BodeCODES™ - An automated software package for post Genotyper data review

<u>Minh Nguyen</u>1, Charles Barna2, Christopher Cave1, Brian Chen1, Ko Endo1, Mitch Holland1, Robyn Wingrove1, Tim Zolandz1, James Schumm1 1The Bode Technology Group, 7364 Steel Mill Drive, Springfield, VA 22150 2Michigan State Police, 714 South Harrison, East Lansing, MI 48823

In the laboratories at The Bode Technology Group (Bode), the generation of convicted offender STR profiles includes multiplex PCR amplification, capillary electrophoretic fragment separation and detection, and analysis with GeneScan and Genotyper softwares. Manual analysis of Genotyper results are then performed independently by two different DNA analysts. Final profiles from the analysts are compared, and consistent results are provided to a Technical Reviewer for final review. Bode has now developed and validated software to assist Technical Reviewers. This software platform, called BodeCODESTM, automates the review process and is available to CODIS laboratories that work with Bode. BodeCODES is a custom written, Microsoft Visual Basic based graphical user interface (GUI) software package that filters profiles through a set of user-defined interpretation guidelines and automatically creates lists of passed samples that are ready for CODIS entry, failed samples that require reprocessing in the wet laboratory, and any samples that require additional manual analysis or review. The software takes three tab delimited files as the data input. One file contains the internal lane standard (ILS) information corresponding to a set of profiles. The second file contains the base pair size, peak height, peak area, and allele call information made prior to human analysis (i.e. Genotyper automatic allele calls after running a Kazaam macro). The final file contains the base pair size, peak height, peak area, and allele call information made after manual analysis. BodeCODES then performs a series of calculations and filtering: checking the ILS, ladders, positive, negative and reagent blank controls, comparing the unanalyzed file against the analyzed file to find manual edits that were made by either analyst. It also checks allele calls and peak heights for such metrics as imbalance, peak height limits, pullup and stutter. It automatically deposits the profiles into Pass, Fail and To Be Checked bins. The accuracy and precision of these calculations and filtering algorithms have been thoroughly tested. The software package was used to process a test data set of 5000 real samples processed using the Promega PowerPlex16 multiplex kit and run on the ABI 3100 Genetic Analyzer. The results of the BodeCODES analysis were compared to the decisions made by a Technical Reviewer. An additional 1000 samples were created electronically to simulate anomalous profiles to test the various metrics in the system such as pullup, stutter, peak imbalance and peak height limits. A subset of these samples has been created to calibrate the software. The GUI program allows for easy user navigation throughout the various panels and input screens. Filter

criteria for automatic pass and fail actions are customized by the user through GUI screens. Because samples will have gone through the prerequisite double analyses, there will be a high rate of automatically passed samples which reduces the need for a final human check of the profiles. Conversely, any faulty samples which may have eluded both analysts will be caught by the software at this point, providing a strong final quality control step. In this way, BodeCODES provides a solution for automation of the review required in forensic human identification while still allowing for the necessary security of human expertise in the nuances of profile analysis. This simultaneously simplifies the Technical Reviewer's work while increasing confidence in the final result.