

## 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 mixtures (Lyon).

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

Recently, a paper has been published in the *Journal of Forensic Sciences* (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)

[Excel sheet](#)

[Documentation](#)

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

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

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

[MixtureCalc v1.2 Excel sheet](#)

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**30.11.2010:** Torben's mixture separation package: "mixsep". The package is available at [project.org/web/packages/mixsep/](http://project.org/web/packages/mixsep/) including documentation

## David Balding's software described in

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

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

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

## Bruce Weir's DNA mixture calculation

DNAMIX is a computer program that will calculate the likelihood of mixed DNA samples encountered in forensic cases. Curran JM, Triggs CM, Buckleton J. *Journal of Forensic Sciences* 2004; 49: 100-110. Appropriate for complex mixtures as well

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

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](http://www.sciencedirect.com)



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Forensic  
Science  
International

[www.elsevier.com/locate/forensiint](http://www.elsevier.com/locate/forensiint)

## Characterization of human DNA in environmental samples

Mary H. Toothman<sup>a</sup>, Karen M. Kester<sup>a</sup>, Jarrod Champagne<sup>b,d</sup>, Tracey Dawson Cruz<sup>b</sup>,  
W. Scott Street IV<sup>c</sup>, Bonnie L. Brown<sup>a,\*</sup>

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IL CANCELLIERE  
Maria Centorrino

- Prof.ssa Francesca Torricelli -