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Validation of LRmix

Oskar Hansson

Statistical methods in forensic genetics 7-10 October 2013, Copenhagen

SEVENTH FRAMEWORK PROGRAMME

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Recent paper…

Forensic Science International: Genetics 7 (2013) 251–263

Contents lists available at SciVerse ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

A new methodological framework to interpret complex DNA profiles using likelihood ratios

P. Gill [a,b,*], H. Haned [c]

[a] Norwegian Institute of Public Health, Oslo, Norway
[b] University of Oslo, Oslo, Norway
[c] Netherlands Forensic Institute, Department of Human Biological Traces, The Hague, The Netherlands

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Validation of simulation models

"validation is a demonstration that a model within its domain of applicability possesses a satisfactory range of accuracy consistent with the intended application of the model".

Rykiel et al.

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A framework for probabilistic model comparison

a) Provide a 'basic model' as open-source software.
b) Provide version control: LRmix sources are available (within the Forensim package) from the R-Forge collaborative platform, which offers software versioning, and code checks. This ensures that all changes made to the program are recorded and documented via a revision control system. The changes logs and all previous versions of the package can be downloaded from https://r-forge.r-project.org/projects/forensim/.
c) Provide a *standard set* of example data to create a 'test-set' that can be universally applied to any model (see supplementary files).
d) In addition we provide a method to enable comparative studies to be carried out across divergent methods of analysis, based on non-contributor tests.

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A validation schema

a) *Face validity*: Is the model output and its behaviour reasonable?
b) *Comparison to other models*: see an example in Haned et al. [1].
c) *Sensitivity analysis and Extreme condition testing*: The model output should reflect extreme events e.g. when Pr(D) is set to zero and the profile has evidence of dropout then the LR should be very low.
d) *Non-contributor performance tests*: If the *contributor of interest*, e.g. the suspect is replaced by simulated random man in the specific model, then the resulting LR distribution should be distinguished from the LR observed when the *contributor of interest* is analysed.

a - c Rykiel et al.

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Estimating P(D) and P(C)

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Forensic Science International: Genetics 6 (2012) 679–688

Contents lists available at SciVerse ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR typing results that may include drop-out and/or drop-in using probabilistic methods

P. Gill [a,b,*], L. Gusmão [c], H. Haned [d], W.R. Mayr [e], N. Morling [f], W. Parson [g], L. Prieto [h], M. Prinz [i], H. Schneider [j], P.M. Schneider [k], B.S. Weir [l]

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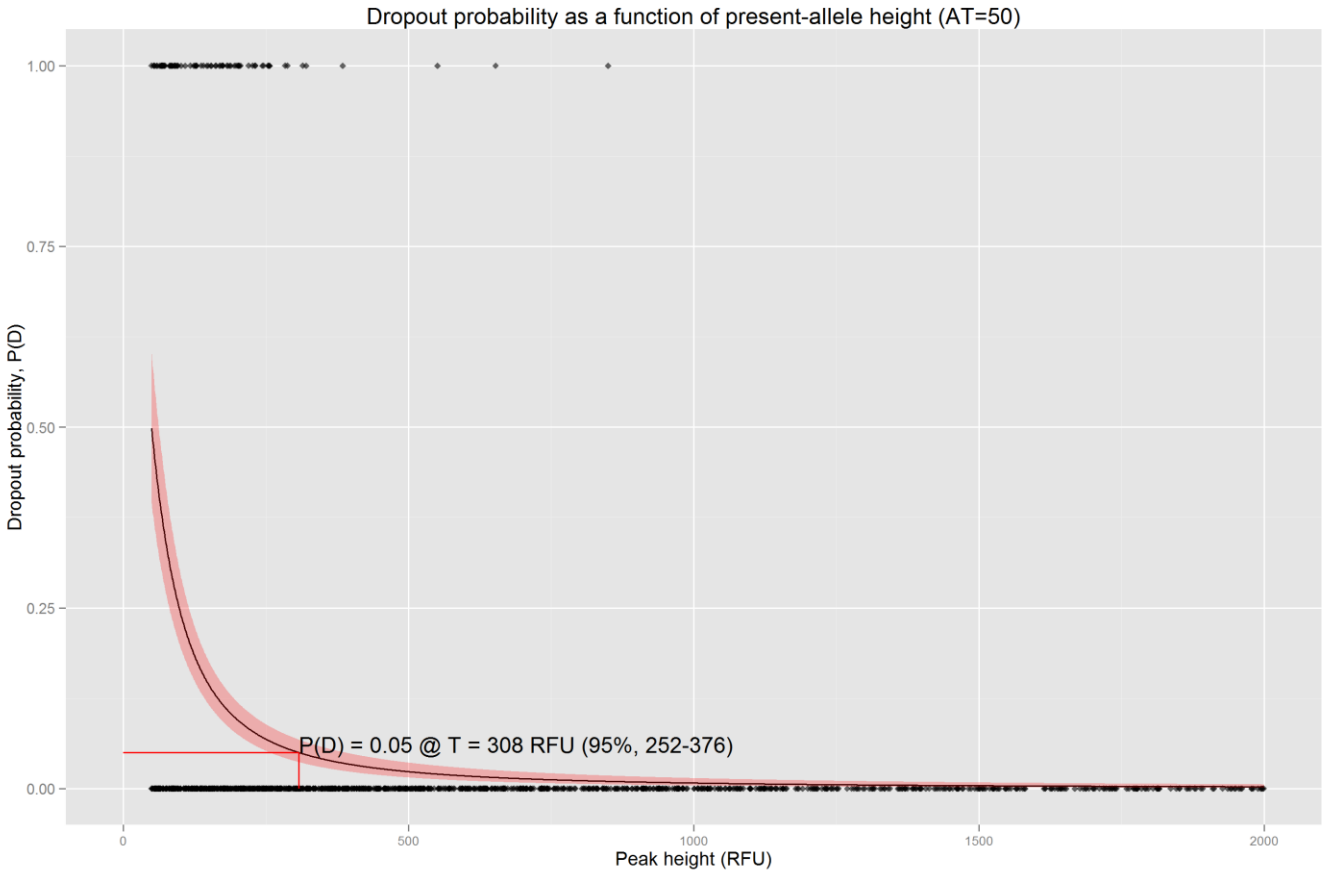
Appendix B is describes the process for dropout

Consider different sample types…



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Drop-in

- Is not discussed in detail…
- Negative controls can be used to estimate the drop-in
- x spurious alleles are observed in n controls, Pr(C)=x/n
- Level will increase by the sensitivity of the process:
  - Increased number of PCR cycles
  - New instruments (e.g. 3500)
  - More robust and sensitive kits

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Drop-in

- Consider the ‘scope’ of your negative controls:
  - PCR negative controls
  - Extraction negative controls
  - Extraction negative controls with blank swab/FTA
  - Negative controls that follow from stain collection?…
- Remember to distinguish from gross contamination
  - Allow only 1 or 2 drop-ins per control

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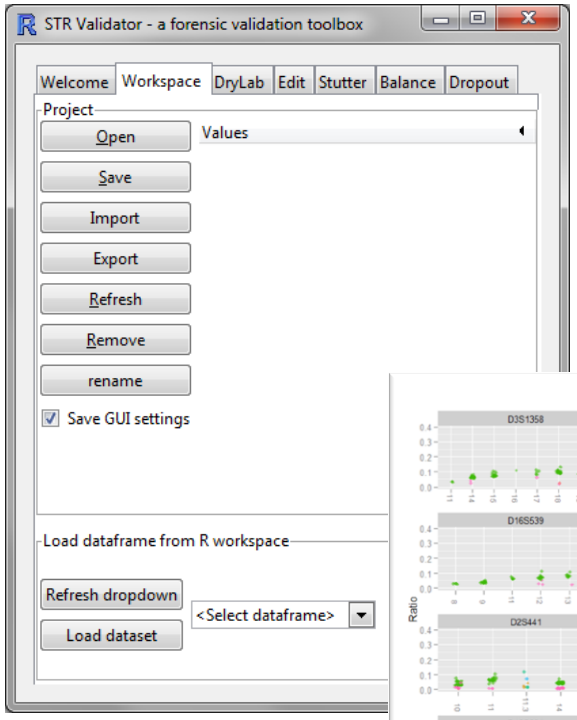
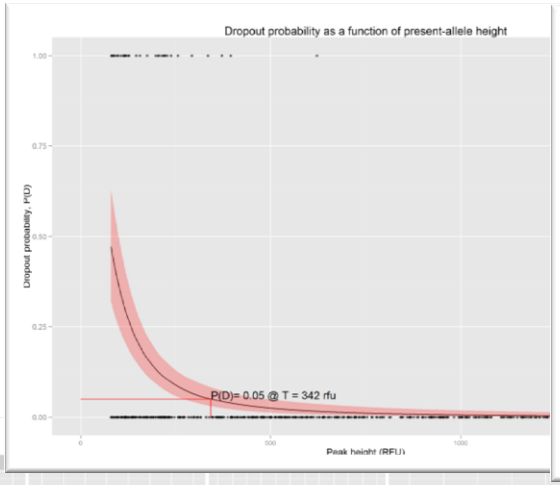
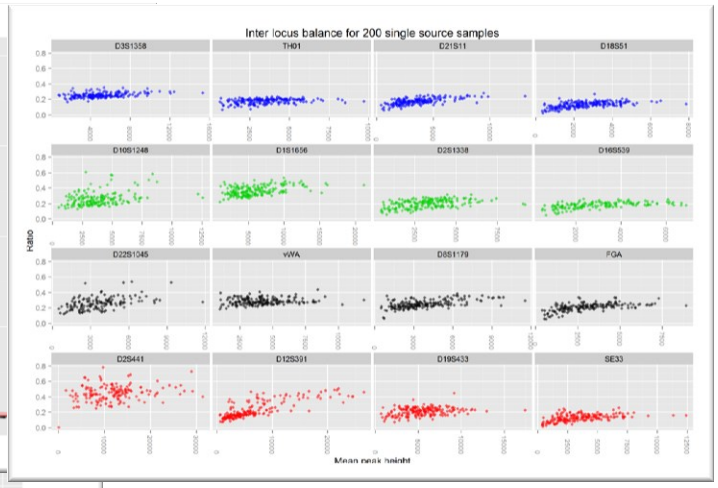
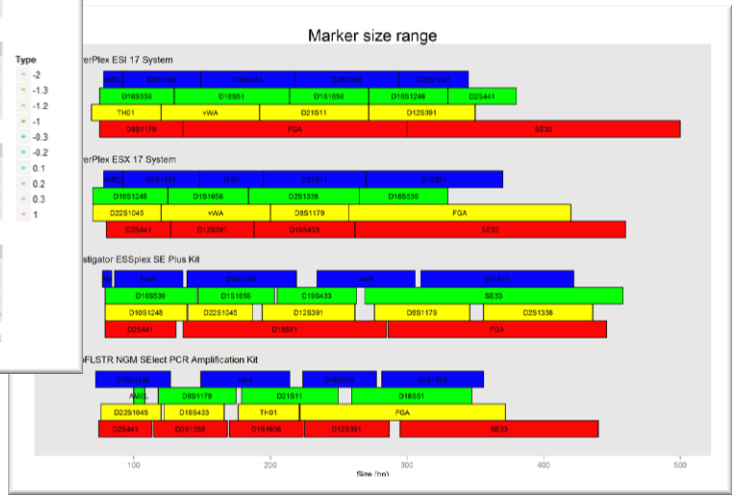
STR validator









https://sites.google.com/site/forensicapps/strvalidator
https://github.com/OskarHansson/strvalidator
http://cran.r-project.org/web/packages/strvalidator/index.html

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