. For conditionally independent evidence:

$$LR_{\text{combined}} = LR_1 LR_2 \implies W_{\text{combined}} = W_1 + W_2.$$

Historical notes

- ▶ Before the introduction of the LR framework, forensic results were often communicated through categorical conclusions such as “identification” or “exclusion”, or qualitative expressions such as “consistent with”.
- ▶ In other cases, experts reported only the frequency of a characteristic in a population.
- ▶ The mathematical foundations of Bayesian forensic statistics can be found in the work of I. J. Good, who interpreted the ratio between the probabilities of the evidence under two hypotheses as a measure of the weight of evidence.

Historical notes

- ▶ In the 1970s, Dennis Lindley brought this reasoning into forensic science (Lindley, 1977). It clearly stated that the scientist's task was not to calculate the probability that a person was guilty, but to assess how much more probable the observed findings were under one proposition than under another.
- ▶ During the 1980s, Ian Evett and other forensic statisticians began to translate this principle into a methodology that could be applied in caseworks ((Evett et al., 2000), (Cook et al., 1998a)).
- ▶ The expansion of forensic DNA analysis since the 1990s made this approach particularly important.
- ▶ In the following years, the use of LR extended beyond DNA and was incorporated into professional guidelines, particularly in Europe (European Network of Forensic Science Institutes, 2015).
- ▶ LR methods are highly developed in forensic genetics, while qualitative or categorical evaluations continue to be used in other forensic disciplines.

Why Bayesian rather than frequentist?

- ▶ A trial concerns a specific event that has already happened. The uncertainty is epistemic and arises from our incomplete knowledge of that event.
- ▶ A strictly frequentist interpretation, in which probability describes the long-run behaviour of repeatable experiments, cannot work.
- ▶ The Bayesian framework allows sequential updating, when new evidence becomes available, the posterior assessment based on the earlier evidence becomes the new starting point
- ▶ However, forensic science does not reject frequentist methods, useful for estimating population frequencies, measuring error rates and validating laboratory procedures.

Likelihood ratios and Bayes factors

, the updating framework is Bayesian but a LR calculated using fixed parameter estimates is not necessarily Bayesian.

- When uncertainty about the parameters is represented by probability distributions and integrated into the calculation, the resulting quantity is more precisely a *Bayes factor*.

Likelihood ratio: fixed parameter values

$$\text{LR}(\theta; E) = \frac{f(E \mid \theta, H_p, I)}{f(E \mid \theta, H_d, I)}.$$

Bayes factor: parameter uncertainty integrated out

$$\text{BF}(E) = \frac{\int_{\Theta_p} f(E \mid \theta_p, H_p, I) \pi_{\text{Pr}}(\theta_p \mid H_p, I) d\theta_p}{\int f(E \mid \theta_d, H_d, I) \pi_d(\theta_d \mid H_d, I) d\theta_d}.$$

Hierarchy of propositions

The second principle of interpretation says that there must be two competing propositions, in Cook et al. (1998a) the authors propose a hierarchy of the competing propositions as follows:

- ▶ Sub-source level
- ▶ Source level
- ▶ Activity level
- ▶ Crime level

Let's see some example.

Hierarchy of propositions

Table: Examples of propositions

Level	Generic	Examples
III	Offence	A Mr A committed the burglary Another person committed the burglary
		B Mr B raped Ms Y Some other man raped Ms Y
		C Mr C assaulted Mr Z Mr C had nothing to do with the assault of Mr Z
II	Activity	A Mr A is the man who smashed window X Mr A was not present when window X was smashed
		B Mr B had sexual intercourse with Ms Y Some other man had sexual intercourse with Ms Y
		C Mr C is the man who kicked Mr Z in the head Mr C was not present at the kicking of Mr Z
I	Source	A The glass fragments came from window X They came from some other broken glass object
		B The semen came from Mr B The semen came from some other man
		C The blood on Mr C's clothing came from Mr Z The blood on Mr C's clothing came from an unknown person

Hierarchy of propositions: sub-source level

- ▶ Sub-source evaluation asks whose DNA is present, without addressing the type of biological material:
 - ▶ H_p : the DNA came from the defendant
 - ▶ H_d : the DNA came from an unknown unrelated person.
- ▶ It is necessary to have a DNA trace to address this level
- ▶ This level got most of the methodological attention and is now relatively well established
- ▶ Current research increasingly focuses on activity-level propositions, that is developing rapidly, but it remains less mature and less standardized than sub-source evaluation.

Moving Up the Hierarchy

Source and sub-source level

- ▶ Focus on the origin of a trace.
- ▶ Usually require limited contextual information.
- ▶ May produce very large likelihood ratios.
- ▶ However, they do not explain *how* or *when* the material was deposited.
- ▶ It is necessary to recover a trace.

Whose DNA is it?

Activity level

- ▶ Addresses questions that are more directly relevant to the case.
- ▶ Requires additional information about transfer, persistence, recovery and background levels.
- ▶ May also require witness statements and other circumstantial information.
- ▶ The absence of evidence is also informative.

How did the DNA get there?

Hierarchy of propositions: Crime level

- ▶ Crime-level propositions concern whether the defendant committed the crime
- ▶ Depend on all the evidence in the case and are generally outside the role of the forensic scientist.
- ▶ The level matters because the same findings can have different values at different levels.
- ▶ A large sub-source LR should not automatically be interpreted as equally strong evidence about the activity or the offence.

Exclusive not exhaustive propositions

The competing propositions must be mutually exclusive and should preferably be exhaustive. This latter is not compulsory, but when the propositions are both mutually exclusive and exhaustive:

- ▶ LR can be converted into $\Pr(H_p \mid E, I)$, and vice versa:

$$\Pr(H_p \mid E) = \frac{LR \times o}{1 + LR \times o}$$

where $o = \frac{\Pr(H_p|I)}{\Pr(H_d|I)}$ is the prior odds

- ▶ An LR greater than 1 tells us that the evidence is more probable under H_p than under H_d . It also implies that observing E increases the probability of H_p and decreases the probability of H_d .

Example

Suppose there are three mutually exclusive and exhaustive propositions:

$$H_p, \quad H_d, \quad H_o,$$

where h_o represents an explanation not included in the original comparison.

Assume the prior probabilities are

$$\Pr(H_p) = 0.40, \quad \Pr(H_d) = 0.40, \quad \Pr(h_o) = 0.20.$$

Suppose that

$$\Pr(E | H_p) = 0.20, \quad \Pr(E | H_d) = 0.10, \quad \Pr(E | h_o) = 0.90.$$

Comparing only H_p and H_d gives

$$LR_{p,d} = \frac{0.20}{0.10} = 2 > 1.$$

Thus, the evidence favours H_p over H_d .

Does $\Pr(H_p)$ Increase?

The total probability of the evidence is

$$\begin{aligned}\Pr(E) &= \Pr(E \mid H_p) \Pr(H_p) + \Pr(E \mid H_d) \Pr(H_d) \\ &\quad + \Pr(E \mid h_o) \Pr(h_o) \\ &= (0.20)(0.40) + (0.10)(0.40) + (0.90)(0.20) \\ &= 0.30.\end{aligned}$$

Therefore,

$$\Pr(H_p \mid E) = \frac{(0.20)(0.40)}{0.30} = 0.267.$$

Although

$$LR_{p,d} = 2 > 1,$$

the probability of H_p decreases:

$$\Pr(H_p) = 0.40 \longrightarrow \Pr(H_p \mid E) = 0.267.$$

The Role of Exhaustiveness

Why?

In the example, the evidence supports h_o much more strongly than either H_p or H_d . It increases the relative odds of H_p against H_d , while shifting probability mass towards the omitted proposition h_o .

- ▶ If H_p and H_d are mutually exclusive and exhaustive,

$$LR > 1 \implies \Pr(H_p | E) > \Pr(H_p).$$

- ▶ If they are mutually exclusive but not exhaustive,

$$LR > 1 \implies \frac{\Pr(H_p | E)}{\Pr(H_d | E)} > \frac{\Pr(H_p)}{\Pr(H_d)},$$

but $\Pr(H_p | E)$ may increase or decrease.

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Fallacy of the transposed conditional

In simple examples, it is easy to see that

$$\Pr(A \mid B) \neq \Pr(B \mid A).$$

For example, let

- ▶ A : the animal is an elephant;
- ▶ B : the animal has four legs.

In forensic contexts, it is much easier to confuse these two conditional probabilities.

Prosecutor fallacy

Imagine that a DNA trace has been retrieved on the crime scene. Let E_c be the event describing the observation of its profile.

Consider the following propositions:

- ▶ H_p : the suspect left the trace;
- ▶ H_d : another person left the trace.

Suppose that:

$$\Pr(E_c \mid H_d) = \gamma = \frac{1}{1000}.$$

Prosecutor fallacy

$$\Pr(E_c \mid H_d) = \gamma = \frac{1}{1000}.$$

The correct statement would be:

The probability of observing this profile if the trace was left by someone other than the suspect is one in one thousand.

An incorrect statement is:

The probability that the profile was left by someone other than the suspect is one in one thousand.

The incorrect statement replaces $\Pr(E_c \mid H_d)$ with $\Pr(H_d \mid E_c)$.

It may then lead to the further incorrect conclusion that

$$\Pr(H_p \mid E_c) = \frac{999}{1000}.$$

The LR version of the prosecutor fallacy

Suppose that $LR = 100$.

The following statement is incorrect:

The proposition H_p is 100 times more probable than H_d .

The correct interpretation is:

The observed evidence is 100 times more probable under H_p than under H_d .

Formally,

$$\frac{\Pr(E \mid H_p, I)}{\Pr(E \mid H_d, I)} \neq \frac{\Pr(H_p \mid E, I)}{\Pr(H_d \mid E, I)}.$$

The relationship between the two quantities is

$$\frac{\Pr(H_p \mid E, I)}{\Pr(H_d \mid E, I)} = LR \frac{\Pr(H_p \mid I)}{\Pr(H_d \mid I)}.$$

If the prior odds are equal to one, the posterior odds are numerically equal to the LR.

The defence attorney fallacy

Suppose that:

- ▶ a profile found at the crime scene has population frequency 1/1000;
- ▶ the relevant population contains 100 000 people.

An incorrect argument is:

There must be 100 people with this profile. The suspect is only one of these 100 people, so the probability that the suspect is the source is 1/100.

This reasoning contains two problems.

First, 100 is the expected number of people with the profile:

$$\mathbb{E}(Y) = 100\,000 \times \frac{1}{1000} = 100.$$

The defence attorney fallacy

If $Y \sim \text{Binomial}\left(100\,000, \frac{1}{1000}\right)$,
then the actual number of people with the profile is uncertain
($\Pr(81 < Y < 121) = 0.95$).

Second, the argument assumes that all people with that DNA profile have the same prior probability of being the source. It ignores information such as age, sex, location, opportunity and alibi.

The number of people expected to share a profile does not, by itself, determine the posterior probability that the suspect is the source.

People vs. Collins

Practical exercise 1.

Lessons from the Collins' case

The Collins case shows very clearly that:

- ▶ multiplying probabilities is valid only if the individual probabilities are empirically supported and their dependence structure is correctly modelled;
- ▶ the frequency of a set of characteristics is not the probability that the defendants are innocent or guilty;
- ▶ the relevant population must be explicitly defined;
- ▶ witness reliability and uncertainty in the reported description are part of the probabilistic model;
- ▶ the procedure used to select the characteristics and the suspects can affect the value of the evidence;
- ▶ a rare combination of characteristics does not imply that the matching couple is unique;
- ▶ an impressive numerical result can be mathematically correct under its assumptions, but still answer the wrong forensic question.

Supreme court vs O.J.Simpson

Practical Exercise 2

Lessons from the Simpson's case

The Simpson case clearly illustrates that:

- ▶ a frequency is not a probability of guilt;
- ▶ a likelihood ratio must always refer to two explicitly defined competing propositions;
- ▶ the value of the evidence changes when moving from the source level to the activity level;
- ▶ the relevant population, the number of contributors and operational errors are part of the statistical model;
- ▶ very large numbers may correctly answer a narrow question, but become misleading when used to answer a different one.

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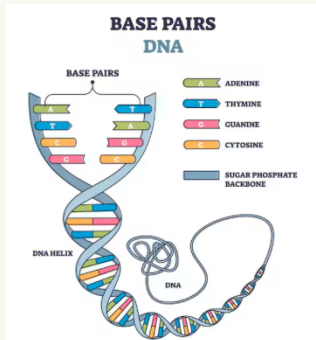
What Does a Forensic DNA Profile Measure?

DNA can be represented as a very long sequence written with four letters:

A, C, G, T.

The human genome contains approximately three billion letters in each copy.

- ▶ Most DNA is shared by all humans.
- ▶ A smaller part varies between individuals.



A DNA Profile Is Not the Whole Genome

A traditional forensic profile examines a limited number of preselected positions in the DNA, known to be polymorphic.

Locus

A locus is a particular position or region of the genome.

A forensic profile records the **values** observed at each selected locus:

$$\text{profile} = (\text{genotype at locus } 1, \dots, \text{genotype at locus } k).$$

A match means that the same values were observed at all the loci examined. It does not mean that every DNA base was compared.

But what values?

STR Loci and Alleles

Many forensic loci are **Short Tandem Repeats**, or STRs.
At an STR locus, a short DNA sequence occurs repeatedly:

GATA GATA GATA ...
a variable number of repetitions

Different numbers of repetitions define different **alleles**.
An allele is one possible version observed at a locus.

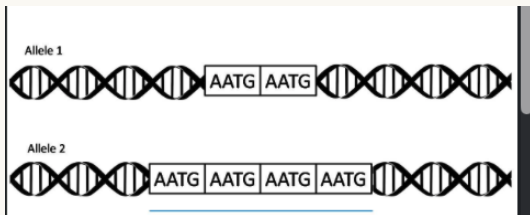


Figure: STR loci

STR loci

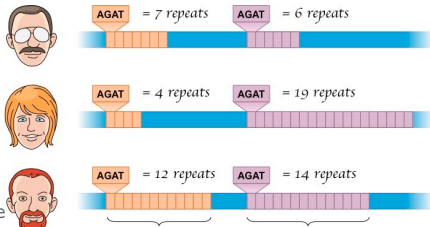
At an autosomal locus, a person normally has two alleles.

The genotype is written as (A, B) , the order does not matter:

- ▶ (A, B) is a heterozygous genotype.
- ▶ (A, A) is a homozygous genotype.

$$(A, B) = (B, A).$$

The labels A and B represent STR repetitions at the locus. They do not represent the DNA bases adenine and thymine.



Different People Can Have the Same Profile

At a specific locus, the same allele may be shared by many people in the population. Two people may therefore have the same observed allele because:

1. they inherited copies from a common ancestor, or
2. the allele is present in both family lines by chance.

The probability of matching alleles decreases with the number of loci analyzed in the profile increase.

Anyway

A DNA-profile match does not, by itself, identify one unique person.

More Loci, Rarer Matching Profiles

Evolution of forensic DNA systems

Period	System
1980s	Early DNA fingerprinting used VNTR band patterns, not a fixed panel of STR loci.
UK, 1995	SGM: 6 STR loci, plus a sex marker.
UK, late 1990s	SGM Plus: 10 STR loci, plus a sex marker.
UK, since 2014	DNA-17: 16 STR loci, plus a sex marker.
USA, 1997–2016	CODIS: 13 core STR loci.
USA, since 2017	CODIS: 20 core STR loci.

Many loci provide high discrimination

With a complete profile based on many informative STR loci, the probability that an unrelated person has the same profile can be extremely small.

Profile frequency and random match probability

Throughout this workshop, we will often use the approximation

$$\Pr(G_c = G_s \mid H_d, I) = \gamma,$$

where γ is the frequency of the suspect's DNA profile in the relevant population. In words, we assume that the probability that an alternative donor matches the suspect is equal to the population frequency of the profile.

This is a useful simplification, but it is not always valid.

- ▶ The alternative donor may be genetically related to the suspect.
- ▶ The relevant population may have substructure.
- ▶ Allele frequencies are estimated and therefore uncertain.
- ▶ The profile may be partial or mixed.
- ▶ Laboratory errors may produce false matches or false exclusions.

More generally, the denominator of the LR is

$$\Pr(G_c = G_s \mid H_d, G_s, I),$$

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The Island Problem: One Trace, Many Suspects, Only One Profiled

Background information I :

- ▶ A crime is committed on a remote island with $N + 1$ inhabitants.
- ▶ No one has arrived or left during the last few days.

Evidence E :

- ▶ A recovered saliva trace has profile Γ .

Source-level propositions:

- ▶ H_p : the suspect left the trace.
- ▶ H_d : someone else on the island left the trace.

Let γ be the probability that a randomly selected person on the island has profile Γ .
Assume that γ is known.

The Island Problem: One Trace, Many Suspects, Only One Profiled

This example is useful because it removes the problem of defining the relevant population.

Simple case:

- ▶ All inhabitants, including the suspect, have the same prior probability of being the offender:

$$\Pr(H_p | I) = \frac{1}{N+1}, \quad \Pr(H_d | I) = \frac{N}{N+1}.$$
$$\frac{\Pr(H_p | I)}{\Pr(H_d | I)} = \frac{\frac{1}{N+1}}{\frac{N}{N+1}} = \frac{1}{N}.$$

Therefore, the prior odds are

$$\frac{\Pr(H_p | I)}{\Pr(H_d | I)} = \frac{1}{N}.$$

From the theory of a single-trace match, in the absence of laboratory errors, if

The Island Problem

Consider the posterior odds:

$$\underbrace{\frac{\Pr(H_p | E_s, E_c, I)}{\Pr(H_d | E_s, E_c, I)}}_{\text{posterior odds}} = \underbrace{\frac{\Pr(E_s, E_c | H_p, I)}{\Pr(E_s, E_c | H_d, I)}}_{\text{likelihood ratio}} \underbrace{\frac{\Pr(H_p | I)}{\Pr(H_d | I)}}_{\text{prior odds}}$$
$$= \frac{1}{\gamma} \frac{1}{N} = \frac{1}{N\gamma}.$$

The posterior probability of H_p is therefore

$$\Pr(H_p | E_s, E_c, I) = \frac{1}{N\gamma + 1}.$$

Two interesting cases:

- ▶ If $\gamma = 1/N$.
- ▶ If $\gamma = 1$.

Even though the profile is rare when $\gamma = 1/N$, the probability that the suspect left the trace is only 50%.

The Island Problem: Extended Version

The previous example relies on the assumptions that:

- ▶ Every person has the same probability of having left the trace¹;
- ▶ $\Pr(E_c \mid E_s, H_d) = \Pr(E_c \mid H_d) = \gamma$ for every inhabitant.

For example, suppose that the suspect has a brother who lives on the island. This would invalidate the approximation

$$\Pr(E_c = \Gamma \mid E_s = \Gamma, H_d, I) = \Pr(E_c = \Gamma \mid H_d, I) = \gamma.$$

Why?

¹Including children and very elderly people

The Island Problem: Extended Version

Let $i \in \{1, \dots, N\}$ identify each island inhabitant other than the suspect.

- ▶ The prior probabilities may differ across individuals:

$$\Pr(H_p | I) = \pi_0, \quad \Pr(H_{d_i} | I) = \pi_i, \quad \Pr(H_d | I) = \sum_i \pi_i = 1 - \pi_0.$$

- ▶ Let

$$\Pr(E_c | E_s, H_p, I) = 1, \quad \Pr(E_c | E_s, H_{d_i}, I) = P_i.$$

Then

$$\Pr(H_p | E_s, E_c, I) = \frac{\pi_0}{\pi_0 + \sum_i \pi_i P_i} = \frac{1}{1 + \sum_i \frac{\pi_i}{\pi_0} P_i} = \frac{1}{1 + \sum_i \omega_i P_i}.$$

N.b. If all inhabitants have the same $P_i = P = 10^{-6}$ and

$$\pi_0 = \pi_i = \frac{1}{N+1} \quad \forall i,$$

we obtain the previous result, with posterior odds $\frac{\Pr(H_p | E_s, E_c, I)}{\Pr(H_d | E_s, E_c, I)} = \frac{1}{NP} = 10$.

The Island Problem: Extended Version

Suppose that we know that the suspect has a brother, denoted by b . It can be proved that $P_b = \Pr(E_c = \Gamma, | E_s = \Gamma, H_{d_b}) = \frac{1}{4}$ (for a genotype at a single locus).

Assuming equal prior probabilities for all individuals, so that $\omega_i = 1$:

$$\Pr(H_p | E_s, E_c, I) = \frac{1}{1 + \sum_i \omega_i P_i} = \frac{1}{1 + \sum_i P_i} = \frac{1}{1 + 0.25 + (N - 1)10^{-6}} = 0.7407.$$

The posterior odds are

$$\frac{\Pr(H_p | E_s, E_c, I)}{\Pr(H_d | E_s, E_c, I)} = \frac{1}{0.25 + 0.1} = 2.85.$$

I	N	p	$\Pr(H_p E_s, E_c, I)$	$O(H_p E_s, E_c, I)$
$P_i = p \quad \forall i$	10^5	10^{-6}	0.9091	10
$P_b = 0.25, P_i = p \quad \forall i \neq b$	10^5	10^{-6}	0.7407	2.85

Merely allowing for the possibility that a brother committed the crime reduces the odds from 10 to 2.85.

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So far, we have considered a case in which someone left a trace at the crime scene.

We now consider a situation in which a trace from the crime scene was transferred to a person.

Imagine that a victim lost a large amount of blood after being stabbed.

A suspect is arrested and the suspect's clothes are examined in the laboratory. A detected blood stain has profile X , which matches the victim's profile and differs from the suspect's profile.

The main difference from the classical case is that the weight of evidence depends on both the DNA profile and the presence of the trace itself. We are reasoning at the activity level.

Introduction

Let $E = (E_1, E_2, E_v, E_s)$ denote the evidence to be evaluated, where

- ▶ E_1 : a bloodstain is present on the suspect's clothes;
- ▶ E_2 : the recovered blood has genotype X ;
- ▶ E_v : the victim has genotype X ;
- ▶ E_s : the suspect has genotype $Y \neq X$.

The propositions are at activity level:

- ▶ H_p : the suspect was present when the victim was killed;
- ▶ H_d : the suspect was not present when the victim was killed.

The background information I states that:

- ▶ no mechanism other than presence at the stabbing could have transferred the victim's blood to the suspect. If the blood was not transferred during the assault, it must have been present beforehand.

The likelihood ratio becomes

$$\begin{aligned} &= \frac{\Pr(E_1, E_2, E_v, E_s \mid H_p, I)}{\Pr(E_1, E_2, E_v, E_s \mid H_d, I)} \\ &= \frac{\Pr(E_1, E_2, E_v \mid E_s, H_p, I) \Pr(E_s \mid H_p, I)}{\Pr(E_1, E_2, E_v \mid E_s, H_d, I) \Pr(E_s \mid H_d, I)}. \end{aligned}$$

The second ratio is equal to one.

$$= \frac{\Pr(E_1, E_2 \mid E_v, E_s, H_p, I) \Pr(E_v \mid E_s, H_p, I)}{\Pr(E_1, E_2 \mid E_v, E_s, H_d, I) \Pr(E_v \mid E_s, H_d, I)}.$$

The second ratio is again equal to one. Under H_d , there is no reason for E_v to affect the background evidence:

$$= \frac{\Pr(E_1, E_2 \mid E_v, E_s, H_p, I)}{\Pr(E_1, E_2 \mid E_s, H_d, I)}.$$

$$= \frac{\Pr(E_1, E_2 \mid E_v, E_s, H_p, I)}{\Pr(E_1, E_2 \mid E_s, H_d, I)}.$$

NUMERATOR

Let T the event that blood was transferred from the victim to the person present during the assault, not necessarily to the suspect.

Let $t = \Pr(T)$.

Using the law of total probability:

$$\begin{aligned} \Pr(E_1, E_2 \mid E_v, E_s, H_p) &= \overbrace{\Pr(E_1, E_2 \mid T, E_v, E_s, H_p)}^1 \overbrace{\Pr(T \mid E_v, E_s, H_p)}^{\Pr(T)=t} \\ &+ \underbrace{\Pr(E_1, E_2 \mid \bar{T}, E_v, E_s, H_p, I)}_{\text{without transfer, the evidence is independent of } E_v} \Pr(\bar{T} \mid E_v, E_s, H_p) \\ &= t + \underbrace{\Pr(E_1, E_2 \mid \bar{T}, E_s, H_p, I)}_{\Pr(E_1, E_2 \mid E_s, H_d, I)} (1 - t). \end{aligned}$$

If no transfer occurred during the assault, the blood must have been present beforehand. Its probability is therefore the same as in the denominator of the LR.

DENOMINATOR

Let B represent the event that the blood was already present as background.

$$\begin{aligned}\Pr(E_1, E_2 \mid E_s, H_d, I) &= \Pr(E_1 \mid E_s, H_d, I) \Pr(E_2 \mid E_1, E_s, H_d, I) \\ &= \underbrace{\Pr(E_1 \mid E_s, H_d, I)}_{\text{probability of an earlier transfer}} \underbrace{\Pr(E_2 \mid H_d, I)}_{\text{frequency of genotype } X} \\ &= b\gamma.\end{aligned}$$

Here, b is the probability that a blood trace not belonging to the suspect is found on the suspect's clothes for reasons unrelated to the assault.

The LR becomes

$$= (1 - t) + \frac{t}{b\gamma} \approx \frac{t}{b\gamma}.$$

The approximation applies when

$$b\gamma \ll 1, \quad \text{so that} \quad \frac{t}{b\gamma} \gg 1 - t.$$

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The Island Problem: how was the suspect identified?

In the previous versions of the Island Problem, we did not consider **how the suspect was identified**.

Suppose that the inhabitants are tested sequentially:

- ▶ the first k inhabitants do not match the crime-scene profile;
- ▶ the next inhabitant produces a match;
- ▶ the search is stopped, and this person becomes the suspect.

Question

Is this match more or less probative than a match obtained after testing a suspect selected independently of the DNA profile?

The observed profile is the same, but the process by which the suspect was selected is different.

Sequential search on the island

Initially, the island has $N + 1$ inhabitants.

After k inhabitants have been excluded, $N + 1 - k$ possible donors remain: the person who is tested next and $N - k$ alternative donors.

Let I_k the background information after this k profiling, namely that :

- ▶ The island has $N + 1$ inhabitants;
- ▶ the donor belongs to the island population;
- ▶ all inhabitants have the same probability of being the donor;
- ▶ the first k individuals tested do not have the crime-scene profile;
- ▶ there are no laboratory errors or false-negative results.

Sequential search on the island

Before observing the match,

$$\Pr(H_p | I_k) = \frac{1}{N+1-k}, \quad \Pr(H_d | I_k) = \frac{N-k}{N+1-k},$$

and therefore

$$\frac{\Pr(H_p | I_k)}{\Pr(H_d | I_k)} = \frac{1}{N-k}.$$

If γ is the probability of random-matching, then

$$\text{LR} = \frac{\Pr(E | H_p, I_k)}{\Pr(E | H_d, I_k)} = \frac{1}{\gamma}.$$

Sequential search on the island

Thus,

$$\frac{\Pr(H_p \mid E, I_k)}{\Pr(H_d \mid E, I_k)} = \frac{1}{(N - k)\gamma},$$

and

$$\Pr(H_p \mid E, I_k) = \frac{1}{1 + (N - k)\gamma}.$$

That is actually stronger evidence than in the case the suspect was identified independently of the evidence.

- ▶ The result might seem counterintuitive, but think of the case in which the suspect is actually the last person to be searched: then, $\Pr(H_p \mid E, I_k) = 1$.
- ▶ Each individual who is found not to have Γ is excluded from suspicions and reduces the pool of possible culprits.
- ▶ The remaining persons become more likely to be guilty
- ▶ Also, the reason why the suspect has prior probability equal to all the others in the classical case (suspect apprehended before evidence) is because we assume that the reason for which the suspect is apprehended does not constitute evidence (see Balding, pag.6-17)

From the island to a general database search

The Island Problem is a simplified database-search problem. Let:

- ▶ C = the true donor
- ▶ D = the set of individuals in the database
- ▶ S be the only database member whose profile matches the trace.

Two different questions can then be asked:

$$C = S \quad \text{versus} \quad C \neq S \quad \text{or} \quad C \in D \quad \text{versus} \quad C \notin D.$$

These are different pairs of propositions and, therefore, generally produce different LR's.

$$\text{Let } LR_S := \frac{\Pr(E_S|C=S)}{\Pr(E_S|C \neq S)} \text{ and } LR_D := \frac{\Pr(E_S|C \in D)}{\Pr(E_S|C \notin D)}$$

Deriving LR_S : assumptions and notation

Let $E_S = \{S \text{ is the unique matching individual in } D\}$.

Define $A_{-S} = \{\text{no database member other than } S \text{ matches the trace}\}$.

Thus,

$$E_S = \{S \text{ matches}\} \cap A_{-S}.$$

For this simplified derivation, assume that:

- ▶ the true donor necessarily matches the crime-scene profile;
- ▶ there are no laboratory errors or false exclusions;
- ▶ an unrelated non-donor matches S 's profile with probability p_S ;
- ▶ the probability of A_{-S} is the same in the numerator and denominator.

The numerator: $C = S$

Consider $\Pr(E_S \mid C = S, I)$.

If $C = S$, then S is the true donor and therefore necessarily matches the crime-scene profile: $\Pr(S \text{ matches} \mid C = S, I) = 1$.

For S to be the *unique* match, all the other database members must fail to match. Therefore,

$$\begin{aligned}\Pr(E_S \mid C = S, I) &= \Pr(S \text{ matches}, A_{-S} \mid C = S, I) \\ &= 1 \times \Pr(A_{-S} \mid C = S, I).\end{aligned}$$

Let $q_{-S} := \Pr(A_{-S} \mid C = S, I)$.

Hence,

$$\Pr(E_S \mid C = S, I) = q_{-S}.$$

The denominator: $C \neq S$

We now consider

$$\Pr(E_S \mid C \neq S, I).$$

Under $C \neq S$, the true donor may be:

1. another member of the database, $C \in D \setminus \{S\}$;
2. outside the database, $C \notin D$.

Using the law of total probability,

$$\begin{aligned} \Pr(E_S \mid C \neq S, I) &= \Pr(E_S \mid C \in D \setminus \{S\}, I) \Pr(C \in D \setminus \{S\} \mid C \neq S, I) \\ &\quad + \Pr(E_S \mid C \notin D, I) \Pr(C \notin D \mid C \neq S, I). \end{aligned}$$

If the true donor is another database member

Suppose that

$$C \in D \setminus \{S\}.$$

Under the assumption of no false exclusions, the true donor would necessarily match the crime-scene profile.

Therefore, if S also matched, S could not be the unique match.

Hence,

$$\Pr(E_S \mid C \in D \setminus \{S\}, I) = 0.$$

The denominator consequently reduces to

$$\Pr(E_S \mid C \neq S, I) = \Pr(E_S \mid C \notin D, I) \Pr(C \notin D \mid C \neq S, I).$$

The likelihood ratio for $C = S$ versus $C \neq S$

Combining the numerator and denominator,

$$LR_S = \frac{\Pr(E_S \mid C = S, I)}{\Pr(E_S \mid C \neq S, I)}.$$

Since $\Pr(E_S \mid C = S, I) = q_{-S}$ and $\Pr(E_S \mid C \neq S, I) = p_S q_{-S} \Pr(C \notin D \mid C \neq S, I)$, we obtain

$$\begin{aligned} LR_S &= \frac{q_{-S}}{p_S q_{-S} \Pr(C \notin D \mid C \neq S, I)} \\ &= \boxed{\frac{1}{p_S \Pr(C \notin D \mid C \neq S, I)}}. \end{aligned}$$

Because

$$\Pr(C \notin D \mid C \neq S, I) \leq 1,$$

Two equivalent posterior questions

Let D be the set of tested individuals and let E_S denote the result that S is the unique matching individual in D .

Assuming that the true donor would necessarily match the crime-scene profile, all the other database members are excluded as possible donors.

Therefore, **conditional on** E_S , $C = S \iff C \in D$, and $C \neq S \iff C \notin D$.
Hence,

$$\Pr(C = S \mid E_S, I) = \Pr(C \in D \mid E_S, I),$$

and

$$\Pr(C \neq S \mid E_S, I) = \Pr(C \notin D \mid E_S, I).$$

The evidential value of a unique database match

Let $E_S = \{S \text{ is the unique matching individual in database } D\}$.

Consider the propositions $H_p : C = S$, $H_d : C \neq S$.

Under H_d , observing E_S requires:

1. The true donor not to be another member of D ;
2. S to produce a coincidental match.

Therefore,

$$\text{LR}_S = \frac{\Pr(E_S \mid C = S, I)}{\Pr(E_S \mid C \neq S, I)} = \frac{1}{p_S \Pr(C \notin D \mid C \neq S, I)}.$$

Since $\Pr(C \notin D \mid C \neq S, I) \leq 1$, we obtain

$$\boxed{\text{LR}_S \geq \frac{1}{p_S}}.$$

The evidence includes not only the match with S , but also the exclusion of all other members of the database.

Exercise

Prove that $LR_C \leq 1/p_s$.

It follows that $LR_C \leq \frac{1}{p_s} \leq LR_S$.

Regina vs. Adams

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