PACE

New AI tool significantly increases DNA analysis speed, accuracy and consistency!

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Learn how PACE streamlines artifact management and determines NOC's in a mixture

Probabilistic Assessment Contributor Estimator

No end to DNA submissions

The number of annual DNA testing submissions and the complexity of cases continues to increase. Labs working to keep backlogs to a minimum turn to leading edge tools to efficiently resolve these cases.

PACE to the Rescue

The PACE[1] technology leverages machine learning to address two key bottlenecks in the DNA analysis pipeline:

Bottleneck #1
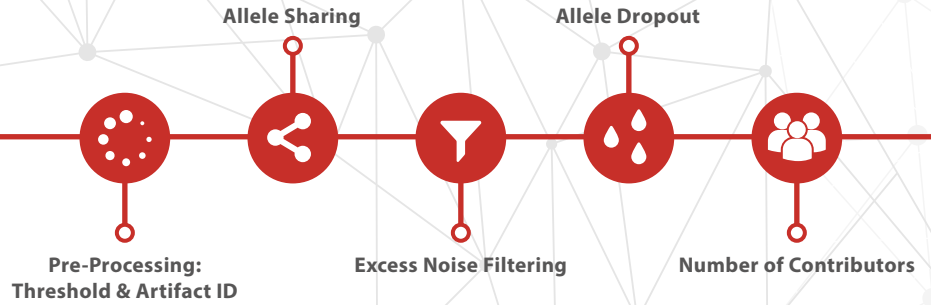**Tedious, time consuming, manual review of authentic peaks and artifacts.**

PACE performs artifact management starting from a direct import of raw files (.hid/.fsa) to:
- ✔ automatically identify authentic peaks
- ✔ remove all artifacts including pull up peaks, stutter peaks (reverse or forward, traditional or non-traditional) and remove excess noise over baseline.

Bottleneck #2
Determination of number of contributors in a forensic mixture.

Using machine learning, PACE very accurately and quickly determines the correct number of contributors in a complex mixture for up to four contributors. Machine learning allows PACE to simultaneously examine over 20 empirically derived features for each locus in every sample to provide a fast, objective, and accurate fully continuous probabilistic prediction of the correct number of contributors in challenging forensic mixtures.

Allele Sharing

Allele Dropout

**Pre-Processing:
Threshold & Artifact ID**

Excess Noise Filtering

Number of Contributors

Determine the correct number of contributors in a challenging forensic sample in seconds!

PACE completes the automated artifact management with over 90% accuracy and extremely quickly (approximately 20 seconds per sample) completing a full 96 well plate in about 30 minutes!

PACE technology has been trained and tested with:

✓ Over 10,000 samples from 15 different laboratories

✓ 18 different instruments (31XX and 3500)

✓ Samples ranging from 3.0 pg to 5.1 ng with multiple injection times/voltage

PACE is ready for immediate internal validation in your laboratory!

AVAILABLE KIT(S)
GlobalFiler, Fusion 5C, Fusion 6C
*Additional models being developed for common kits. Call us for information.

PUBLISHED DATA

1. PACE: Probabilistic Assessment for Contributor Estimation – A machine learning-based assessment of the number of contributors in DNA mixtures. M. Marciano, J. Adelman. FSI Genetics 27: 2917, 82-91.

2. A hybrid approach to increase the informedness of CE-based data using locus-specific thresholding and machine learning. M. Marciano, V. Williamson, J. Adelman. FSI Genetics 35: 2018, 26-37.

COMPUTER SPECIFICATIONS
64bit Windows PC (Win 7 or above, 1.8GHz 4MB RAM)

PACE is exclusively licensed from Syracuse University and was developed by Dr. Michael Marciano and Dr. Jonathan Adelman at the Forensic & National Security Institute.

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