



# WISCONSIN STATE CRIME LABORATORIES

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## WSCL Probabilistic Genotyping [i.e. STRmix™] Request Guidelines

Effective 2/10/2020

The Wisconsin State Crime Laboratories (WSCL) have recently implemented a new DNA interpretation technology, Probabilistic Genotyping<sup>1</sup> (PG) [i.e. STRmix™]. As a result, the following policies were created to provide guidance to privileged parties making requests for use of this technology in DNA cases on their behalf:

### PROBABILISTIC GENOTYPING REQUEST ACCEPTANCE

- I. The use of PG is limited to cases in which DNA analysis was performed using the currently validated DNA testing kit and analysis equipment. DNA testing performed prior to January 1<sup>st</sup>, 2019 may not be eligible for PG as a result. Please consult the reporting DNA Analyst if you have questions about this concern.
- II. To accommodate timely results for all agencies and parties throughout Wisconsin, PG requests must be provided to the WSCL at least four weeks in advance of any approaching jury trial dates. Requests made within four weeks of a jury trial may not allow adequate time for analysis to be performed; therefore, they will only be accepted on a limited basis.
- III. The PG submission timeline above is applicable to requests requiring no additional laboratory work; if additional laboratory work is needed, please refer to the general DNA Evidence Submission Guidelines.
- IV. The WSCL reserves the right to deny any request that does not meet the Division of Forensic Sciences (DFS) policy described herein or that is determined to be otherwise inappropriate.

### INITIAL PROBABILISTIC GENOTYPING INTERPRETATION REQUESTS

- I. If a DNA report issued prior to January 2020 includes profiles that may provide probative value for an active case with additional PG interpretation, please consult the reporting DNA analyst to determine whether additional interpretation is appropriate, and possible, based on the sample profile and validated procedures.
- II. Standards from all relevant individuals, including elimination standards and any available suspect standards, must be submitted if not previously analyzed.
- III. Requests for initial PG interpretation on existing profiles should include the following information:
  - Name, organization, and contact information for the requesting party;
  - WSCL case number or submitting law enforcement agency case number;
  - Submission of DNA standards, if applicable.

### ALTERNATE PROBABILISTIC GENOTYPING INTERPRETATION REQUESTS

- I. To perform statistical analysis, DNA analysts are required to set propositions. The propositions chosen are based on the analyst's assessment of the profile, relevant information regarding the item of evidence, and an effort to concede statistical doubt to the person of interest (POI) when possible. Two propositions (also known as "hypotheses") are used in each statistical calculation:
  - H1 relates to the proposed scenario in which the POI is a donor to the DNA profile
  - H2 relates to the proposed scenario in which the POI is not a donor to the DNA profile

- II. If a reported result from probabilistic genotyping interpretation differs from the theory being presented at trial as related to a specific item of evidence, it may be possible to conduct and report interpretations more directly associated with the trial theory, provided they do not violate laboratory policy. Reasons alternate propositions may be considered include:
  - Different number of DNA contributors based on case scenario;
  - An individual's DNA is expected to be present on an item (other than the POI);
  - The true contributor to the DNA profile is proposed to be a relative of the POI<sup>2</sup>.
- III. A privileged party may only request an alternate structure for the proposition associated with their trial theory. For example, if the prosecution's theory is that an individual is the real contributor to a DNA profile (H1), the prosecuting attorney may not request changes to H2 without agreement from the defense. Depending on the requested change, and absent specific information from the opposing party, WSCL will construct the additional proposition in the manner deemed most consistent with internal policy.
- IV. Requests for alternate PG propositions should include the following information:
  - Name, organization, and contact information for the requesting party;
  - WSCL case number and item number(s) associated with the request;
  - Information relevant to the alternate proposition, including:
    - Which proposition is being requested to change;
    - Proposed number of contributors;
    - Any individuals proposed to be present in the profile;
    - Whether a proposed contributor in H2 is a relative of the POI in H1.
- V. If both parties agree to changes for H1 and/or H2, please include documentation of joint communication to the lab to prevent denial of changes related to the non-communicating party.

Any requested Probabilistic Genotyping analysis that does not adhere to the policy described herein should be discussed with the DNA Technical Unit Leader of the WSCL for consideration of acceptance:

Gretchen DeGroot  
DNA Technical Unit Leader  
(414) 382-7500  
degrootga@doj.state.wi.us

Any questions concerning the policy should be directed to:

Nicole Roehm, M.S.  
Administrator  
WI Division of Forensic Sciences  
(414) 216-8769  
roehmnl@doj.state.wi.us

Thank you for your cooperation in helping the WSCL provide consistent, quality service to agencies throughout Wisconsin. We look forward to working with you.

<sup>1</sup>Probabilistic genotyping refers to the use of biological modeling, statistical theory, computer algorithms, and probability distributions to calculate likelihood ratios and/or infer genotypes for the DNA typing results of forensic samples. Probabilistic genotyping is a tool to assist a DNA analyst in the interpretation of forensic DNA typing results. It is not intended to replace the human evaluation of the forensic DNA typing results or the human review of the output prior to reporting. Probabilistic genotyping provides statistical weight in the form of a likelihood ratio.

<sup>2</sup>If a specific relative (i.e. Joe's brother John) is proposed as a true contributor, a standard of that individual should be submitted for direct comparison to the relevant profile(s). Propositions considering the possible presence of DNA from a relative address hypothetical unknown relatives ("a brother"), not specific known relatives ("his brother John").