



Corrigendum

Corrigendum to “Evaluation of the IrisPlex DNA-based eye color prediction assay in a United States population” [Forensic Sci. Int. Genet. (2014) 111–117]



Gina M. Dembinski, Christine J. Picard*

Department of Biology and Forensic and Investigative Sciences Program, Indiana University-Purdue University Indianapolis, 723 W. Michigan Street, Indianapolis, IN 46202, USA

After further scrutiny of the genotype and eye color data of the 200 samples used in the dataset while analyzing it for post-published purposes, some inconsistencies were noted which the authors would like to further report here. There were 9 samples (5 in training set, 4 in the validation set) that had their genotypes shifted by one sample in the data so that the true genotype of the sample was not correctly aligned. The erroneously shifted genotypes were corrected and allele frequencies were recalculated for 4 SNPs. These corrections were made to the model parameters and all analyses repeated.

Maximum prediction accuracies following allele frequency adjustment went from 58% to 77% for brown, from 95% to 79% for blue, and 11% to 65% for intermediate (Table 3). The figures and tables were corrected and are shown below (Figs. 2 and 3 and Tables 3–5). Briefly to summarize the changes, there was a small increase of sensitivity for blue eye color with all models with an increase from 93% to 95%, and a decrease for brown and intermediate eye colors, 97% to 89% and 93% to 0%, respectively (Table 5). For all models, there was an increase in correct prediction rates for intermediate eye color from 11% to 65% and blue eye color from 55% to 79%, but a decrease in brown eye color from 98% to 57%. Overall frequencies of predictions (Figs. 2 and 3) mostly decreased in inconclusive results, but also increased in the number of incorrect predictions. AUC values were approximately the same across all models, except with a decrease in intermediate from 0.88 to 0.77 (Table 4). There was no overall change from original conclusions made that the Bayesian network model should still be considered as an optimal prediction model method (over MLR), this is especially true for intermediate sample predictions.

Table 3

The corrected prediction rates (%) by color category of the verification set (N=100) was evaluated against the IrisPlex regression parameters and the adjusted regression parameters. The verification set was then evaluated using the Bayesian network with either set of *a priori* odds.

Parameters	Threshold	Original			Corrected		
		Brown (%)	Intermediate (%)	Blue (%)	Brown (%)	Intermediate (%)	Blue (%)
MLR: IrisPlex	0.5	88	0	95	90	0	93
	0.7	76	0	95	79	0	91
MLR: Adjusted	0.5	58	19	93	79	53	77
	0.7	42	11	95	79	41	64
Bayesian: Equal odds ^c	0.5	55	20	80	79	65	64
	0.7	55	20	98	74	41	27
Bayesian: Adjusted ^c	0.5	67	30	98	79	65	66
	0.7	55	15	98	72	41	57

^cEqual odds = 0.33 each eye color category, adjusted odds = 0.39 brown, 0.44 blue, 0.17 intermediate.

DOI of original article: <http://dx.doi.org/10.1016/j.fsigen.2013.12.003>

* Corresponding author at: 723 W. Michigan Street, SL 306, Indianapolis, IN 46202, USA. Tel.: +1 317 278 1050.

E-mail addresses: gdembins@iupui.edu (G.M. Dembinski), cpicard@iupui.edu (C.J. Picard).

<http://dx.doi.org/10.1016/j.fsigen.2016.06.002>

1872–4973/© 2013 Elsevier Ireland Ltd. All rights reserved.

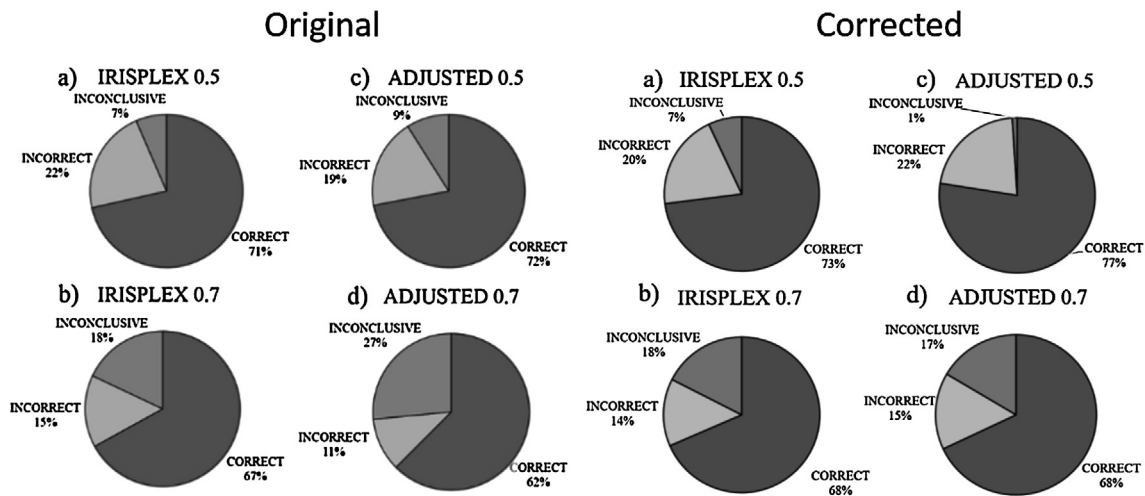


Fig. 2. Corrected frequency of overall correct, incorrect, and inconclusive eye color predictions using the multinomial regression model. a) Predictions under IrisPlex parameters at the 0.5 threshold, b) predictions under adjusted parameters at the 0.5 threshold, c) predictions under IrisPlex parameters at the 0.7 threshold, and d) predictions under adjusted parameters at the 0.7 threshold.

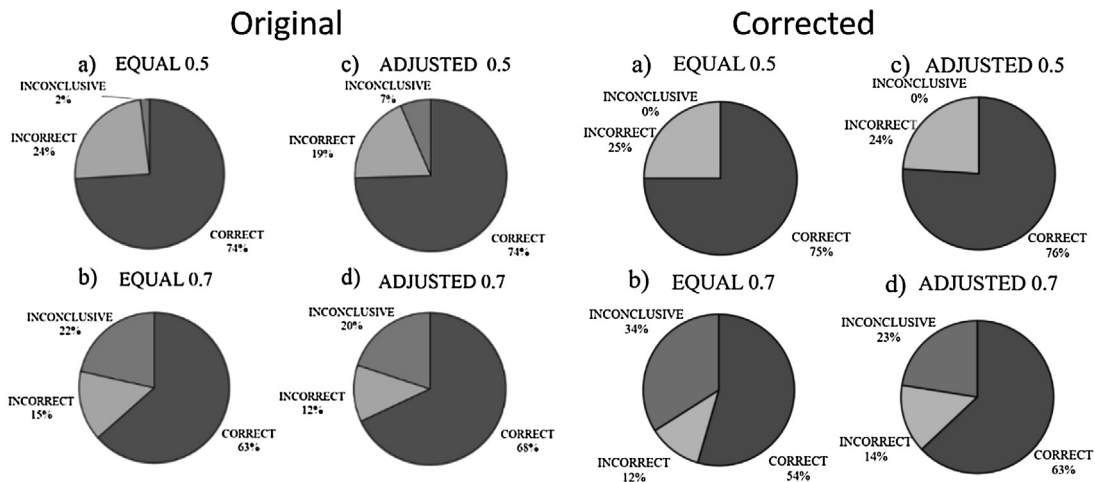


Fig. 3. The corrected frequencies of overall correct, incorrect, and inconclusive eye color predictions using the Bayesian model. a) Predictions under equal odds at the 0.5 threshold, b) predictions under adjusted frequency odds at the 0.5 threshold, c) predictions under equal odds at the 0.7 threshold, and d) predictions under adjusted frequency odds at the 0.7 threshold.

Table 4
Corrected AUC values of each prediction model evaluating the training set (N = 100). AUC reflects model performance (ability to make accurate predictions). Higher AUC value indicates better model performance.

Prediction Model	Original			Corrected		
	Blue	Intermediate	Brown	Blue	Intermediate	Brown
Liu et al. [1]	0.91	0.73	0.93	0.91	0.73	0.93
IrisPlex parameters [2]	0.97	0.84	0.95	0.98	0.83	0.95
Adjusted parameters	0.97	0.89	0.97	0.97	0.77	0.95
Bayesian: Equal Odds	0.97	0.88	0.96	0.97	0.75	0.95
Bayesian: Adjusted	0.97	0.86	0.96	0.97	0.77	0.95

Table 5

Corrected prediction model performance test characteristics (%) of both regression and Bayesian parameter sets after analysis of the training set (N = 100).

Model	Test Characteristics	Original			Corrected		
		Blue	Intermediate	Brown	Blue	Intermediate	Brown
MLR: IrisPlex	Sensitivity	95	93	84	95	94	87
	Specificity	91	41	85	91	29	85
	PPV	93	54	77	93	50	80
	NPV	93	89	89	93	87	90
MLR: Adjusted	Sensitivity	95	95	93	96	98	89
	Specificity	86	64	85	86	6	82
	PPV	93	73	89	95	33	82
	NPV	90	93	91	90	83	89
Bayesian: Equal odds	Sensitivity	93	92	97	95	0	92
	Specificity	91	76	77	89	100	79
	PPV	91	65	94	93	0	86
	NPV	93	95	87	91	83	88
Bayesian: Adjusted	Sensitivity	93	93	87	95	0	92
	Specificity	93	41	82	89	100	79
	PPV	91	54	80	93	0	86
	NPV	95	89	88	91	83	88

PPV = positive prediction value (correctly predicted positives), NPV = negative prediction value (correctly predicted negatives).

References

- [1] F. Liu, K. van Duijn, J. Vingerling, A. Hofman, A. Uitterlinden, A. Janssens, M. Kayser, Eye color and the prediction of complex phenotypes from genotypes, *Curr. Biol.* 19 (2009) R192–R193.
- [2] S. Walsh, F. Liu, K.N. Ballantyne, M. van Oven, O. Lao, M. Kayser, IrisPlex: a sensitiveDNA tool for accurate prediction of blue and brown eye colour in the absence of ancestryinformation, *Forensic Sci. Int. Genet.* 5 (2011) 170–180.