From the team that brought you STRmix™

DBLR™ (database likelihood ratios) is an application designed for the rapid calculation of likelihood ratios (*LR*s) using STRmix™ deconvolutions.

DBLR™

www.STRmix.com/dblr

STRmix™ EMPOWERING FORENSIC SCIENCE 10 YEARS Since 2012

Telarc. Registered ™ Quality ISO 9001

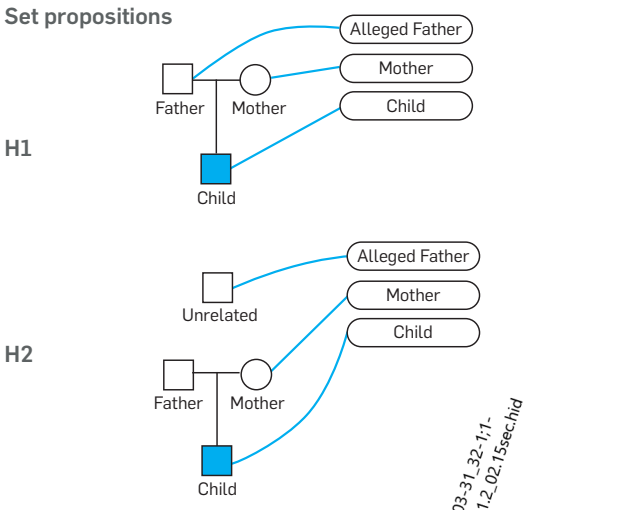
FAST DBLR™ calculates millions of *LR*s in seconds.

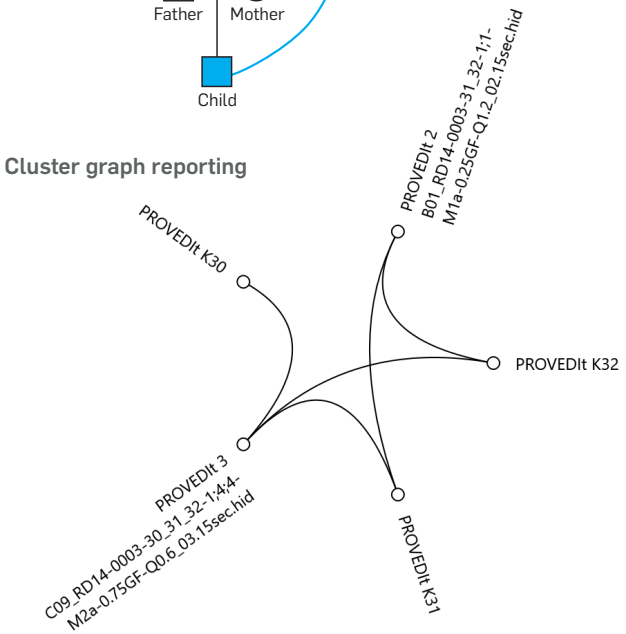
ACCESSIBLE DBLR™ runs on a user's PC, without the need for high-performance computing.

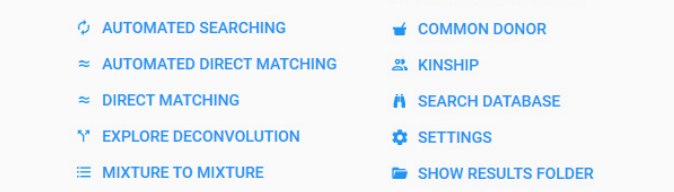
ENABLING DBLR™ enables you to get more value from your DNA evidence.

WITH DBLR™ YOU WILL BE ABLE TO:

- Achieve superfast database searches.
- Visualise the value of your DNA mixture evidence.
- Undertake mixture to mixture matches.
- Determine whether there is a common donor between samples.
- Calculate any kinship relationship conceivable (including modelling of linkage, mutation and F_{ST}).
- Assign Kinship *LR*s for profiles.







WHAT CAN DBLR™ DO?

- **APPLY POPULATION STRATIFICATION** in the Kinship, Search Database and Explore Deconvolution modules *(New in DBLR™ v1.3)*
- **LEVERAGE PROBABILISTIC LINKS** within the Kinship module to probabilistically condition on the presence of a sample donor *(New in DBLR™ v1.3)*
- **UTILISE SEQUENCE BASED DATA** from STRmix™ NGS or a UAS Sample Details Report within the Kinship, Search Database and Explore Deconvolution modules. *(New in DBLR™ v1.3)*
- **UNDERTAKE DIRECT COMPARISON** of one or many components of a forensic DNA mixture to a database of known individuals (i.e. "Who contributed to the profile?").
- **CARRY OUT FAMILIAL SEARCHING** for a range of different relationships including siblings, half-siblings, parents, and children (i.e. "Is there a relative of the donor in the database?").
- **SEARCH FOR COMMON CONTRIBUTORS** between mixed DNA profiles (mixture to mixture comparisons). These *LR*s can be visualised using a heat map, and include cluster graphs.
- **DETERMINE THE PROFILES** of the most likely contributors to a profile.
- **VISUALISE THE VALUE** of evidence by calculating expected *LR*s for one or many components of forensic DNA profiles for true and non-contributors using randomly generated individuals.
- **MANAGE AUTOMATED SEARCHES** for one or many DNA profiles against one or many databases of known individuals. Includes direct matching between databases.
- **MANAGE DATABASES** of known contributors and STRmix™ deconvolutions from unsolved casework for easy matching.
- **COMBINE MULTIPLE EVIDENCE PROFILES** under the assumption that there is a common contributor within the different samples (Common Donor).
- **BUILD ANY PEDIGREE** imaginable and calculate likelihood ratios given the different propositions (Kinship).
- **MODEL** linkage, mutation and F_{ST} in the Kinship module
- **PROTECT YOUR SETTINGS** with a user defined password.

HOW DOES DBLR™ WORK?

DBLR™ uses efficient algorithms for the fast calculation of *LR*s. With DBLR™ the user can import STRmix™ deconvolutions or single source-profiles and visualise the value of the evidence or carry out fast database searches. The DBLR™ Kinship function is both powerful and flexible. The user can load STRmix™ deconvolutions or single-source profiles from known individuals and link these with one or more pedigrees. The Common Donor function can better resolve the genotypes of queried contributors and search these against a database to identify possible donors.

VALIDATION

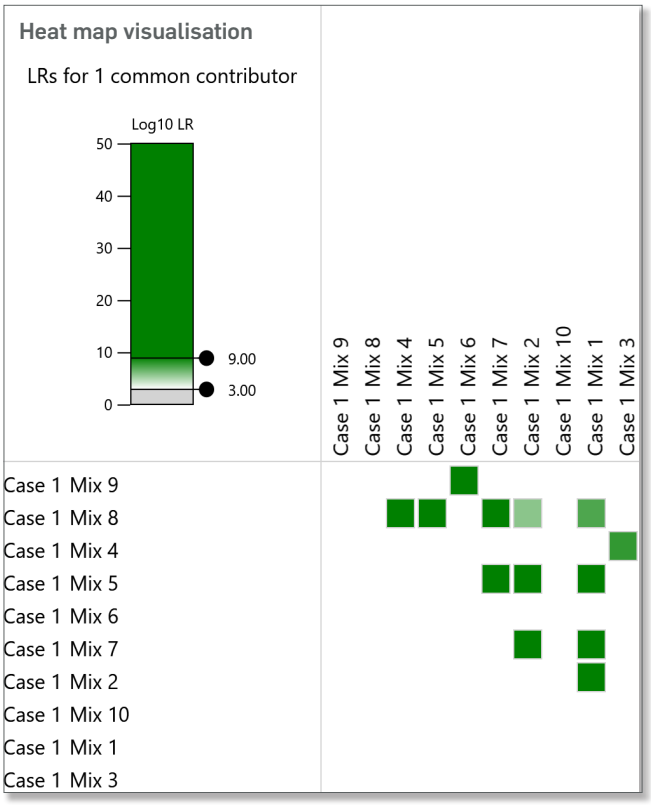
DBLR™ has been extensively validated by the STRmix™ team based at ESR, New Zealand.

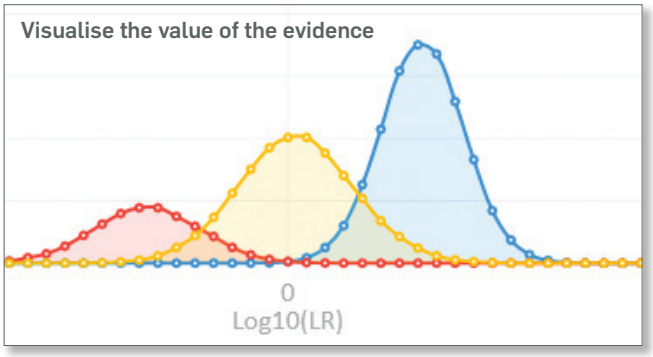
SPECIFICATIONS

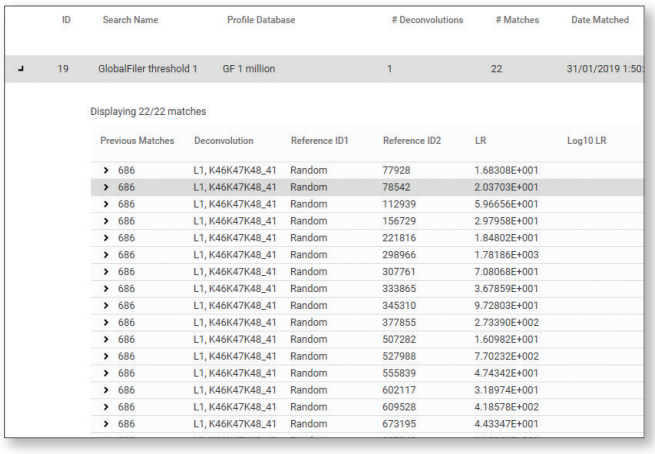
DBLR™ is designed to run standalone on an individual DNA analyst's PC. For guidance on hardware and software specifications please go to:
www.strmix.com/dblr/specifications/

CERTIFICATION

The STRmix™ team's quality management system is certified to ISO 9001:2015.







ID	Search Name	Profile Database	# Deconvolutions	# Matches	Date Matched
19	GlobalFiler threshold 1	GF 1 million	1	22	31/01/2019 1:50:

Displaying 22/22 matches

Previous Matches	Deconvolution	Reference ID1	Reference ID2	LR	Log10 LR
686	L1, K46K47K48_41	Random	77928	1.68308E+001	
686	L1, K46K47K48_41	Random	78542	2.03703E+001	
686	L1, K46K47K48_41	Random	112939	5.96656E+001	
686	L1, K46K47K48_41	Random	156729	2.97958E+001	
686	L1, K46K47K48_41	Random	221816	1.84802E+001	
686	L1, K46K47K48_41	Random	298966	1.78186E+003	
686	L1, K46K47K48_41	Random	307761	7.08068E+001	
686	L1, K46K47K48_41	Random	333865	3.67859E+001	
686	L1, K46K47K48_41	Random	345310	9.72803E+001	
686	L1, K46K47K48_41	Random	377855	2.73390E+002	
686	L1, K46K47K48_41	Random	507282	1.60982E+001	
686	L1, K46K47K48_41	Random	527988	7.70232E+002	
686	L1, K46K47K48_41	Random	555839	4.74342E+001	
686	L1, K46K47K48_41	Random	602117	3.18974E+001	
686	L1, K46K47K48_41	Random	609528	4.18578E+002	
686	L1, K46K47K48_41	Random	673195	4.43347E+001	

PUBLISHED DATA

The following papers describe the mathematics, validation and application of DBLR™:

[1] Slooten K. Identifying common donors in DNA mixtures, with applications to database searches. Forensic Science International: Genetics 2017;26:40-7.

[2] Kruijver M, Bright J-A, Kelly H, Buckleton J. Exploring the probative value of mixed DNA profiles. Forensic Science International: Genetics 2019;41: 1-10.

[3] Bright J-A, Taylor D, Kerr Z, Buckleton J, Kruijver M. The efficacy of DNA mixture to mixture matching. Forensic Science International: Genetics 2019;41: 64-71.

[4] Taylor D, Rowe E, Kruijver M, Abarno D, Bright J-A, Buckleton J. Inter-sample contamination detection using mixture deconvolution comparison. Forensic Science International: Genetics 2019; 40: 160-167.

[5] J.-A. Bright, M. Jones Dukes, S.N. Pugh, I.W. Evett, J.S. Buckleton, Applying calibration to LRs produced by a DNA interpretation software. Australian Journal of Forensic Sciences. 2019; 1-7.

[6] Taylor D, Kruijver M. Combining evidence across multiple mixed DNA profiles for improved resolution of a donor when a common contributor can be assumed. Forensic Science International: Genetics 2020; 49.

[7] H. Kelly, Z. Kerr, K. Cheng, M. Kruijver, J.-A. Bright, Developmental validation of a software implementation of a flexible framework for the assignment of likelihood ratios for forensic investigations. Forensic Science International: Reports. 2021; Volume 4, 100231 https://doi.org/10.1016/j.fsir.2021.100231

[8] M. Kruijver, D. Taylor, J.-A. Bright, Evaluating DNA evidence possibly involving multiple (mixed) samples, common donors and related contributors, Forensic Science International: Genetics. 2021; 54 https://doi.org/10.1016/j.fsigen.2021.102532

[9] Kruijver M, Kelly H, Bright J-A, Buckleton J. Evaluating DNA Mixtures with Contributors from Different Populations Using Probabilistic Genotyping. Genes. 2023; 14(1):40. https://www.mdpi.com/2073-4425/14/1/40

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INSTITUTE OF ENVIRONMENTAL SCIENCE AND RESEARCH (ESR)

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