

SOFTWARE

FORENSIC SOFTWARE RESOURCES

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LATEST NEWS

The **forensim package** for the open source **R statistical software** is dedicated to forensic DNA mixtures interpretation. It provides tools to simulate mixture cases, and analytical tools to interpret them (Lyon).

<http://forensim.r-forge.r-project.org/>

Recently, a paper has been published in the *Journal of Forensic Science* (in press) [DOI Link](#)

Torben Tvedebrink's online mixture interpretation tool

Torben Tvedebrink's thesis contains publications on population genetics, including drop-out events. He has created a tool designed to deconvolute 2-person mixtures described in his thesis (link as above):

Mixture Analysis: A freeware solution to aid the interpretation of mixtures using peak height / or area information using an Excel spreadsheet (Copyright P.D. Gill, Glasgow)

Evaluating the weight of evidence data in DNA mixtures. T. Tvedebrink *Applied Statistics* 59(5): 855-874

[Excel sheet](#)

Identifying contributors of DNA mixture from STR typing. T. Tvedebrink, PS Eriksson *Journal of Computational Biology* (in press)

[Documentation](#)

MixtureCalc v1.2 (Free software for the interpretation of mixtures by using data from an exported Authority - submitted by Berthoin *Journal of Forensic Genetics* - June 2010)

- MixtureCalc v1.2 Excel sheet
- [License Agreement](#)
- [Standard Operation Procedure](#)
- [Workshop Examples](#)

David Balding's software described in

Balding DJ, Buckleton J, *Interpreting low template DNA profiles* *Journal of Forensic Science*, 4: 1-10, 2009 [DOI Link](#)

can be retrieved from his personal website (see section **Software**):

<http://www.zebfontaine.eclipse.co.uk/djb/html>

Bruce Weir's DNA mixture calculator

DNAMIX is a computer program that will calculate the likelihood ratio for mixed DNA samples encountered in forensic cases. Curran JM, Triggs CM, Buckleton J. *Journal of Forensic Science*. 2004; 49: 100-104. *Journal of Forensic Science* appropriate for complex mixtures as well

<http://www.biostat.washington.edu/~bweir/>

All software is written in R, and extra features are available: "the code also includes features not described in that paper, such as consideration of relatives of the alleged contributor, and incorporation of replicates and of two unknown contributors. *** 21/6/10 Previous two files LR1unk.R and LR2unk.R are now merged into a single file LTDNALR.R"

- Prof.ssa Francesca Torricelli -



Available online at www.sciencedirect.com

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Characterization of human DNA in environmental samples

Mary H. Toothman^a, Karen M. Kester^a, Jarrod Champagne^{b,d}, Tracey Dawson Cruz^b,
W. Scott Street IV^c, Bonnie L. Brown^{a,*}

- Prof.ssa Francesca Torricelli -

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IL CANCELLIERE
Maria Centorrino