CITY OF COLUMBUS - BID WAIVER INFORMATION FORM
TO ACCOMPANY LEGISLATION WHICH WAIVES ANY PROVISIONS OF
COLUMBUS CITY CODES CHAPTER 329
(PLEASE LIMIT YOUR RESPONSE TO THIS SHEET)

1. In accordance with section 329.27 of the Columbus City Code, City Council may determine that the City's best interest is served by waiving the City Code Formal Bid procedures for the following reason(s): (Note that these reasons are all based on time. Currently, formal bid average completion time is 160 calendar days.)

☐ An unanticipated breakdown created an unplanned, emergency need.

☐ The item to be purchased is of a perishable nature, the price or availability will perish before the formal bid process can be completed.

☐ Need to extend an existing contract for one year or more where no provision for extension was included in the original bid/contract.

☐ Need to increase a contract for additional supplies/services, although the original contract obligations have been fulfilled.

☐ A new law or regulation requires immediate compliance; there is insufficient time to accomplish formal competitive bidding and satisfy the needs in order to comply.

☒ Other: There is not enough time to obtain formally advertised, competitive sealed bids to satisfy the needs because: _the grant period is expiring soon._

2. Informal bid procedure used: ☒Yes   ☐No   Explain:

I obtained a quote directly from Niche Vision who is the sole distributor of the STRmix software in the U.S.

3. Informal bids received and prices for each:

Bid received from Niche Vision for $66,300.00 which includes two licenses, support, and training

4. If lowest bid was not accepted, Explain:

Ordinance No.: _____
Approved By: Authorized Approval on Corresponding Legislative File

The International Society for Forensic Genetics (ISFG) has published recommendations for the interpretation of low-level mixtures when drop-out is possible, including recommendations on how to utilize a probability of drop-out and probability of drop-in with likelihood ratios. Currently Columbus PD still utilizes Random Match Probabilities and Combined Probabilities of Inclusion in order to perform statistical analysis of low-level or mixed casework samples. Software programs are now available that utilize either a "semi-continuous" approach which incorporates a probability of drop-out into the likelihood ratio, or a "continuous" model of interpretation which incorporates the biological variation within the data itself into the probabilistic statistical assessment.

In June, I attended a week-long intensive evaluation process to determine which of four probabilistic genotyping software programs would best fit the DNA section's long term needs. I evaluated the semi-continuous models utilized in Lab Retriever and LRmix and the continuous models of STRmix and True Allele. Each program was evaluated utilizing hands-on access to the software as well as direct training and guidance from the software developers themselves. This thorough side-by-side comparison allowed me to assess and ultimately conclude that a fully continuous model of probabilistic genotyping will best serve the needs of the DNA section due to its ability to employ mathematical modeling of the DNA profile (utilizing the observed mixture ratio, peak height ratio, stutter, the laboratory's own instrument variation, etc.) to determine the optimal genotypes present by giving weight to each of the results. These weights are determined by performing simulations of the data using the Markov Chain Monte Carlo (MCMC) method.

Having narrowed the choices down to the two software programs which utilize this fully continuous modeling, STRmix and True Allele, I was able to further decide between the two based on several additional factors:

1) True Allele requires expensive servers and is Mac-based, neither of which the DNA section currently has in-house. This will require a further investment in hardware and training. STRmix will run on the current PCs which we have in-house without a need for additional servers.

2) STRmix allows for modeling allele-specific or locus-specific stutter, whereas True Allele only has the capability to model locus-specific stutter.

3) By its own admission, the True Allele software is computer intensive and can take days to process complicated mixtures. True Allele takes almost one hour to process a 2-person mixture. Each True Allele core processor can analyze approximately ten 2 or 3-person mixtures a day. A four-processor system, such as they have at the National Institute of Standards and Technology, can take between 12 to 16 hours to run up to four 3-person mixture samples. By comparison, STRmix can interpret most mixed DNA profiles from two individual in less than five minutes, mixed DNA profiles from three contributors in approximately 20 minutes, and mixed DNA profiles from up to four contributors in less than 2 hours. In a high throughput lab such as Columbus PD, the use of True Allele for casework becomes impractical due to the time constraints it takes for sample analysis.

4) STRmix has been designed by case analysts to be comprehensible to case analysts and outputs the weight for a genotype combination that is highly intuitive and interpretable. Misrepresentation or misunderstanding of the software is mitigated through transparency in how the software works, good diagnostics in the software itself, and thorough training of the scientists that are utilizing it. The amount of front-end training provided and supported by both

ESR and NicheVision Forensics, LLC is imperative to ensuring that the case analysts utilizing the software understand how it is all working. True Allele was developed and is maintained by mathematical specialists. It is not intuitive to case working analysts and is difficult to understand how it is ultimately computing its conclusions.

5) STRmix has been utilized to interpret thousands of profiles in Australia and New Zealand forensic cases, all by forensic laboratories accredited to the ISO 17025 standards similar to Columbus PD. It is also currently in use at USACIL, CAL DOJ and NIST, and undergoing validation at the FBI. The expert witnesses in judiciary hearings associated with these cases are the caseworking scientist themselves, rather than a mathematical specialist as is required with True Allele. This ability to be represented in court by caseworking analysts is imperative when it comes to determining the practicality of validating something for use in everyday casework.

During the week of September 22-25, I and another DNA analyst attended a four day training on the use and validation of the STRmix software. This training was conducted by the actual analysts who designed the STRmix software and also currently use it in their own casework in Australia and New Zealand. A representative from NicheVision was also present to answer technical questions. As NicheVision is located only an hour away in Akron, Ohio we will also be able to obtain hands-on training from NicheVision on the STRmix software once we are ready to implement the software in our lab.

Emma Becker
Forensic Scientist III