



FaSTR™ DNA Published data

Papers describing the validation, features and models of FaSTR™ DNA:

- [1] D. Taylor, A. Harrison, D. Powers, An artificial neural network system to identify alleles in reference electropherograms. *Forensic science international: Genetics* 30 114-126.
- [2] R.M. Goor, L. Forman Neall, D. Hoffman, S.T. Sherry, A mathematical approach to the analysis of multiplex DNA profiles. *Bulletin of mathematical biology*. 2011; 73(8) 1909.
- [3] M.-H. Lin, S.-I. Lee, X. Zhang, L. Russell, H. Kelly, K. Cheng, S. Cooper, R. Wivell, Z. Kerr, J. Morawitz, J.-A. Bright, Developmental validation of FaSTR™ DNA: Software for the analysis of forensic DNA profiles. *Forensic Science International: Reports*. 2021; Volume 3, 100217. <https://www.sciencedirect.com/science/article/pii/S2665910721000487>
- [4] D. Taylor, D. Powers, Teaching artificial intelligence to read electropherograms, *Forensic Science International: Genetics* 25 (2016) 10-18.
- [5] D. Taylor, M. Kitselaar, D. Powers, The generalisability of artificial neural networks used to classify electrophoretic data produced under different conditions, *Forensic Science International: Genetics* 38 (2019) 181-184.
- [6] M. Kruijver, H. Kelly, K. Cheng, M.H. Lin, J. Morawitz, L. Russell, J. Buckleton, J.A. Bright, Estimating the number of contributors to a DNA profile using decision trees, *Forensic science international: Genetics* 50 (2021) 102407.
- [7] L. Volgin, D. Taylor, J.-A. Bright, M.-H. Lin, Validation of a neural network approach for STR typing to replace human reading, *Forensic Science International: Genetics* (2021) 102591.
- [8] T. Kalafut, C. Schuerman, J. Sutton, T. Faris, L. Armogida, J.-A. Bright, J. Buckleton, D. Taylor, Implementation and validation of an improved allele specific stutter filtering method for electropherogram interpretation, *Forensic Science International: Genetics* 35 (2018) 50-56.

