

## **OSIRIS VERSION 2.0: INTELLIGENT DNA PROFILE ANALYSIS AND QUALITY ASSURANCE SOFTWARE**

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DNA profile databases have proven to be a highly successful method of solving and linking crimes over the past decade and are a broadly relied-upon forensic tool in many nations. The National DNA Index System (NDIS) has grown to nearly ten million convicted offender DNA profiles and more than 380,000 forensic profiles with more than 149,000 hits to aid 143,000 investigations in the last decade. States are following the trend to expand offenses for which DNA sample collection for NDIS is mandated to include all arrestees, thereby increasing their case loads and raising the demand for higher throughput to meet required turnaround times for profile inclusion. This need for higher efficiency comes at a time when fiscal austerity further limits already constrained laboratories. Effective and efficient quality control, already a critical component in successful high throughput testing becomes even more important at a time when human resources are already spread thin. Human evaluation of DNA profile quality and decisions regarding reanalysis of poor quality samples remain critical bottlenecks in the DNA laboratory.

We previously reported on the Open Source Independent Review and Interpretation System (OSIRIS) software which uses an independently derived set of algorithms (Goor *et al.*, 2010) that are robust indicators of multiplex STR DNA profile quality to facilitate rapid and simple review and quality assessment. The first publicly available version of OSIRIS could process typical .fsa files in 0.25 seconds with unattended batch processing, resulting in analysis of a 96-well plate in approximately 30 seconds. Here we describe Version 2.0 of OSIRIS, which represents a quantum leap in DNA analysis and quality assurance over the previous version. The new version includes a new software framework, more laboratory-customizable metrics, exquisite recognition of a broad array of artifacts and sample quality issues, sample reanalysis calculation, and LIMS integration.

OSIRIS 2.0 incorporates a new conceptual framework, called the “state message book” which encapsulates the software’s knowledge base. Through this message book laboratories can organize and present artifact messages to determine their priority and reporting status specific to the laboratory’s own protocol and report wording. Among the advantages of this approach is greater analysis transparency, which supports the court’s need for openness in scientific analysis of forensic evidence. We describe OSIRIS 2.0’s ability to add new detection parameters and reanalysis points without changing the core software, enhancing the software’s flexibility while promoting overall stability. Further, we describe OSIRIS integration with popular LIMS that enables automatically generating reanalysis recommendations for export to the LIMS system in the case of poor DNA profile quality. Thus, OSIRIS saves human resources for the most ambiguous samples while communicating specific reanalysis, re-extraction or re-amplification to the LIMS to appropriately re-queue failed samples.

These improvements have made the software much more powerful and flexible, allowing laboratories to customize it to their process rather than customizing their process to the software, and enabling laboratories to implement the software at various points in their laboratory process, depending on the laboratory's specific need.

We demonstrate OSIRIS stand-alone functionality, including improved laboratory customizability, broader artifact recognition, sample reanalysis recommendations, and export for LIMS integration as well as suggesting possible integration into laboratory workflow.

Goor RM, Forman Neall L, Hoffman D, Sherry ST, 2011. A mathematical approach to the analysis of multiplex DNA profiles. *Bulletin of Mathematical Biology* 73(8):1909-31. Epub 2010 Nov 20  
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