LiRa – a new way to evaluate the strength of evidence for complex profiles

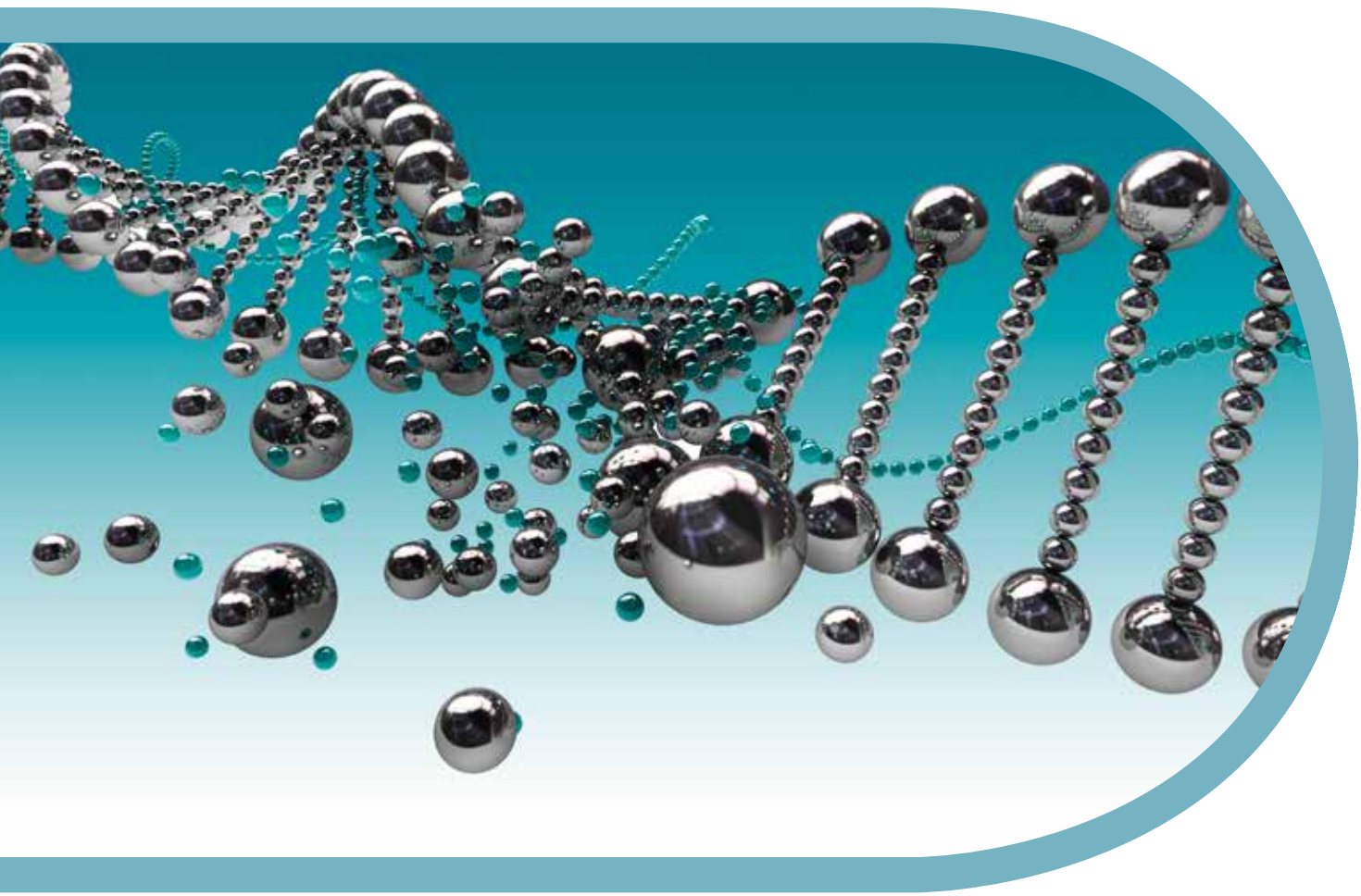
What is LiRa?

LiRa is a web based system for the evaluation of DNA profiles via Likelihood Ratios (LRs). This software has been developed within LGC and uses a probabilistic model to evaluate mixtures.

The statistical method underpinning LiRa has been published and is also described in a separate statistical specification document:

Puch-Solis, R and Clayton T. (2014). Evidential evaluation of DNA profiles using a discrete statistical model implemented in the DNA LiRa software. Forensic Science International: Genetics, Vol. 11, pp 220-228

LiRa is fully validated for use within LGC. LiRa is accredited to ISO/IEC17025:2005 and the LGC schedule of accreditation for the accreditation methods can be viewed through the UKAS website www.ukas.com.



Mixture interpretation

There are two key challenges in the interpretation of mixed DNA profiles:

1. The deconvolution of mixtures to produce a profile which can be used to search the NDNAD to provide intelligence leads.
2. Calculation of strength of evidence when comparing the profile of a nominated individual to a mixed DNA profile from a crime stain sample.

LiRa is now available to increase our capability with this 2nd challenge.

Why do we need a new system?

Standard methods for calculating a likelihood ratio can only handle mixtures with a maximum of two contributors. In addition to this, they also struggle to robustly compute a likelihood ratio where low level profiles are involved.

Where we encounter these challenging profiles we are often unable to assign a numerical value to the strength of evidence and instead may attempt to verbalise the result of the comparison with a reference sample or perform a Qualitative Evaluation (QE). Whilst this has been the best option available until now, it has been open to challenge and will often underestimate the true evidential value.

Due to the increased sensitivity of the new DNA-17 profiling kits introduced in July 2014, the number of mixed profiles being generated and also the number of complex results has increased. The need for an urgent change is now even greater therefore.

What types of profiles can it handle?

The current version of LiRa (LiRa v1.2) has been fully validated and accredited for use with profiles generated with SGM Plus and/or ESI17. LiRa can calculate likelihood ratios for mixed profiles with up to 3 contributors.

Binary/Discrete/Continuous – what does it all mean?

You may have heard people refer to binary, discrete and continuous models when referring to the calculation of likelihood ratios. These are all accepted methods and differ as shown in the table below.

Binary	Discrete	Continuous
Binary models require that all peaks are designated as alleles or ignored completely. No allowance for drop-in or drop-out.	Discrete models use the presence/absence of peaks but do not take their heights into consideration. Drop-in and drop-out are accommodated.	Continuous models take into account the peak heights of each allele as well as their presence or absence. Again, drop-in and drop-out are accommodated.

The method we have used until now is a binary method and we will continue to use that, together with our existing tools (MatchProb and MixIT) for good quality single source profiles and two person mixtures.

LiRa v1.2 uses the discrete model and therefore is more advanced that the binary model as it will take into account random events such as drop-in, drop-out and also account for degradation within a profile.

What types of cases can it be used for?

There is no restriction as to the type of case that can be used with LiRa. However, it is currently considered to be a specialist DNA technique and therefore will be charged under the 03BF/26BF product codes.

Why have we developed our own software?

LGC has its own statistical and software development team. This team has already successfully developed our existing DNA analysis software – Insight – which has demonstrated the advantages of being able to configure the software to meet our own operational needs. Development of our own statistical software means we can directly link this to DNA Insight to allow for a more robust and streamlined workflow.

The development of our own software gives us total ownership of its functionality and allows us to implement any improvements as and when required. We also fully understand and can support the statistical algorithms. As we have carried out the full end to end validation of LiRa, we have assurance around the extent of the software development and validation of the algorithms as well as the more standard operational validation.

As the first cases using LiRa (and other probabilistic models) go through the criminal justice system, there are likely to a number of challenges. We therefore see it as a key strength that our reporting officers will have direct access to our own statistician and IT development team who can attend court if necessary to explain the complex statistics and defend challenges.

Finally, unlike an off-the-shelf product, we are able to continue to refine LiRa to meet our developing needs and those of the CJS.

Future developments

As LiRa v1.2 is now in full operation, the team have started the development of LiRa v2.0. This new version will offer full integration with Insight, the option to run a continuous model (whilst retaining the capability to use the discrete model) and the ability to evaluate mixtures with up to 4 contributors.

Case study

A tiny blood speck was found on a knife believed to be linked to a cold case homicide. Using DNA 17 a low level, partial DNA profile was obtained where no profile had been obtained previously. However, due to the low level nature of the result and the variation in the potential number of contributors between amplifications, the reporting officer was unable to give a weight of evidence using conventional means, i.e. the binary model, but was able to see that the prominent components matched that of the suspect. Using LiRa (discrete model) we have now been able to calculate a likelihood ratio that the evidence is 490 million times more likely if the DNA came from the suspect and an unknown than from two unknowns.

All things forensic

Our DNA expertise complements and integrates seamlessly with other LGC services, providing powerful assistance and expert evidence to support crime investigations, and civil or private disputes. Highly qualified experts are available to discuss your specific casework problems and advise potential, integrated solutions to provide the greatest certainty of a satisfactory outcome.

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