identification process. One issue in libraries of older allelic ladders arises in how they are assembled (e.g., manually selected) and how well does the library cover the variations. The density and dimensionality of the library's coverage, as well as how representative the included ladders are, may also have an impact. Even if all external parameters can be held constant in theory, differences in composition, injection and noise in the measurements can affect how well it represents or fits a typical or particular sample. Another issue in using older allelic libraries is how to select the best fit or sufficiently fit allelic ladder from the allelic ladder library. If the ladders in the ladder library have significant noise or other effects that deviate from a typical or particular sample run, the risk of ambiguous selection increases. For example, ambiguity in ladder selection can occur if two ladders in the ladder library are very similar. In some cases, the peaks in a test sample may be identified identically regardless of which of two ladders is selected for the identification, and the ambiguity is of no concern. In another case, two very different ladders can provide a sufficient fit to the test sample, and only small differences, such as noise, may determine which ladder is ultimately selected as reference for the sample. This has a higher risk of happening if the test sample includes none or a very small numbers of peaks, for example less than five or ten.

[0018] An incorrect identification of a DNA fragment in forensic analysis can have very severe implications, e.g. in criminal investigations by law enforcement, and in judicial criminal and civil trials where the fates of lives of individuals are decided. Therefore, methods to improve the accuracy and speed up the analysis time of sample identification using DNA fragment analysis are needed.

[0018a] An aspect of the present invention provides a method of testing a biological sample comprising deoxyribonucleic acid (DNA) molecules for presence of a plurality of alleles, wherein DNA fragments obtained using the biological sample and corresponding to different alleles of the plurality of alleles have different fragment sizes, the method comprising: obtaining test fragment sizing data by migrating and scanning, using an analysis instrument, a plurality of

labelled DNA fragments corresponding to the biological sample; using a pre-computed model to dynamically generate one or more first synthetic allelic ladders, the pre-computed model based on analysis of a plurality of fragment sizing data sets obtained from a plurality of previously conducted sample runs using either the same analysis instrument or using another comparable analysis instrument to measure fragment sizes; determining whether the one or more first synthetic allelic ladders fits the test fragment sizing data sufficiently for identifying which of the plurality of alleles are present in the biological sample; if the determination is that the one or more first synthetic allelic ladders does not fit the test fragment sizing data sufficiently, then generating one or more additional synthetic allelic ladders based on varying one or more parameters of the pre-computed model and determining whether any of the one or more additional synthetic allelic ladders fits the test fragment sizing data sufficiently for identifying which of the plurality of alleles are present in the biological sample; and once a sufficiently fitting synthetic allelic ladder is identified, using the sufficiently fitting synthetic allelic ladder to determine which of the plurality of alleles are present in the biological sample.

[0018b] Another aspect of the present invention provides a deoxyribonucleic acid (DNA) analysis instrument comprising: a capillary electrophoresis (CE) genetic analyzer comprising: a sample port operable to receive a test biological sample comprising one or more DNA molecules, wherein the DNA molecule comprises one or more DNA loci and each DNA locus is associated with a plurality of alleles; a thermal cycler connected to the sample port comprising a polymerase chain reaction (PCR) chamber operable to perform DNA amplification of DNA fragments of the test biological sample; at least one CE capillary connected to the thermal cycler operable to receive and separate the amplified DNA fragments of the test biological sample; and an optical detector operable to scan the CE capillary to detect fluorescent values of the amplified DNA fragments of the test biological sample; and a signal processor connected to the optical detector and operable to generate test fragment sizing data corresponding to fluorescent values of the amplified DNA fragments of the test biological sample; and a DNA profile generator connected to the CE genetic

analyzer comprising: a pre-computed model to dynamically generate a first synthetic allelic ladder, the pre-computed model having been derived based on statistical analysis of a plurality of fragment sizing data sets obtained from a plurality of sample runs previously conducted on allelic ladder samples using either the same CE instrument or using another comparable CE instrument to measure fragment sizes; a fitter to determine whether the first synthetic allelic ladder fits the test fragment sizing data sufficiently for identifying which of the plurality of alleles are present in the biological sample, and if the fit is not sufficient, then signaling the pre-computed model to generate one or more additional synthetic allelic ladders based on varying one or more parameters of the pre-computed model and determining whether any of the one or more additional synthetic allelic ladders fits the test fragment sizing data sufficiently for identifying which of the plurality of alleles are present in the biological sample; and an allele caller to determine which of the plurality of alleles are present in the biological sample once a sufficiently fitting synthetic allelic ladder is identified.

[0018c] Another aspect of the present invention provides a method of testing a biological sample comprising deoxyribonucleic acid (DNA) molecules for presence of a plurality of alleles, wherein DNA fragments obtained using the biological sample and corresponding to different alleles of the plurality of alleles have different fragment sizes, the method comprising: obtaining test fragment sizing data by migrating and scanning, using a capillary electrophoresis (CE) instrument, a plurality of fluorescently labelled DNA fragments corresponding to the biological sample; using the test fragment sizing data to search a stored allelic ladder library, wherein the stored allelic ladder library comprises one or more stored synthetic allelic ladders that have been synthetically generated using a pre-computed model, the pre-computed model having been derived based on statistical analysis of a plurality of fragment sizing data sets obtained from a plurality of sample runs previously conducted on allelic ladder samples using either the same CE instrument or using another comparable CE instrument to measure fragment sizes; determining whether the one or more stored allelic ladders fits the test fragment sizing data sufficiently to comprise a sufficiently

fitting allelic ladder for identifying which of the plurality of alleles are present in the biological sample; if the one or more stored allelic ladders does not fit the test fragment sizing data sufficiently, then dynamically generating one or more additional synthetic allelic ladders using the pre-computed model based on varying one or more parameters of the pre-computed model and determining whether any of the one or more additional synthetic allelic ladders fits the test fragment sizing data sufficiently to comprise a sufficiently fitting allelic ladder for identifying which of the plurality of alleles are present in the biological sample; and once a sufficiently fitting allelic ladder is identified, using the sufficiently fitting allelic ladder to determine which of the plurality of alleles are present in the biological sample.

[0018d] A non-transitory computer readable medium comprising a memory storing one or more instructions which, when executed by one or more processors of at least one computing device, perform validation of a DNA analysis instrument for testing a biological sample comprising one or more deoxyribonucleic acid (DNA) molecules, wherein the DNA molecule comprises one or more DNA loci and each DNA locus is associated with a plurality of alleles, by: obtaining test fragment sizing data corresponding to fragment sizing values corresponding to a plurality of fragments of a control biological sample, the plurality of fragments detected by an electrophoresis genetic analyzer of the DNA analysis instrument; and using a pre-computed model to dynamically generate one or more first synthetic allelic ladders, the pre-computed model having been derived based on statistical analysis of a plurality of fragment sizing data sets obtained from a plurality of sample runs previously conducted on allelic ladder biological samples using either the same electrophoresis instrument or using another comparable electrophoresis instrument to measure fragment sizes; determining whether the first synthetic allelic ladder fits the control sample fragment sizing data sufficiently for identifying which of the plurality of alleles are present in the control biological sample and satisfies a pre-specified set of validation criteria; if the first synthetic allelic ladder does not fit the control sample fragment sizing data sufficiently, then generating one or more additional synthetic allelic ladders based on varying one or more parameters of the pre-

computed model and determining whether any of the one or more additional synthetic allelic ladders fits the test fragment sizing data sufficiently for identifying which of the plurality of alleles are present in the control biological sample and satisfies a pre-specified set of validation criteria; and once a sufficiently fitting synthetic allelic ladder is identified, determining whether the plurality of alleles of the control biological sample match a corresponding plurality of alleles of the sufficiently fitting synthetic allelic ladder.

[0018e] A non-transitory computer readable medium comprising a memory storing one or more instructions which, when executed by a one or more processors of at least one computing device, perform testing of a biological sample comprising one or more deoxyribonucleic acid (DNA) molecules, wherein the DNA molecule comprises one or more DNA loci and each DNA locus is associated with a plurality of alleles, by: obtaining test fragment sizing data by migrating and scanning, using an analysis instrument, a plurality of labelled DNA fragments corresponding to the biological sample; using a pre-computed model to dynamically generate at least one first synthetic allelic ladder, the pre-computed model based on analysis of a plurality of fragment sizing data sets obtained from a plurality of previously conducted sample runs using either the same analysis instrument or using another comparable analysis instrument to measure fragment sizes; determining whether any of the first synthetic allelic ladders fit the test fragment sizing data sufficiently for identifying which of the plurality of alleles are present in the biological sample; if first synthetic allelic ladder does not fit the test fragment sizing data sufficiently, then generating one or more additional synthetic allelic ladders based on varying one or more parameters of the pre-computed model and determining whether any of the one or more additional synthetic allelic ladders fits the test fragment sizing data sufficiently for identifying which of the plurality of alleles are present in the biological sample; and once a sufficiently fitting synthetic allelic ladder is identified, using the sufficiently fitting synthetic allelic ladder to determine which of the plurality of alleles are present in the biological sample.

[0019] Embodiments of the present invention describe a method of testing a biological sample comprising deoxyribonucleic acid (DNA) molecules for presence of a plurality of alleles, wherein DNA fragments obtained using the biological sample and corresponding to different alleles have different fragment sizes. A