



### **B104 The Use of Standardized Microsoft® Office Excel Templates for Forensic Casework to Reduce Human Error and Analyst Time**

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After attending this presentation, attendees will understand the steps needed to create a standardized, multi-instrument and sample input / output Excel template system. The audience will be lead through an example of template use and be shown that a simple, yet effective, Excel template will help ease the processing of samples, especially in a batch process laboratory where different analysts will work on various stages of the STR analysis process.

This presentation will impact the forensic community by demonstrating how templates built using the ubiquitous Microsoft® Office spreadsheet program, Excel, can more efficiently manage sample and data organization, as well as perform repetitive calculations without error. Standardization of documentation in the forensic community is of the utmost importance. Templates allow analysts within a given lab to seamlessly integrate different instruments, record quality control data effortlessly, and reduce transcription and manual calculation errors.

Reducing human error will result in more accurate reports. As well, decreased analyst time per case will mean that a single analyst can process more cases overall. Improved accuracy and efficiency benefits the criminal justice community and the public that a laboratory serves.

Until recently, a DNA analyst or technician at the Harris County Medical Examiner's Office (HCMEO) had to manually record sample names at all steps using Microsoft Office WORD forms, input all sample names into all instruments used, calculate appropriate dilutions and normalization volumes, and calculate master mix volumes for all reactions. On all forms used, quality control (QC) information, such as kit and lot ID numbers, were manually entered. Since all documents and worklists were produced manually, there was no soft copy backup of the documents being generated for routine casework. The hard-copy forms resided solely within each case file.

Human error can be introduced at any of these steps. In order to meticulously avoid error, the DNA analyst and reviewer were required to spend considerable time checking and re-checking the forms, calculations, and data. This was especially difficult in our high- throughput, batch process laboratory. In addition, the process of completing the forms was not standardized among analysts making the review process even more difficult. With many DNA analysts working at different stages of the STR testing in our batch-process laboratory, the importance of stream-lining these tasks throughout the Quant/Amp/Run stages became apparent.

By employing Microsoft Office EXCEL, a template was prepared that allows the user to input sample names and, using a series of links, formulas, data validation lists, and macros, the template generates all required documentation, QC data, normalization calculations, master mix volumes, and import sheets for various instruments.

The user inputs sample names into a blank template initially and this sample is populated through all sheets in the template automatically. After typing in all samples into a quant grid sheet, master mix volume for the reaction is calculated automatically. An import sheet is also generated automatically through a series of links in order to import plate setup information into the ABI Prism® 7000 Sequence Detection System or the Applied Biosystems 7500 Real-Time PCR System. Following quantification on either machine the results are exported from the sequence detection software and subsequently added to the template. The next step involves the template recognizing, without analyst intervention, which samples require dilutions, due to extremely high quantitative value (>1000 ng/μL), and which samples are reagent blanks. The template then automatically performs normalization calculations for optimum amplification input DNA levels, as well as master mix volumes for both AmpF!STR® Profiler Plus® PCR Amplification reactions and for AmpF!STR® COfiler® PCR Amplification reactions. All QC data, including kit lot IDs, expiration dates, and thermocycler used, is available as a drop-down menu selection in the worksheet itself. Through a series of links, grid sheets for amplification and loading on the capillary electrophoresis (CE) instruments are produced automatically in order to show sample well position. On the CE grid sheet, once the instrument that will be used is selected (the ABI PRISM® 3100-Avant Genetic Analyzer or the Applied Biosystems 3130xl Genetic Analyzer), an import sheet is automatically generated. The import sheet adjusts columns such as Analysis Method, GeneMapper ID number, and Results Group in order to be able to import into different CE instruments. Injection times of the samples are also varied according to quantification data, with some samples that have low quantification values allowing a longer injection time, all without analyst intervention or manipulation. The import sheet allows import of plate setup information into the various CE instruments.

After substantial validation, all automatic links, formulas, calculations, and macros within the template have been verified using various sample and data possibilities. The template has been implemented at HCMEO and used in routine casework, validation, and training August of 2006.

#### **Excel, Multi-Protocol, Standardization**