

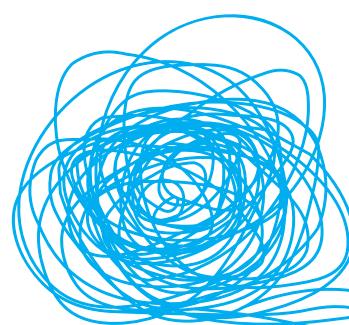
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STRmixTM published data

Papers describing the biological model, mathematics, performance and validation of STRmixTM:

- [1] D.A. Taylor, J.-A. Bright, J. S. Buckleton, The interpretation of single source and mixed DNA profiles. *Forensic Science International: Genetics*. 2013; 7(5): 516-528.
- [2] J.-A. Bright, D.A. Taylor, J. M. Curran, J. S. Buckleton, Developing allelic and stutter peak height models for a continuous method of DNA interpretation. *Forensic Science International: Genetics*. 2013; 7(2): 296-304.
- [3] J.-A. Bright, D.A. Taylor, J. Curran, J.S. Buckleton, Degradation of forensic DNA profiles, *Australian Journal of Forensic Sciences*. 2013 45(4): 445-449.
- [4] J.-A. Bright, D.A. Taylor, J. M. Curran, J. S. Buckleton, Searching mixed DNA profiles directly against profile databases. *Forensic Science International: Genetics*. 2014; 9: 102-110.
- [5] D.A. Taylor, Using continuous DNA interpretation methods to revisit likelihood ratio behaviour, *Forensic Science International: Genetics*. 2014; 11: 144-153.
- [6] J.-A. Bright, J.M. Curran and J.S. Buckleton, The effect of the uncertainty in the number of contributors to mixed DNA profiles on profile interpretation. *Forensic Science International: Genetics*. 2014; 12: 208-214.
- [7] J.-A. Bright, I.W. Evett, D.A. Taylor, J.M. Curran and J.S. Buckleton, A series of recommended tests when validating probabilistic DNA profile interpretation software. *Forensic Science International: Genetics*. 2015; 14: 125-131.
- [8] J.-A. Bright, K.E. Stevenson, J.M. Curran and J.S. Buckleton, The variability in likelihood ratios due to different mechanisms. *Forensic Science International: Genetics*. 2015; 14:187-190.
- [9] D.A. Taylor, J.-A. Bright and J.S. Buckleton, Considering relatives when assessing the evidential strength of mixed DNA profiles. *Forensic Science International: Genetics*. 2014; 13: 259-263.
- [10] T.W. Bille, S.M. Weitz, M.D. Coble, J.S. Buckleton and J.-A. Bright, Comparison of the performance of different models for the interpretation of low level mixed DNA profiles. *Electrophoresis*. 2014; 35:3125-33.
- [11] D.A. Taylor, J.-A. Bright and J.S. Buckleton, The 'factor of two' issue in mixed DNA profiles. *Journal of Theoretical Biology*. 2014; 363: p. 300-306.
- [12] D.A. Taylor and J.S. Buckleton, Do low template DNA profiles have useful quantitative data? *Forensic Science International: Genetics*. 2015; 16:13-6.
- [13] D.A. Taylor, J.S. Buckleton and I. Evett, Testing likelihood ratios produced from complex DNA profiles. *Forensic Science International: Genetics*. 2015; 16:165-171.
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- [15] J.-A. Bright, D.A. Taylor, C.E. McGovern, S.J. Cooper, L.J. Russell, D.V. Abarno and J.S. Buckleton, Developmental validation of STRmixTM, expert software for the interpretation of forensic DNA profiles. *Forensic Science International: Genetics*. 2016; 23:226-239.



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- [16] D.A. Taylor, J.-A. Bright, C.E. McGovern, C. Hefford, T. Kalafut, J.S. Buckleton, Validating multiplexes for use in conjunction with modern interpretation strategies. *Forensic Science International: Genetics*. 2016; 20:6-19.
- [17] D.A. Taylor, J.S. Buckleton, J.-A. Bright, Factors affecting peak height variability for short tandem repeat data. *Forensic Science International: Genetics*. 2016; 21:126-133.
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- [33] D. Taylor, J.-A. Bright, L. Scandrett, D. Abarno, S.-I. Lee, R. Wivell, H. Kelly, J. Buckleton, Validation of a top-down DNA profile analysis for database searching using a fully continuous probabilistic genotyping model. *Forensic Science International: Genetics*. 2021; 2021/05/1;52:102479.
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