

**From the team
that brought
you STRmix™**

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

DBLR™



Quality
ISO 9001

www.STRmix.com/dblr

FAST DBLR™ calculates millions of *LRs* 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.

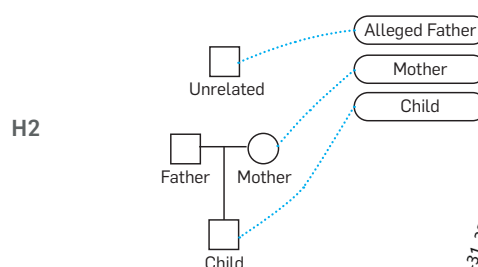
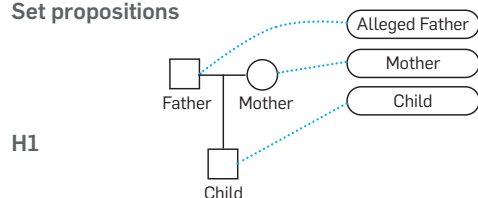
WITH DBLR™ YOU WILL BE ABLE TO:

- 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 (now including modelling of linkage, mutation and F_{ST}).
- Assign Kinship *LRs* for single source NGS profiles.

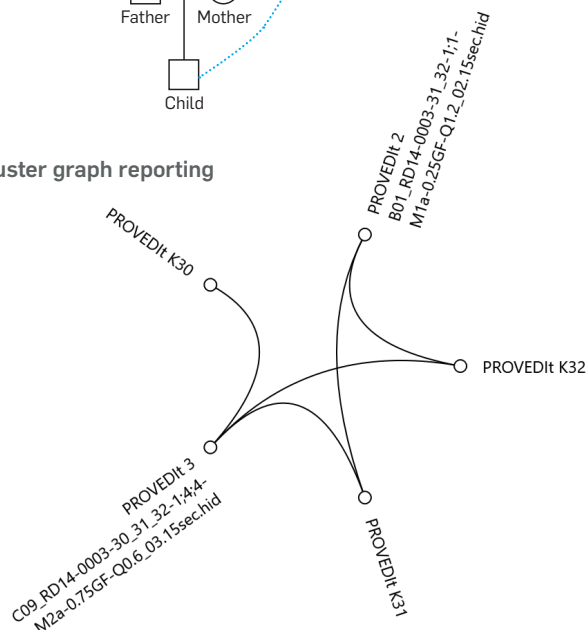


- 🔍 AUTOMATED SEARCHING
- ≈ AUTOMATED DIRECT MATCHING
- ≈ DIRECT MATCHING
- 🔍 EXPLORE DECONVOLUTION
- ≡ MIXTURE TO MIXTURE
- 👤 COMMON DONOR
- 👤 KINSHIP
- 🔍 SEARCH DATABASE
- ⚙️ SETTINGS
- 📁 SHOW RESULTS FOLDER

Set propositions



Cluster graph reporting



WHAT CAN DBLR™ DO?

- **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 *LRs* can be visualised using a heat map, and now include cluster graphs (New in DBLR™ v1.2).
- **DETERMINE THE PROFILES** of the most likely contributors to a profile.
- **VISUALISE THE VALUE** of evidence by calculating expected *LRs* 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. Now includes direct matching between databases (New in DBLR™ v1.2).
- **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 (New in DBLR™ v1.2).
- **ASSIGN *LRs*** within the Kinship module for single source profiles containing both STR and SNP loci generated using Next Generation Sequencing (NGS) technology (New in DBLR™ v1.2).
- **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.

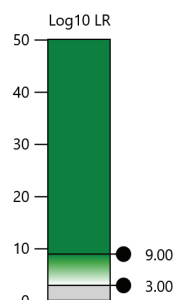
PUBLISHED DATA

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

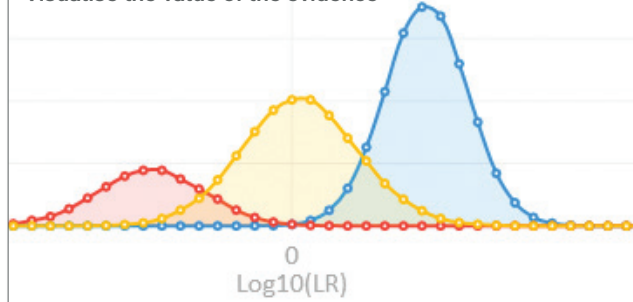
- [1] Slooten K. Identifying common donors in DNA mixtures, with applications to database searches. *Forensic Science International: Genetics* 2017;26:40-7.
- [2] Kruijver M, Bright J-A, Kelly H, Buckleton J. Exploring the probative value of mixed DNA profiles. *Forensic Science International: Genetics* 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 LR_s 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://www.sciencedirect.com/science/article/pii/S2665910721000621?via%3Dihub> (external link)
- [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>

Heat map visualisation

LR_s for 1 common contributor



Visualise the value of the evidence



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	

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INSTITUTE OF ENVIRONMENTAL SCIENCE AND RESEARCH (ESR)

ESR is New Zealand's Crown Research Institute specialising in science for communities. ESR uses world-leading science to safeguard our health, keep our communities safer, protect our food-based economy, and improve the health of our water and natural environment.

FORENSIC SCIENCE SA (FSSA)

FSSA provides independent, expert scientific evidence, opinion and information to the justice system and carries out award-winning research in forensic science.

STRMIX LIMITED

STRmix Limited is a subsidiary of ESR, founded to better serve international users of STRmix™.