



Priority Action Report

Biology

Biology Data Interpretation and Reporting Committee

Mechthild Prinz

February 22, 2016





Subcommittee Leadership

Position	Name	Organization	Term	Email
Chair	Robyn Ragsdale, Ph.D.	FDLE	4	robynragdale@fdle.state.fl.us
Vice Chair	Mechthild Prinz, Ph.D.	John Jay College of Criminal Justice	2	mprinz@jj.cuny.edu
Executive Secretary	Catherine Grgicak, Ph.D.	Boston University School of Medicine	3	cgrgicak@bu.edu



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3	Michael Coble, Ph.D.	NIST	4	mcoble@nist.gov
4	Kathleen Corrado, Ph.D.	Onondaga County Center for Forensic Sciences	2	kcorrado@ongov.net
5	Julie French	GE Health Care	4	julie.french@ge.com
6	Bill Gartside	San Bernardino County Sheriff's	3	bgartside@sbcasd.org
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8	Susannah C. Kehl	FBI	2	susannah.kehl@ic.fbi.gov
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10	Steven Myers	California Department of Justice Jan Bashinski DNA Laboratory	3	Steven.Myers@doj.ca.gov
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12	Peg (Margaret) Schwartz, Ph.D.	Vermont Forensic Laboratory (retired)	2	mbschwartzvt@gmail.com
13	Carl Sobieralski	Indiana State Police Laboratory Department	4	csobieralski@isp.in.gov
14	Joel Sutton	DFSC -USACIL	2	joel.d.sutton2.civ@mail.mil
15	Christian G. Westring, Ph.D.	NMS Labs	3	christian.westring@NMSlabs.com
16	Charlotte J. Word, Ph.D.	Self Employed as a Private Consultant	3	cjword@comcast.net
17	Sandy Zabell, Ph.D.	Northwestern University, Department of Mathematics	4	zabell@math.northwestern.edu



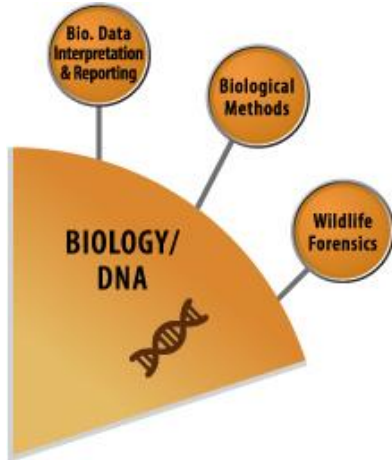
Affiliates



	Name	Organization/Employer	Task Group
	Dr. Michael Adamowicz	University of New Haven	Probabilistic Genotyping
	Dr. James Curran	University of Auckland, NZ	Probabilistic Genotyping
	Dr. Adele Mitchell	Merck	Probabilistic Genotyping
	Mark Powell	San Francisco Police Department Crime Lab	Probabilistic Genotyping
	Dr. Charles Brenner	Self	Software Validation
	Malena Jimenez	STACS DNA	Software Validation
	Dr. Desmond Lum	Rutgers University	Software Validation
	Jessica Charak	Las Vegas Metropolitan Police Department	Mixture Interpretation
	Kristen Fripp	Georgia Bureau of Investigation	Mixture Interpretation
	Marla Kaplan	Oregon State Police	Mixture Interpretation
	Beth Ordeman	Pinellas County Forensic Laboratory	Mixture Interpretation



Biological Data Interpretation and Reporting Committee



This Subcommittee (formerly called DNA Analysis 2) will focus on standards and guidelines related to forensic DNA laboratory interpretation.

The Biological Data Interpretation Committee will focus on establishing best practices, guidelines, and standards for inclusion in the OSAC Registry. The goal is to foster quality and consistency within the forensic community through the standardization of scientifically valid methods of interpretation, statistical analysis and reporting of biological results.

Summary of Standards/Guidelines Priority Actions

Priority	Working Title of Document
1	Validation Standards for Probabilistic Genotyping Systems
2	Standards for Validation Studies of DNA Mixtures and the Development and Verification of a Laboratory's Mixture Interpretation Protocol
3	Biology/DNA Software Validation
4	Statistical Interpretation



Standards/Guidelines Development Priority 1 Document

Document Title: Validation Standards for Probabilistic Genotyping

Scope: These standards are to be used by laboratories for the validation of probabilistic genotyping systems related to interpreting autosomal STR results.

Objective/rationale: If a laboratory wishes to use probabilistic genotyping in interpreting their casework, it must first be appropriately validated as with any new method prior to use. No standards currently exist for laboratories validating and implementing probabilistic genotyping systems.

Issues/Concerns: No standards currently exist for laboratories validating and implementing probabilistic genotyping systems.

Task Group Name: Probabilistic Genotyping

Task Group Chair Name: Joel Sutton

Task Group Chair Contact Information:

joel.d.sutton2.civ@mail.mil

Date of Last Task Group Meeting: 28 Jan 2015





Standards/Guidelines Development Priority 1 Document

Key Components of Standard:

Developmental validation studies needed

Internal validation studies needed

Sample types to be run with each validation study

Underlying scientific principles for the method need to be published
in a peer-reviewed journal for reference

Software modification considerations





Priority 1: Validation Standards for Probabilistic Genotyping
Task Group/Subcommittee Action Plan

Planned Actions	OSAC Process Stage (e.g., SDO 100)	Assignee	Estimated Completion Date
Review SAC comments and adjudicate	SDO-300	Task Group	04 Feb 2016
Post to Kavi for BDIRC to review and vote on changes	SDO-300	Task Group Chair	11 Feb 2016
Submit to SAC for vote	SDO-300	BDIRC Chair	?



Standards/Guidelines Development Priority 2 Document



Document Title: Standards for Validation Studies of DNA Mixtures and the Development and Verification of a Laboratory's Mixture Interpretation Protocol

Scope: These standards are for the design and evaluation of validation studies for mixed DNA samples and the development of appropriate interpretation protocols for mixtures based on the validation studies performed.

Objective/rationale: Determine standards to allow for verification of a laboratory's mixture interpretation protocol

Issues/Concerns: No existing standards

Task Group Name: Mixture Interpretation Verification
Task Group Chair Name: Carl Sobieralski/Shawn Montpetit
Task Group Chair Contact Information:
csobieralski@isp.in.gov / smontpetit@pd.sandiego.gov
Date of Last Task Group Meeting: 01/29/2016



Standards/Guidelines Development

Priority 2: Standards for Validation Studies of DNA Mixtures and the Development and Verification of a Laboratory's Mixture Interpretation Protocol

Key Components of Standard:

The laboratory shall only interpret mixed DNA data for which there are supporting internal validation studies and data, supporting publications when available, and relevant and appropriate interpretation protocols in the laboratory.

- The mixture studies performed as part of internal validation studies will include representative samples of those to be interpreted in casework
- The data from mixture studies performed by the laboratory shall be evaluated and summarized
- The laboratory shall verify and document that the mixture interpretation protocols developed from the validation studies generate reliable and consistent interpretations and conclusions for the types of mixed DNA samples typically encountered by the laboratory



Priority 2: Standards for Validation Studies of DNA Mixtures and the Development and Verification of a Laboratory's Mixture Interpretation Protocol

Task Group/Subcommittee Action Plan

Planned Actions	OSAC Process Stage (e.g., SDO 100)	Assignee	Estimated Completion Date
Fill in required forms. Initiate project.	SDO-0	Task Group	01/29/2016
Move draft document to next level (BDRIC, Methods SC, RC, SAC)	SDO-200/SDO-300	Task Group	02/05/2016





Standards/Guidelines Development Priority 3 Document

Document Title: Biology/DNA Software Validation

Scope: This document includes guidelines for the validation of software used in a forensic DNA laboratory that impacts the integrity of the evidence, the analytical process, interpretations and/or statistical conclusions. Additional guidelines and standards may be applicable to specialized software packages.

Objective/rationale: Few standards are available for the validation of software used by a forensic DNA laboratory.

Issues/Concerns: Newly developed or modified software programs should be validated prior to implementation.

Task Group Name: Biology/DNA Software Validation

Task Group Chair Name: Susannah Kehl

Task Group Chair Contact Information:

susannah.kehl@ic.fbi.gov

Date of Last Task Group Meeting: Jan 29, 2016



Standards/Guidelines Development Priority 3 Document: Bio/DNA Software Validation

Key Components of Standard:

The goal is to provide standards or guidelines for the validation of software used by forensic laboratories when conducting forensic DNA testing.

Establish standards or guidelines for the validation of software programs and upgrades that impact the integrity of the evidence, the analytical process, interpretation and/or conclusions.



Priority 3: Bio/DNA Software Validation

Task Group/Subcommittee Action Plan

Planned Actions	OSAC Process Stage (e.g., SDO 100)	Assignee	Estimated Completion Date
Provide draft document to relevant subcommittees for input, revise as appropriate	SDO-0	Susannah Kehl	March 1, 2016
Provide draft document to resource committees and SAC for input, revise as appropriate	SDO-0	Susannah Kehl	May 1, 2016
Create Project and fill in required forms	SDO-0	Task Group	Jan 29, 2016
Submit SDO Submission Form	SDO-100	Susannah Kehl	Jan 29, 2016
Move draft document to next level	SDO-200/300	Task Group	June 1, 2016



Standards/Guidelines Development Priority 4 Document

Document Title: Statistical Interpretation

Scope: Description of existing methods and delineating appropriate areas of application

Objective/rationale: State generally accepted methods and limitations for statistical analysis of single source and mixed DNA profiles

Issues/Concerns: Concerns have been raised about the correct application of different statistical approaches used in the interpretation of mixtures.

Task Group Name: Statistical Interpretation

Task Group Chair Name: Sandy Zabell

Task Group Chair Contact Information:

zabell@math.northwestern.edu

Date of Last Task Group Meeting: January 28, 2016



Standards/Guidelines Development Priority 4 Document

Key Components of Standard:

Description of existing methods, and guidance on appropriate areas of application

Note: Our understanding is that SWGDAM will very shortly release for comment a substantial revision of its 2010 “SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories”. The work of the Task Group has been temporarily suspended until this document is available for review to avoid duplication of effort.





Priority 4: Statistical Interpretation

Task Group/Subcommittee Action Plan

Planned Actions	OSAC Process Stage (e.g., SDO 100)	Assignee	Estimated Completion Date
Review of documents	SDO 100	Dr. Zabell	May 1, 2016
Drafting of standard	SDO 100	Members of TG	October 1, 2016





Standards/Guidelines Development Priority 5 Document

- Review and standardization of terminology within the field using current documentation.
 - Being performed in conjunction with other Biology subcommittees

Task Group Name: Terminology

Task Group Chair Name: Christian Westring, Ph.D.

Task Group Chair Contact Information:

christian.westring@NMSSlabs.com





Priority 5: Terminology

Task Group/Subcommittee Action Plan

- SAC level task group encompassing all of the DNA subcommittees
- Working on collating terms used in forensic biology analysis



Summary of Standards/Guidelines Priority Actions

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1	Validation Standards for Probabilistic Genotyping Systems
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3	Biology/DNA Software Validation
4	Statistical Interpretation
5	Terminology (SAC wide task group)



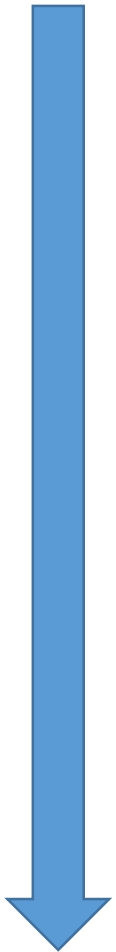
Items of Interest Identified

- **Analytical and stochastic thresholds** – guidance on valid approaches on how to determine these thresholds
- **Front end evaluation of DNA profile data** – guidance on determining suitability for various interpretation approaches
- **Hypothesis building for LRs** – guidance on assumptions, numerator, denominator
- **Monitoring analysts performance for DNA interpretation** – guidance on internal assessment of interpretation competency including statistical evaluations
- **Reporting of DNA conclusions for mixtures** – standard defining required components

Research Gaps Identified - 1

(in order of evidence analysis process)



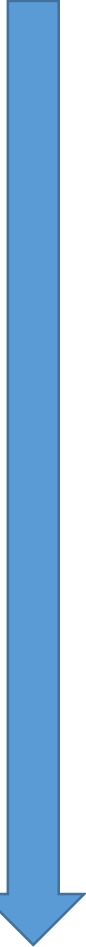
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- More efficient collection of DNA at the scene and from evidence items
 - Quantitative interpretation of color signals for serology testing results
 - More efficient extraction of DNA from evidence items
 - Assessment of specific classes of evidence types to determine the necessity to quantify DNA before amplification



Research Gaps Identified - 2

(in order of evidence analysis process)



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- Develop software to tools to assist in characterization and utilization of STR typing validation data
 - **Software solutions for Y-STR mixture deconvolution**
 - Research on how to design proficiency tests for complex data interpretation and probabilistic genotyping
 - **Impacts of laboratory, assumptions, and model decisions on continuous likelihood ratios**
 - Best practices to avoid biases in interpretation of DNA profiles





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