

# Glossary of Terms and Acronyms as used in DNAmix 2021

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The purpose of this glossary is to detail specific terms/acronyms and their associated definitions as used in this study. We recognize that not all of these terms are used in the same way universally: this glossary is to specify how these terms are used in this study, to avoid misunderstandings or ambiguity in our analyses of your responses.

<b>Amp/CE settings</b>	<p>A specific combination of settings used in preparing an electropherogram, including the amplification kit, number of amplification cycles, volume of amplification reaction, CE instrument, and injection time/voltage.</p> <p>In the <i>NoC Subtest</i> and <i>ICSA Subtest</i>, the electropherograms will be created using the most popular combinations of Amp/CE settings (as reported during registration) in an attempt to accommodate the standard operating procedures used by participating laboratories.</p>
<b>Casework scenarios questionnaire</b>	<p>Subtest of this study intended to assess analysis procedures or decisions that may vary depending upon the case scenario, and the nature of participating laboratories' mixture casework.</p>
<b>Comparison</b>	<p>The examination of a <i>DNA mixture profile</i> with respect to a <i>reference profile</i> to assess the degree of similarity or difference.</p> <p>In the <i>ICSA Subtest</i>, the comparison of <i>DNA mixture profile</i> with respect to the <i>person of interest reference profile</i> results in a <i>comparison conclusion</i> and/or <i>statistical analysis</i> results.</p>
<b>Comparison conclusion</b>	<p>Categorical conclusion (e.g. <i>exclusion</i>, <i>inconclusive</i>, <i>inclusion</i>) resulting from a <i>comparison</i>, generally supported by <i>statistical analysis</i> results.</p>
<b>Comparison packet</b>	<p>Data provided in the <i>ICSA Subtest</i>, containing</p> <ul style="list-style-type: none"> <li>• 1 <i>DNA mixture profile</i></li> <li>• 1 <i>person of interest reference profile</i></li> <li>• (for <i>SAK Comparison packets</i>):             <ul style="list-style-type: none"> <li>○ 1 <i>victim reference profile</i></li> <li>○ 0 or 1 <i>consensual partner reference profile</i></li> </ul> </li> <li>• (for <i>Non-SAK Comparison packets</i>):             <ul style="list-style-type: none"> <li>○ 0 or 1 <i>expected contributor reference profile</i></li> </ul> </li> <li>• Textual information:             <ul style="list-style-type: none"> <li>○ <i>Amp/CE Settings</i></li> <li>○ Quantitation data (as measured by Quantifiler Trio during quantitation of the mixture)</li> </ul> </li> <li>• Quality assurance files for each mixture profile and each reference profile:             <ul style="list-style-type: none"> <li>○ Amplification positive control</li> <li>○ Amplification negative control</li> <li>○ 2 allelic ladders</li> </ul> </li> </ul>
<b>Consensual partner</b>	<p>For the purposes of this study, an individual known to have had consensual intimate contact with a <i>victim</i> of a sexual assault.</p> <p><i>Comparison packets</i> that are <i>simulated sexual assault kits (SAKs)</i> include 0 or 1 <i>consensual partner reference profiles</i>.</p>
<b>DNA mixture profile</b>	<p>A <i>profile</i> that contains more than one contributor.</p>
<b>Exclusion</b>	<p>An analyst's <i>comparison conclusion</i>, based upon the results of <i>comparison</i> and/or <i>statistical analysis</i>, that a known individual is eliminated as a possible contributor to a <i>DNA mixture profile</i>.</p>
<b>Expected contributor</b>	<p>A known individual who is expected or assumed to be a contributor to a <i>DNA mixture profile</i>, such as the owner of an item or a member of a household.</p> <p><i>Non-SAK comparison packets</i> include 0 or 1 <i>expected contributor reference profiles</i>.</p> <p>(<i>Reference profiles</i> in <i>SAK comparison packets</i> do not use the term "expected contributor" in order to explicitly label <i>victim</i> and <i>consensual partner reference profiles</i>.)</p>
<b>HID File</b>	<p>A format used for files generated by the Applied Biosystems 3500 series genetic analyzers that has become a de facto interchange standard (replacing the earlier FSA file format).</p> <p>The <i>profiles</i> used in this study are electropherograms in HID file format.</p>

<b>ICSA Subtest</b>	<i>Interpretation, comparison, and statistical analysis</i> — a subtest of this study intended to assess the <i>categorical conclusions</i> and <i>statistical analysis</i> reported in response to a <i>comparison packet</i> . Each participant will complete the <i>ICSA Subtest</i> for 7 <i>comparison packets</i> .
<b>Inclusion</b>	An analyst's <i>comparison conclusion</i> , based upon the results of a <i>comparison</i> and/or <i>statistical analysis</i> , that a known individual may be considered a possible contributor to a <i>DNA mixture profile</i> .
<b>Inconclusive</b>	An analyst's <i>comparison conclusion</i> , based upon the results of a <i>comparison</i> and/or <i>statistical analysis</i> , that a known individual can neither be <i>excluded</i> nor <i>included</i> as a possible contributor to a <i>DNA mixture profile</i> .
<b>Interpretation</b>	The process of evaluating a <i>DNA mixture profile</i> for purposes including, but not limited to, defining assumptions related to the mixture profile, distinguishing between alleles and artifacts, assessing the possibility of degradation, inhibition, and stochastic effects, and determining whether the profile is suitable for comparison. This study evaluates interpretation in the <i>ICSA Subtest</i> , and some aspects of interpretation in the <i>NoC Subtest</i> .
<b>Non-SAK Comparison packet</b>	A <i>comparison packet</i> that is not a simulated sexual assault kit (SAK).
<b>Number of contributors (NoC)</b>	In this study, the number of individuals known (under controlled conditions or very specific casework scenarios) or assumed (as estimated by an analyst for casework profiles) to have contributed to a <i>DNA mixture profile</i> .
<b>NoC Packet</b>	Data provided in the <i>NoC Subtest</i> , containing <ul style="list-style-type: none"> <li>• 1 <i>DNA mixture profile</i></li> <li>• Textual information: <ul style="list-style-type: none"> <li>○ <i>Amp/CE Settings</i></li> <li>○ Quantitation data (as measured by Quantifiler Trio during quantitation of the mixture)</li> </ul> </li> <li>• Quality assurance files: <ul style="list-style-type: none"> <li>○ Amplification positive control</li> <li>○ Amplification negative control</li> <li>○ 2 allelic ladders</li> </ul> </li> </ul>
<b>NoC Subtest</b>	The <i>NoC Subtest</i> of this study is being conducted to assess the variability of assessments of suitability and number of contributors.
<b>Policies and procedures (P&amp;P) questionnaire</b>	Subtest of this study intended to capture information pertaining to participating laboratories' standard operating procedures (SOPs) relevant to DNA mixture <i>interpretation, comparison, and statistical analysis</i> .
<b>Person of interest (POI)</b>	An individual whose contribution to the mixture is in question (such as an alleged perpetrator). In the <i>ICSA Subtest</i> , one <i>person of interest reference profile</i> will be provided in each <i>comparison packet</i> .
<b>Profile</b>	A DNA electropherogram provided in <i>HID format</i> . A <i>DNA mixture profile</i> contains more than one contributor (containing known and/or unknown individuals). A <i>reference profile</i> contains one known contributor ( <i>person of interest, victim, consensual partner, or expected contributor</i> ).
<b>Reference profile</b>	A <i>profile</i> for a single subject.
<b>SAK Comparison packet</b>	A <i>comparison packet</i> that is a simulated sexual assault kit (SAK).
<b>Statistical analysis</b>	The computation of weight of evidence for the comparison of a <i>reference profile</i> with a <i>DNA mixture profile</i> . Potential statistical analysis results include the combined probability of inclusion/exclusion (CPI/CPE), random match probability (RMP), modified random match probability (mRMP), or likelihood ratio (LR).
<b>Suitable / Suitable for comparison</b>	An analyst's determination during <i>interpretation</i> that a <i>DNA mixture profile</i> is appropriate for use in <i>comparisons</i> and/or <i>statistical analyses</i> . (not <i>unsuitable</i> )
<b>Unsuitable / Unsuitable for comparison</b>	An analyst's determination during <i>interpretation</i> that a <i>DNA mixture profile</i> cannot be used for <i>comparisons</i> and/or <i>statistical analyses</i> for reasons including (but not limited to) poor or limited data quality, mixture complexity, or a failure to meet laboratory quality assurance requirements. (not <i>suitable</i> )

**Victim**

For the purposes of this study, the complainant in a sexual assault from whom *simulated sexual assault kit* samples are collected.

In the *ICSA Subtest*, one *victim reference profile* will be provided in each *SAK comparison packet*.