

**COMPUTATIONAL MODEL FOR BETTER SELECTION OF  
GENETIC LOCI FOR FORENSIC HUMAN IDENTIFICATION**

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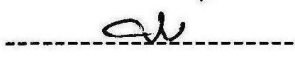


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## DEDICATION

This thesis is dedicated to my parents with thanks for everything throughout the years, to my mother who waited so long for this.

This thesis would be incomplete without a mention of the support given me by my brother Dr. Salem, to whom this thesis is dedicated.

Miss Dania Masadeh, without her lifting me up when this thesis seemed interminable, I doubt it should ever have been completed.

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## LIST OF CONTENTS

Title	Pages
Committee Decision	ii
Dedication	iii
Acknowledgment	iv
List of contents	v
List of Tables	vi
List of Figures	x
List of Abbreviations	xi
Abstract	xii
1. Introduction	1
1.1 Bioinformatics and Computational Biology	1
1.2 Biological Concepts	5
1.3 The Biological Tasks of Bioinformatics	12
1.4 DNA Fingerprints and Community Service	15
1.5 Forensic Science and Human Identification	17
1.6 Selection of Genetic Markers for Forensic Applications	19
1.7 Objectives of the Study	20
1.8 Proposed Computed System	22
1.9 Thesis Structure	23
2. Literature Review	24
3. Materials and Methods	33
3.1 Perl Programming Language	33
3.2 STR Genetic Loci Row Data	35
3.3 Biostatistics of Forensic Parameters	48
3.4 Model Flowchart	50
3.5 Use Case Diagram	52
3.6 Web Diagram	53
3.7 The computed system User's Guide	54
4. Results	59
5. Discussion	176
6. Conclusions and Future Works	185
References	186
Abstract (in Arabic)	192

## LIST OF TABLES

No.	Title	Page
1	The CSF1PO STR Genetic Locus	35
2	The D13S317 STR Genetic Locus	36
3	The D16S539 STR Genetic Locus	36
4	The D18S51 STR Genetic Locus	37
5	The D21S11 STR Genetic Locus	38
6	The D3S1358 STR Genetic Locus	39
7	The D5S818 STR Genetic Locus	39
8	The D7S820 STR Genetic Locus	40
9	The D8S1179 STR Genetic Locus	40
10	The F13A1 STR Genetic Locus	41
11	The FES/FPS STR Genetic Locus	42
12	The FGA STR Genetic Locus	42
13	The Penta D STR Genetic Locus	43
14	The Penta E STR Genetic Locus	44
15	The TH01 STR Genetic Locus	45
16	The TPOX STR Genetic Locus	45
17	The vWA STR Genetic Locus	46
18	STR Allelic Windows	47
19	The Observed and Expected Genotypic Frequency Distributions of the CSF1PO STR Genetic Locus in Jordanian Population	59
20	The CSF1PO Allelic Frequency Distributions	60
21	The Forensic Parameters for the CSF1PO STR Genetic Locus	61
22	The Observed and Expected Genotypic Frequency Distributions of the D3S1358 STR Genetic Locus in Jordanian Population	61
23	The D3S1358 Allelic Frequency Distributions	62
24	The Forensic Parameters for the D3S1358 STR Genetic Locus	63
25	The Observed and Expected Genotypic Frequency Distributions of the D5S818 STR Genetic Locus in Jordanian Population	63
26	The D5S818 Allelic Frequency Distributions	64
27	The Forensic Parameters for the D5S818 STR Genetic Locus	64
28	The Observed and Expected Genotypic Frequency Distributions of the D7S820 Genetic Locus in Jordanian Population	65
29	The D7S820 Allelic Frequency Distributions	66
30	The forensic Parameters for the D7S820 STR Genetic Locus	66
31	The Observed and Expected Genotypic Frequency Distributions of the D8S1179 STR Genetic Locus in Jordanian Population	67
32	The D8S1179 Allelic Frequency Distributions	68
33	The Forensic Parameters for the D8S1179 STR Genetic Locus	69
34	The Observed and Expected Genotypic Frequency Distributions of the D13S317 STR Genetic Locus in Jordanian Population	69
35	The D13S317 Allelic Frequency Distributions	70
36	The Forensic Parameters for the D13S317 STR Genetic Locus	70
37	The Observed and Expected Genotypic Frequency Distributions of the D16S539 STR Genetic Locus in Jordanian Population	71
38	The D16S539 Allelic Frequency Distributions	72

39	The Forensic Parameters for the D16S539 STR Genetic Locus	72
40	The Observed and Expected Genotypic Frequency Distributions of the D18S51 STR Genetic Locus in Jordanian Population	73
41	The D18S51 Allelic Frequency Distributions	75
42	The Forensic Parameters for the D18S51 STR Genetic Locus	75
43	The Observed and Expected Genotypic Frequency Distributions of the D21S11 STR Genetic Locus in Jordanian Population	76
44	The D21S11 Allelic Frequency Distributions	78
45	The Forensic Parameters for the D21S11 STR Genetic Locus	78
46	The Observed and Expected Genotypic Frequency Distributions of the F13A1 STR Genetic Locus in Jordanian Population	79
47	The F13A1 Allelic Frequency Distributions	81
48	The Forensic Parameters for the F13A1 STR Genetic Locus	81
49	The Observed and Expected Genotypic Frequency Distributions of the FES/FPS STR Genetic Locus in Jordanian Population	82
50	The FES/FPS Allelic Frequency Distributions	82
51	The Forensic Parameters for the FES/FPS STR Genetic Locus	83
52	The Observed and Expected Genotypic Frequency Distributions of the FGA STR Genetic Locus in Jordanian Population	83
53	The FGA Allelic Frequency Distributions	85
54	The Forensic Parameters for the FGA STR Genetic Locus	85
55	The Observed and Expected Genotypic Frequency Distributions of the Penta D STR Genetic Locus in Jordanian Population	86
56	The Penta D Allelic Frequency Distributions	88
57	The Forensic Parameters for the Penta D STR Genetic Locus	88
58	The Observed and Expected Genotypic Frequency Distributions of the Penta E STR Genetic Locus in Jordanian Population	89
59	The Penta E Allelic Frequency Distributions	91
60	The Forensic Parameters for the Penta E STR Genetic Locus	92
61	The Observed and Expected Genotypic Frequency Distributions of the TH01 STR Genetic Locus in Jordanian Population	92
62	The TH01 Allelic Frequency Distributions	93
63	The Forensic Parameters for the TH01 STR Genetic Locus	93
64	The Observed and Expected Genotypic Frequency Distributions of the TPOX STR Genetic Locus in Jordanian Population	94
65	The TPOX Allelic Frequency Distributions	95
66	The Forensic Parameters for the TPOX STR Genetic Locus	95
67	The Observed and Expected Genotypic Frequency Distributions of the vWA STR Genetic Locus in Jordanian Population	96
68	The vWA Allelic Frequency Distributions	97
69	The Forensic Parameters for the vWA STR Genetic Locus	97
70	Virtual Observed and Expected Genotypic Frequency Distributions for the CSF1PO STR Genetic Locus	98
71	Virtual CSF1PO Allelic Frequency Distributions	100
72	Virtual CSF1PO Forensic Parameters	100
73	Virtual Observed and Expected Genotypic Frequency Distributions for the D3S1358 STR Genetic Locus	101
74	Virtual D3S1358 Allelic Frequency Distributions	102
75	Virtual D3S1358 Forensic Parameters	103

76	Virtual Observed and Expected Genotypic Frequency Distributions for the D5S818 STR Genetic Locus	103
77	Virtual D5S818 Allelic Frequency Distributions	104
78	Virtual D5S818 Forensic Parameters	105
79	Virtual Observed and Expected Genotypic Frequency Distributions for the D7S820 STR Genetic Locus	105
80	Virtual D7S820 Allelic Frequency Distributions	107
81	Virtual D7S820 Forensic Parameters	107
82	Virtual Observed and Expected Genotypic Frequency Distributions for the D8S1179 STR Genetic Locus	108
83	Virtual D8S1179 Allelic Frequency Distributions	111
84	Virtual D8S1179 Forensic Parameters	112
85	Virtual Observed and Expected Genotypic Frequency Distributions for the D13S317 STR Genetic Locus	112
86	Virtual D13S317 Allelic Frequency Distributions	113
87	Virtual D13S317 Forensic Parameters	114
88	Virtual Observed and Expected Genotypic Frequency Distributions for the D16S539 STR Genetic Locus	114
89	Virtual D16S539 Allelic Frequency Distributions	115
90	Virtual D16S539 Forensic Parameters	116
91	Virtual Observed and Expected Genotypic Frequency Distributions for the D18S51 STR Genetic Locus	116
92	Virtual D18S51 Allelic Frequency Distributions	124
93	Virtual D18S51 Forensic Parameters	125
94	Virtual Observed and Expected Genotypic Frequency Distributions for the D21S11 STR Genetic Locus	125
95	Virtual D21S11 Allelic Frequency Distributions	133
96	Virtual D21S11 Forensic Parameters	134
97	Virtual Observed and Expected Genotypic Frequency Distributions for the F13A1 STR Genetic Locus	134
98	Virtual F13A1 Allelic Frequency Distributions	136
99	Virtual F13A1 Forensic Parameters	137
100	Virtual Observed and Expected Genotypic Frequency Distributions for the FES/FPS STR Genetic Locus	137
101	Virtual FES/FPS Allelic Frequency Distributions	138
102	Virtual FES/FPS Forensic Parameters	138
103	Virtual Observed and Expected Genotypic Frequency Distributions for the FGA STR Genetic Locus	138
104	Virtual FGA Allelic Frequency Distributions	150
105	Virtual FGA Forensic Parameters	152
106	Virtual Observed and Expected Genotypic Frequency Distributions for the Penta D STR Genetic Locus	152
107	Virtual Penta D Allelic Frequency Distributions	155
108	Virtual Penta D Forensic Parameters	156
109	Virtual Observed and Expected Genotypic Frequency Distributions for the Penta E STR Genetic Locus	156
110	Virtual Penta E Allelic Frequency Distributions	161
111	Virtual Penta E Forensic Parameters	162
112	Virtual Observed and Expected Genotypic Frequency Distributions for the	162



	TH01 STR Genetic Locus	
113	Virtual TH01 Allelic Frequency Distributions	164
114	Virtual TH01 Forensic Parameters	164
115	Virtual Observed and Expected Genotypic Frequency Distributions for the TPOX STR Genetic Locus	165
116	Virtual TPOX Allelic Frequency Distributions	166
117	Virtual TPOX Forensic Parameters	166
118	Virtual Observed and Expected Genotypic Frequency Distributions for the vWA STR Genetic Locus	167
119	Virtual vWA Allelic Frequency Distributions	168
120	Virtual vWA Forensic Parameters	169
121	Summary of Results	170

## LIST OF FIGURES

No.	Title	Page
1	Bioinformatics Software Cycle	25
2	Cyclical Refinement of Predictive Computer Models used to Define Further Biological Experiments	25
3	Diagram of the Pise Interface Generator Architecture	26
4	Modular Organization of BioSuite	27
5	The Alternative Software Architectures of the Pathway Tools.	29
6	Forensic Parameters Model Flowchart	51
7	Use Case Diagram	52
8	Web diagram	53
9	Registration Form	54
10	Login Form	54
11	Options Menu	55
12	New population and experiment Menu	56
13	New experiment data Form	56
14	New experiment data-Continued	57
15	Options Menu	57
16	Admin Tools	58
17	Statistical Analysis	58
18	Statistical Analysis for population	58
19	Statistical Analysis data for population-Continued	171
20	Statistical Analysis Graph / PD	172
21	Statistical Analysis Graph / Observed Homo	173
22	Statistical Analysis Graph / Observed Hetero	173
23	Statistical Analysis Graph / PI	174
24	Statistical Analysis Graph / PIC	174
25	Statistical Analysis Graph / I <sub>G</sub>	175

## LIST OF ABBREVIATIONS

DNA	Deoxyribo Nucleic Acid
HWE	Hardy-WEINBERG Equilibrium
PCR	Polymerase Chain Reaction
STR	Short Tandem Repeat
BLAST	Basic Local Alignment Search Tool
NCBI	National Center for Biotechnology Information
Homo <sub>obs</sub>	Observed Homozygosity
PIC	Polymorphism Information Content
P <sub>D</sub>	Power of Discrimination
P <sub>I</sub>	Power of Identity
I <sub>G</sub>	Impossible Genotypes
(VH <sub>obs</sub> ) <sub>max</sub>	Maximum Observed Heterozygosity
(VTP <sub>D</sub> ) <sub>max</sub>	Maximum Virtual Target Power of Discrimination

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## **ABSTRACT**

Short Tandem Repeat (STR) sequences have been established as genetic markers in forensic investigations due to their ability to individualize or identify accused persons. The choice for inclusion of STR genetic locus into a forensic genetic STR panel depends on several genetic parameters including its independent inheritance and polymorphic nature.

Three biological concepts were implemented in order to determine the most applicable STR genetic loci in forensic settings for the Jordanian population. The biological concepts comprise the maximum virtual target power of discrimination  $(VTP_D)_{max}$ , maximum observed heterozygosity  $(VH_{obs})_{max}$ , and the number of impossible genotypes  $(I_G)$  for each STR genetic locus. Computer software was designed

considering these three concepts. The selection of the most applicable STR sequences for inclusion in a forensic panel of genetic loci for DNA fingerprinting in Jordanian individuals was successfully achieved.

This study has shown that out of the seventeen implemented STR genetic loci that included the TPOX, D16S539, Penta D, Penta E, VWA, FGA, CSF1PO, TH01, D21S11, D18S51, D13S317, D8S1179, D7S820, D5S818, D3S1358, F13A1 and FES/FPS, four STR genetic loci could be reasonably used for forensic application in the Jordanian population. The four STR markers are the TH01, Penta D, FES/FPS, and the D18S51 loci. They exhibited a relatively reasonable power of discrimination of 0.999987 for the Jordanian population which does not exceed 5.5 million individuals.

## (1) INTRODUCTION

### 1.1 Bioinformatics and Computational Biology

Defining the terms of bioinformatics and computational biology is not an easy task; both of them although distinct have become completely interchangeable terms. Bioinformatics and computational biology are multidisciplinary fields, involving researchers from different areas of specialty, including statistics, computer science, physics, biochemistry, genetics, molecular biology and mathematics (Rouchka, 2003). Both disciplines apply principles of information sciences and technologies to make the vast, diverse, and complex life sciences data more understandable and useful.

The National Institute of Health Biomedical Information Science and Technology Initiative Consortium in United States of America recognized that no definition of bioinformatics and computational biology could completely eliminate overlap with other activities or preclude variations in interpretation by different individuals and organizations (Wu et al, 2002). Bioinformatics was defined as the research, development, or application of computational tools and approaches for expanding the use of biological, medical, behavioral or health data, including those to acquire, store, organize, archive, analyze, or visualize such data. While computational biology is the development and application of data-analytical and theoretical methods, mathematical modeling and computational simulation techniques to the study of biological, behavioral, and social systems.

The field of bioinformatics is rapidly growing as a research tool in biological sciences. It dates back to the 1960s following the discovery of the DNA double helix and cracking the genetic code. This allowed for the ability to treat genes as strings of information that guide the building of cellular components, the faithful reproduction of an organism's genetic material and its ability to evolve (Buehler and Rashidi, 2005).

However, the term "Bioinformatics" first appears in the literature in 1989 (Retrieved October 19, 2006, from <http://www.bioinformatics.vg/what-is-bioinformatics.shtml>). The beginning of bioinformatics can be traced back to 1968 where a collection of protein sequences known as the Atlas of Protein Sequence and Structure were established (Fox, 2005). This was one of the early significant experiments in bioinformatics where a sequence similarity searching program for identification of the origins of a viral gene was applied (Doolittle et al., 1983). In their study, Fox and coworkers used a computer program for determining the similarities between a cancer causing viral sequence and the human gene for the platelet-derived growth factor. Their work provided important mechanistic insights for biologists working on how a viral sequence could cause cancer (Waterfield et al., 1983). From this first initial application of computers to biology, the field of bioinformatics has exploded. The rapid growth of bioinformatics can be illustrated by the growth of DNA sequences contained in the public repository of nucleotide sequences called GenBank (Luscombe et al., 2001). As a result of this surge in genetic data, computers have become indispensable to biological research because of the ease with which computers can handle large quantities of data and probe the complex dynamics observed in nature.

Large-scale activities that use bioinformatics and computational biology are genomics and proteomics (Fox, 2005). Genomics refers to the analysis of genomes. A genome can be thought of as the complete set of DNA sequences that codes for the hereditary material that is passed on from generation to generation. These DNA sequences include all of the genes which are defined as the functional and physical unit of heredity passed from parent to offspring. Thus, genomics refers to the sequencing and analysis of all of these genomic entities, including genes and transcripts, in an organism. Proteomics refers to the analysis of the complete set of proteins or proteome.

In addition to genomics and proteomics, there are many more areas of biology (Siitari and Koivistoinen, 2004) where bioinformatics is being applied (i.e., metabolomics, transcriptomics, bioindustry). Each of these important areas in bioinformatics aims to understand complex biological systems.

The future of bioinformatics is integration of several data sources to come up with a prediction. For example, integration of a wide variety of clinical and genomic data will allow us to use disease symptoms to predict genetic mutations and vice versa (Fox, 2005). The integration of Geographical Information System (GIS) data such as maps and weather systems with crop health and genotype data will allow us to predict successful outcomes of agriculture experiments (Fox, 2005). Another future area of research in bioinformatics is large-scale comparative genomics. For example, the development of tools that can do 10 way comparisons of genomes will push forward the discovery rate in this field of bioinformatics (Fox, 2005). Along these lines, the modeling and visualization of full networks of complex systems could be used in the future to predict, for example, how the system (or cell) reacts to a drug. A technical set of challenges faces bioinformatics and is being addressed by faster computers, technological advances in disk storage space, and increased bandwidth, but by far one of the biggest hurdles facing bioinformatics today, is the small number of researchers in the field. This is changing as bioinformatics moves to the forefront of research, but this lag in expertise has led to real gaps in the knowledge of bioinformatics in the research community.

In general, the aims of bioinformatics include organizing the generated data in a way that allows researchers to access existing information, to submit new entries as they are produced and carry out data analysis (Luscombe et al, 2001). moreover, to develop



tools and resources that aid in the analysis of data. For example, having sequenced a particular protein, it is of interest to compare it with previously characterized sequences.

## 1.2 Biological Concepts

Each human individual is made up of several hundred billions of microscopic cells in addition to a considerable noncellular material such as bones and water. Cells come in a variety of shapes and sizes. Some are rounded, some flat, some angular, some irregular, and some such as nerve cells have long projections. A typical cell, such as a white blood cell, is about 1/2,000-inch in diameter. The part of greatest genetic interest, the nucleus, is usually roughly spherical. All the cells in the body are descended from a single fertilized egg, which by successive divisions has produced the vast number and various cell types that the human body comprises. The nucleus contains a number of wormlike or threadlike microscopic bodies, called chromosomes. Each species has a characteristic number of chromosomes - somatic human cells have 46. The nucleus of a fertilized human egg starts out with 23 chromosomes from the mother's egg and a corresponding set of 23 from the father's sperm. A sperm or egg cell, containing a single set of chromosomes, is said to be haploid. A cell with two sets, a total of 23 pairs or 46 chromosomes, is diploid (Berg and Singer, 1992; Campbell and Reece, 2007; Lewin, 1990; Mange and Mange, 1999; Snustad and Simmons, 2000; Twyman, 1998; Watson et al., 1987).

The fertilized egg divides into two, these two into four, and so on throughout embryonic development, and differentiate into many kinds of cells, throughout life. The process of cell division (mitosis) distributes these chromosomes precisely. Before the cell divides, each chromatid goes to each daughter cell. Thus, after cell division, each of the daughter cells has identical chromosomes, the same as in the parent cell. This precise process assures that every cell in the body has an identical 46-chromosome makeup in its nucleus. In the formation of a sperm or egg, the chromosome number is halved. By the process of meiosis, the chromosomes are allocated so that each gamete

(sperm or egg) has one representative of each pair, for a total of 23. The members of different pairs behave independently in meiosis. If the chromosome from the number 1 pair in a sperm is maternal, that is, derived from the mother, the chromosome from the number 2 pair is equally likely to be either maternal or paternal, and so on. For convenience, the human chromosomes are identified by number, starting with the largest. Most chromosomes have a short and a long arm, designated by p and q respectively. The two members of a chromosome pair, as seen in the microscope, are identical in shape and size. There is, however, an exception, the sex chromosomes. In the human male cell, the Y chromosome is much smaller than the X chromosome. A body cell from a female has two X chromosomes; a cell from a male has an X and Y. Through the process of meiosis, an egg has a single X chromosome in addition to the 22 other autosomal chromosomes. A sperm has either an X or a Y. The chance event at fertilization, whether the successful sperm carries an X or Y chromosome, determines whether the developing embryo will be female or male. The X and Y chromosomes are not numbered, so the chromosomes of a gamete are numbered 1 through 22, plus X or Y (Berg and Singer, 1992; Campbell, 2007; Lewin, 1990; Mange and Mange, 1999; Snustad et al, 2000; Twyman, 1998; Watson et al., 1987).

Each chromosome is a three-dimensional object, and appears during division as a condensed sausage-shaped object, and a long, often invisible thread at other stages of cell cycle. The core of the chromosome is a very long, extremely thin thread of deoxyribonucleic acid (DNA). The DNA molecule is a double thread, coiled into a helix. The genetically important constituents of DNA are the four nucleotides Adenine (A), Thymine (T), Guanine (G), and Cytosine(C). The double thread consists of two phosphate-sugar strands bridged by complementary pairs of nucleotides, AT, TA, GC, or CG. A always pairs with T and G with C. The DNA molecule can be thought of as a

twisted rope ladder with four kinds of stair steps. Each chromosome has the base pairs in a specific order. The genetic difference between one gene and another, or one person and another, is not in the kinds of base pairs; always the same four are used. The genetic reference is the sequence in which the four bases occur and hence determining the genetic individuality. With an enormous number of base pairs, the number of orders is astronomical. No wonder we are all different; yet at the DNA level we are remarkably alike. In this context, the chromosomes of a sperm or egg contain about 3 billion base pairs, so a body cell has 6 billion. The whole set of base pairs in a gamete is the genome. The precise processes of DNA replication and cell division ensure to a large extent that each cell contains the same sequence of DNA bases. Any two human genomes are alike for the overwhelming majority of their bases; DNA samples from two unrelated persons differ on the average at only about one base per thousand. Yet  $1/1,000$  of 6 billion is 6 million. These 6 million base differences are sufficient to produce all the genetic differences of those two persons. Although any two genomes differ at some  $1/1,000$  of their bases, these are not necessarily the same bases as those that are different in another pair of genomes. So the great diversity of shapes, sizes, color, behavior, disease susceptibility, and so on that characterize humanity is no surprise. Even though two persons share an overwhelming proportion of their DNA, there are still enough differences that no two are genetically alike, unless they are identical twins. If we had the complete sequence of the DNA from two persons, or even 1 percent of the DNA, we could (except for identical twins) be certain if they came from one person or two. However, in practice a much smaller fraction of DNA is analyzed so that identification becomes probabilistic rather than certain. In addition to differences in individual nucleotides, there are also variations in their number. There are some DNA regions in which a small number of bases are repeated a variable number of times, so

the total amount of DNA in different individuals is not exactly the same. Some of the regions that are of the greatest use forensically are such repeated sequences in which the number of repeats varies from person to person (Berg and Singer, 1992; Campbel, 2007; Lewin, 1990; Mange and Mange, 1999; Snustad and Simmons, 2000; Twyman, 1998; Watson et al., 1987).

The aim of the Human Genome Project is to determine the complete sequence of base pairs in a representative person or a composite of several persons in order to utilize the complete encoded genetic information for the determination of genes responsible for the developmental outcome. A gene is a stretch of DNA from 1,000 to 100,000 or more base pairs in length that has a specific function; usually a gene is responsible for the production of particular protein. Alternative forms of the gene are called alleles. Alleles that express their characteristic trait only when present in duplicate are called recessive. Those alleles, that are effective when present in duplicate or singly, are called dominant. An individual with two representatives of the same allele, *aa* or *AA*, is a homozygous. If the two are different, *Aa*, the individual is a heterozygous. Hence, the genetic makeup (i.e. the genotype) of an individual could be homozygous or heterozygous. The genotypic designation may be extended to include several gene loci. Phenotype, on the other hand, is the trait or character inflicted by the individual's genotype. A phenotype could be the color of the eye if observed externally or a metabolic defect if measured chemically. It may include several traits or it may be a quantitative measure such as height (Berg and Singer, 1992; Campbel, 2007; Lewin, 1990; Mange and Mange, 1999; Snustad and Simmons, 2000; Twyman, 1998; Watson et al., 1987).

The rules of inheritance can be deduced from the behavior of chromosomes in meiosis and fertilization. However, before the mechanism of inheritance was understood, the rules were inferred by the Austrian monk, Gregor Mendel, from his

experiments breeding garden peas. Although his studies were reported in 1865, they remained unknown until the principles were rediscovered in 1900. It was immediately obvious that Mendel's hereditary factors followed the same rules as chromosomes; hence the genes must be carried by chromosomes.

Each gene occupies a specific position (or locus) on a specific chromosome. There at least two different alleles at a locus in a population. There may be hundreds in some extreme cases, but of course any fertilized egg has at most two kinds. A locus with more than two alleles in the population is said to be polymorphic. Highly polymorphic loci are particularly useful for forensic identification. In the process of meiosis one member of each chromosome pair is included in the gamete. Early in meiosis, the two homologous chromosomes pair up. While lined up side by side they often break at corresponding sites and exchange genetic material with their partners. Thus, two genes that were formerly on the same chromosome may end up on different chromosomes. The tendency for two different genes on the same chromosome to be inherited together is called linkage. The closer together two genes are on the chromosome, the less probable it is that a break will occur between them and the more probable that they are to be inherited together. This property has been used in classical genetics to "map" the position of genes on the chromosome; the closer together two genes are, the more tightly linked they are in inheritance (Berg and Singer, 1992; Campbel, 2007; Lewin, 1990; Mange and Mange, 1999; Snustad and Simmons, 2000; Twyman, 1998; Watson et al., 1987).

Genes are ordinarily transmitted from generation to generation unchanged. Sometimes, however, the gene is changed by a rare process called mutation. When a gene mutates, the mutant form is as stable and as regularly transmitted as the original. Mutations come in all sizes. A mutation may be a substitution of one base for another,

or one or more bases may be gained or lost, or the order of a group of bases may be changed, inverted for example. Chromosomes are sometimes broken and reattached in new ways. Or a whole chromosome may be lost or duplicated. All of these come under the general name of mutation, although the term is more often restricted to those changes that are transmitted as a Mendelian unit (Berg and Singer, 1992; Campbel, 2007; Lewin, 1990; Mange and Mange, 1999; Snustad and Simmons, 2000; Twyman, 1998; Watson et al., 1987).

The genes make up only a tiny fraction of the DNA. The rest, the great bulk -about 97 percent- has no known function. It is sometimes referred to as “junk DNA.” Nevertheless, these nongenic regions show the same genetic variability that genes do, in fact usually more. These differences are not overt, but can be detected by laboratory tests. Regions of DNA that are used for forensic analysis are usually not genes, but rather are located in those parts of the chromosomes without known functions, or if part of a gene, not in the part that produces a detectable effect. Nevertheless, the words commonly used for describing genes (e.g., allele, homozygous, polymorphic) are carried over to DNA regions used for identification. It is customary to call the genotype for the group of loci involved in a forensic analysis a profile (Berg and Singer, 1992; Campbel, 2007; Lewin, 1990; Mange and Mange, 1999; Snustad and Simmons, 2000; Twyman, 1998; Watson et al., 1987).

The loci that have been most extensively used in forensics are regions in which a short segment of DNA is repeated tandemly many times. For example, a length of 20 bases may be repeated dozens or even hundreds of times. Such long sequences are much more mutable than genes usually are, the mutations being an increase or decrease in length. If the DNA is cut by a restriction enzyme on both sides of such a region or specific primer sequences are used in an amplification reaction such as the PCR, the

region may be isolated and its size measured. Thus, different numbers of repeats are identified by their size, and this polymorphic trait (DNA fingerprints) was implemented in forensic investigations (Berg and Singer, 1992; Campbel, 2007; Lewin, 1990; Mange and Mange, 1999; Snustad and Simmons, 2000; Twyman, 1998; Watson et al., 1987).



### 1.3 The Biological Tasks of Bioinformatics

The need for Bioinformatics capabilities has been precipitated by the explosion of publicly available genomic information resulting from the Human Genome Project (Retrieved November 01, 2006, from <http://kbrin.a-bldg.louisville.edu/~rouchka/HOMEPAGE/definition.html>). The importance of the large genomic information generated from the Human Genome Project in understanding human diseases and in the identification of new molecular targets for drug discovery (Retrieved November 01, 2006 from <http://kbrin.a-bldg.louisville.edu/~rouchka/HOMEPAGE/definition.html>) was recognized by many universities, government institutions and pharmaceutical firms. These authorities formed bioinformatics groups, consisting of computational biologists and bioinformatics computer scientists to unravel the mass of information generated by large scale human genome sequencing efforts in laboratories around the world. In this context, bioinformatics is used for unlimited number of tasks.

These tasks included several biological examples such as finding homologs ('twins') of a gene in a certain species given a sequence in a model species. For example finding a rice gene given the sequence of an Arabidopsis gene which has been characterized already (Retrieved October 19, 2006, from <http://www.bioinformatics.vg/what-is-bioinformatics.shtml>) or comparing the similarity between two or more gene sequences to get a measure of their relatedness can be achieved (Retrieved October 19, 2006, from <http://www.bioinformatics.vg/what-is-bioinformatics.shtml>).

Other examples included the design of specific primers for sequencing or amplifying unknown or interesting genes. In this case, the primers must not anneal to other primers nor to themselves forming undesirable dimers or hairpin loops respectively - these are things a program can check very quickly - but which would take

human hours. Furthermore, the primer must be specific to be checked easily through a public gene database such as the GenBank to assure their specificity for the species being studied. Lastly, simple calculations such as ideal annealing temperature and molecular weight can also be computed without operator error (Retrieved October 19, 2006, from <http://www.bioinformatics.vg/what-is-bioinformatics.shtml>). Moreover, the work included the reconstruction of genes from Expressed Sequence Tags (EST) sequences. ESTs are short pieces of genes which are expressed, which have been cloned and sequenced - then deposited into the public gene databases. Given a 'zero database' - or no information to begin with, it is possible to reconstruct whole cDNA molecules by using regions of overlap to predict which sequences should fit together. Furthermore, given a known sequence from a different species, ESTs can be aligned against that template with their overlapping ends to allow the construction of a contig, or contiguous sequence (Retrieved October 19, 2006, from <http://www.bioinformatics.vg/what-is-bioinformatics.shtml>). Furthermore, there is a huge amount of work being undertaken to classify the proteins encoded by genes into superfamilies and families. Protein sequences can be compared using an ever-increasing number of methods, their relatedness can be measured, and closely related proteins can then be assigned families. Although grouping should involve the effective comparison of a sequence in GenBank with all the others. Since the number of sequences in GenBank is very large, this would take a long time, so clever methods are used to model groups based upon smaller number of sequences. Protein families are an extremely good example of the use of mathematics to group proteins into families and to make the information resulting from that both useful and accessible (Retrieved October 19, 2006, from <http://www.bioinformatics.vg/what-is-bioinformatics.shtml>).

Indeed, the various potential benefits of bioinformatics made many scientists to find bioinformatics exciting since it holds the potential to dive into a whole new world of uncharted territory. Therefore, scientists are looking into bioinformatics as a new science and a new way of thinking that could potentially lead to many relevant biological discoveries.

Although technology enables bioinformatics, bioinformatics is still very much about biology. Biological questions drive all bioinformatics projects. Important biological questions can be addressed by bioinformatics and include understanding the genotype-phenotype connection for human disease, understanding structure to function relationships for proteins, and understanding biological networks. Bioinformaticians often find that the reagents necessary to answer these interesting biological questions do not exist. Thus, a large part of a bioinformatician's job is building tools and technologies as part of the process of asking the question. For many, bioinformatics is very popular because scientists can apply both their biology and computer skills to developing reagents for bioinformatics research. Many scientists are finding that bioinformatics is an exciting new territory of scientific questioning with great potential to benefit human health and society.

#### 1.4 DNA Fingerprints and Community Service

DNA fingerprints are useful in several community service applications such as the human health care and the justice system. DNA fingerprinting is used to diagnose inherited disorders in both prenatal and newborn babies in hospitals around the world. These disorders may include cystic fibrosis, hemophilia, Huntington's disease, familial Alzheimer's, sickle cell anemia, and thalassemia (Retrieved February, 15, 2007, from [http://www.accessexcellence.org/RC/AB/BA/DNA\\_Fingerprinting\\_Basics.html](http://www.accessexcellence.org/RC/AB/BA/DNA_Fingerprinting_Basics.html)). Early detection of such disorders enables the medical staff and the parents to be prepared for proper treatment of the child. In some programs, genetic counselors use DNA fingerprint information to help prospective parents understand the risk of having an affected child. In other programs, prospective parents use DNA fingerprint information in their decisions concerning affected pregnancies. Research programs to locate inherited disorders on cellular chromosomes depend on the information contained in DNA fingerprints. By studying the DNA fingerprints of relatives who have a history of some particular disorder, or by comparing large groups of people with and without the disorder, it is possible to identify DNA patterns associated with the disease in question. This work is a necessary first step in designing an eventual genetic cure for these disorders (Retrieved February, 15, 2007, from [http://www.accessexcellence.org/RC/AB/BA/DNA\\_Fingerprinting\\_Basics.html](http://www.accessexcellence.org/RC/AB/BA/DNA_Fingerprinting_Basics.html)).

Police laboratories around the world use DNA fingerprints to link suspects to biological evidences including blood, semen stains, hair, and items of clothing found at the scene of a crime. The analyses of specific regions of DNA has become a powerful tool in forensic human identification, and has been utilized extensively in forensic identity testing in areas such as criminal justice and immigration laws. This use examines the science of DNA and the forensic application of DNA-based identity

testing to determine the identity of a person or to evaluate the degree of genetic relatedness between two or more persons. Since 1987, hundreds of cases have been decided with the assistance of DNA fingerprint evidence. Another important use of DNA fingerprints in the court system is to establish paternity in custody and child support litigation. In these applications, DNA fingerprints bring an unprecedented, nearly perfect accuracy to the determination. Because every organ or tissue of an individual contains the same DNA fingerprint, the various authorities around the world utilized DNA fingerprinting techniques for personal identification since it proved to be far superior to the dogtags, dental records, and blood typing strategies currently in use (Retrieved February, 15, 2007, from [http://www.accessexcellence.org/RC/AB/BA/DNA\\_Fingerprinting\\_Basics.html](http://www.accessexcellence.org/RC/AB/BA/DNA_Fingerprinting_Basics.html)).

## 1.5 Forensic Science and Human Identification

Forensic science has come to mean the application of the natural and physical sciences to the resolution of conflicts within a legal setting. In other words, forensic science is the application of scientific methods and techniques to problems in the context of crime and the legal system. Technically, forensic science is a branch of science that involves the application of molecular methodologies to determine the state of a piece of physical evidence. The evidence could be extracted from a crime scene, a victim, a suspect, or other potentially involved individuals. These evidence samples include body fluids, tissues, bone, nail and hair (Inman and Rudin, 1997).

Using scientific methods, deductions are made about how the evidence had come to be in that state (Inman and Rudin, 1997). Thus the ultimate job of a forensic scientist is to use inferences and deductions to interpret the physical fact, so that criminal or civil disputes are resolved (Inman and Rudin, 1997). Thus, the application of science in the legal arena is fundamentally one of reconstruction, that is, trying to assist in determining what happened, where it happened, when it happened, and who was involved. The primary way in which reconstruction occurs is through establishing associations between items.

In forensic science, there are two key concepts by which associations between items are made. The first concept is known as identification while the second is known as individualization (Inman and Rudin, 1997). An item is identified when it can be placed into a class of items with similar characteristics, while an item is individualized when it can be described in such a way that no other item in the universe is like it, even items identified as being similar. Individualization relies on the acquisition of traits that are so rare, either alone or in combination with other traits (Inman and Rudin, 1997). Both concepts are currently analyzed using tandemly repeated DNA sequences known

as genetic markers, in which individuals can be distinguished only by their genetic marker profiles. The more markers compared, the more likely differences between individuals will be revealed (Reynolds and Sensabaugh, 1991). Because of this ability, forensic DNA analysis has played a crucial role in the investigation and resolution of thousands of violent crimes since the late 1980s.

Currently, genetic markers involve short tandem repeats of DNA sequences known shortly as STRs. STRs are the most widely used markers for forensic DNA testing (Retrieved October 21, 2006, from <http://www.dna.gov/research/>). This is because of their high discriminatory power, good resolution of alleles, and the ability to rapidly process samples using multiplexed Polymerase Chain Reaction (PCR). Presently, thirteen STRs have been selected as the core loci upon which the Federal Bureau of Investigations (FBI) National DNA Index System (NDIS) of United States of America has been built (Retrieved October 19, 2006, from <http://www.dna.gov/research/>).

## 1.6 Selection of Genetic Markers for Forensic Applications

Not all genetic markers are suitable for forensic applications. There are several criteria by which genetic markers are evaluated for forensic use. Some of these criteria are related to the method of analysis, while others are related to the nature of the genetic marker.

The method of analysis used to analyze forensic sample must be reliable, rapid, simple to perform, detects unambiguous and qualitative differences between alleles, and consumes very small amount of material. The later is very important since, the smaller quantity of a sample that must be consumed, the greater the opportunity for retyping and analyzing for additional markers (Reynolds and Sensabaugh, 1991; Ludes and Clisson, 2000). With regard to the criteria that are related to the genetic marker, the marker and its alleles must be inherited independently (Tracey, 2001), and shows a high degree of heterozygosity (Reynolds and Sensabaugh, 1991; Ludes and Clisson, 2000). Thus, the dual goals driving the selection of forensic genetic markers are to extend the range of evidence samples from which useful information can be obtained and to enhance the discrimination power ( $P_D$ ).  $P_D$  is defined as the probability that two individuals chosen at random will possess different genotypes for the marker being tested. Higher  $P_D$  values indicate a greater individualization potential because a large portion of the population can be excluded. A higher degree of discrimination among individuals in the population can be obtained when several genetic markers are examined. For a single marker, the greater the number of alleles and more even their distribution throughout a population, the higher the power of discrimination (Jones, 1972; Reynolds and Sensabaugh, 1991).



## 1.7 Objectives Of The Study

Since the advent of STRs as genetic markers for human individualization and identification, population-data bases concerning the allelic and genotypic distribution of variously used STRs have been compiled for use in the different forensic arenas such as human identification and paternity testing. As mentioned earlier, the choice of an STR is greatly dependent on two forensic parameters indicated as Heterozygosity and the Power of Discrimination ( $P_D$ ) which in turn depend on the allelic window for that STR genetic locus. It is established that the larger the allelic window and hence the higher the Heterozygosity and  $P_D$  values (Hamad et al., 2001; Salem et al., 2003; Yasin, 2002), the more powerful the genetic locus as an evidence in issues requiring a high discrimination status. Furthermore, the size of the allelic window was found to vary from one population to another affecting both the heterozygosity and  $P_D$  parameters (Hamad et al., 2001; Salem et al., 2003; Wenz et al.; 1998; Yasin, 2002). Thus, different and controversial heterozygosity and  $P_D$  values were obtained for any single STR genetic locus studied around the world. This means that an STR genetic locus of a high Heterozygosity and  $P_D$  values for one population could be less important for another population which necessitates the search for own-population-optimal STR genetic loci. This indicates that the various human populations do not constitute "ideal" populations according to the mathematical model independently developed by Godfrey H. Hardy and Wilhelm Weinberg in 1908 (Campell, 2007). In their mathematical model, they illustrated the resume of alleles and genotypes in an "ideal" population, one that is free of many of the complications that affect real populations. A set of simple assumptions were put forward to design the model. Firstly, they assumed that individuals of all genotypes have equal rates of survival and equal reproductive success; that is, there is no selection. Secondly, no new alleles are created or converted from one allele into

another by mutations. Thirdly, individuals do not migrate into or out of the population. Fourthly, the population is infinitely large, which in practical terms means that the population is large enough that sampling errors and other random effects are negligible. Finally, individuals in the population mate randomly. Thus, in an "ideal" population, the frequency of alleles does not change from generation to generation. Moreover, after one generation of random mating offspring genotype frequencies can be predicted from the parent allele frequencies and would be expected to remain constant from that point. Therefore, and since the results of different studies have shown variation in the allelic window size and allelic frequencies distribution for real populations, Hardy-Weinberg assumptions can not truly or completely be accounted for because of reasons out of the scope of this study. Hence, the variation in the Heterozygosity and  $P_D$  values, which are allelic-dependent, is amenable among the various human populations.

Since Heterozygosity and  $P_D$  values are important measurement for the power and usefulness of an STR genetic locus, we embarked in this study on a search for the virtual or optimal Heterozygosity and  $P_D$  values to be used as population-reference values in order to determine the fitness of any STR genetic loci for use in the forensic arenas. To accomplish this task, bioinformatics and computational biology aspects were applied using the Jordanian-forensic databases for seventeen STR genetic loci compiled by a group of Jordanian scientists working in forensic DNA analysis at the Hashemite University, Jordan (Hamad et al., 2001; Salem et al., 2003; Yasin, 2002).

## 1.8 Proposed Computed System

A complete system for forensic DNA analysis could enhance user convenience and relieve analysts from performing repetitive, time-consuming and cumbersome tasks. A feature of DNA fingerprinting involves the use of molecular biology techniques to extract molecules representing the solution for a forensic dilemma. Current applied extraction methods often employ automated PCR and gel electrophoresis, both of which we believe are error-prone and financially costly. The extracted results are then subjected to intensive traditional statistical analysis which is time-consuming and subjected to experimental and human errors. Thus, the necessity has appeared to develop an analysis system for forensic STR typing capable of performing all necessary determinations of forensic parameters. Furthermore, such an analysis system has the feature of prediction of the most suitable forensic genetic markers for human identification and individualization in any human population. This analysis system is new computer software that is capable of implementing any statistical procedures used in forensic population genetics.

## 1.9 Thesis Structure

In the introductory chapter, an explanation was provided regarding the differences in terminology between the term of "bioinformatics" and the term of "computational biology". A brief biological background that is required to understand the main concepts and terminology in genetics and molecular biology was included. Examples showing the importance of bioinformatics in biological research were demonstrated. The role of forensic science in the community and the applications of short tandem repeats in criminal and human identification were illustrated. The various characteristics of short tandem repeat sequences were described. Finally, the aim of this study was explained, and a computational model for solving the problem of STR selection was proposed.

Chapter 2 explores the literature review of human identification using conventional statistical analysis of individuals' genotypes. Importance of the computer software model is over the conventional statistical methods is illustrated.

Chapter 3 comprises a description of the design and structure of the computational software model, and describes the complete process of implementation of such model to achieve our target in determining the better genetic loci.

Chapter 4 presents the results of our study as tables and charts. Moreover, we list the results of the various genetic loci that are used in our experiments in order to investigate there results in future works.

Chapter 5 discusses the results of our study and presents a logical analysis of the extracted results. It provides answers to any forensic authorities about the applicability of certain STR genetic loci in their respective populations. It includes concluding remarks and offers directions for future work.

## (2) LITERATURE REVIEW

Majority of researchers are now looking at free bioinformatics software tools publicly available on the Internet such as BLAST, ClustalX, Phylip and many others (Retrieved February 20, 2007, from [http://home.biotec.or.th/newscenter/Uploads/WE\\_pic/rad82B7B.pdf](http://home.biotec.or.th/newscenter/Uploads/WE_pic/rad82B7B.pdf))

Commercial software such as GCG Wisconsin package or those from Accelrys™ are being used sparingly in some universities. There are also attempts to create software that can harvest the CPU cycles of idle computers to solve a computation intensive problem, e.g. comparative genomics which attempts to identify a set of common genes of pathogenic bacteria. There is also another Bioinformatics research that tries to create a model of regulatory pathway by using neural network. More and more Bioinformatics activities are under investigation (Retrieved February 20, 2007, from [http://home.biotec.or.th/newscenter/Uploads/WE\\_pic/rad82B7B.pdf](http://home.biotec.or.th/newscenter/Uploads/WE_pic/rad82B7B.pdf)).

The role of bioinformatics software in biology is hypothesis-driven research cycle as illustrated in Figure 1 (H., 2002). The Cyclical refinement of predictive computer models used to define biological experiments, including the optimization step as shown in Figure 2 (Brusic et al, 2001).

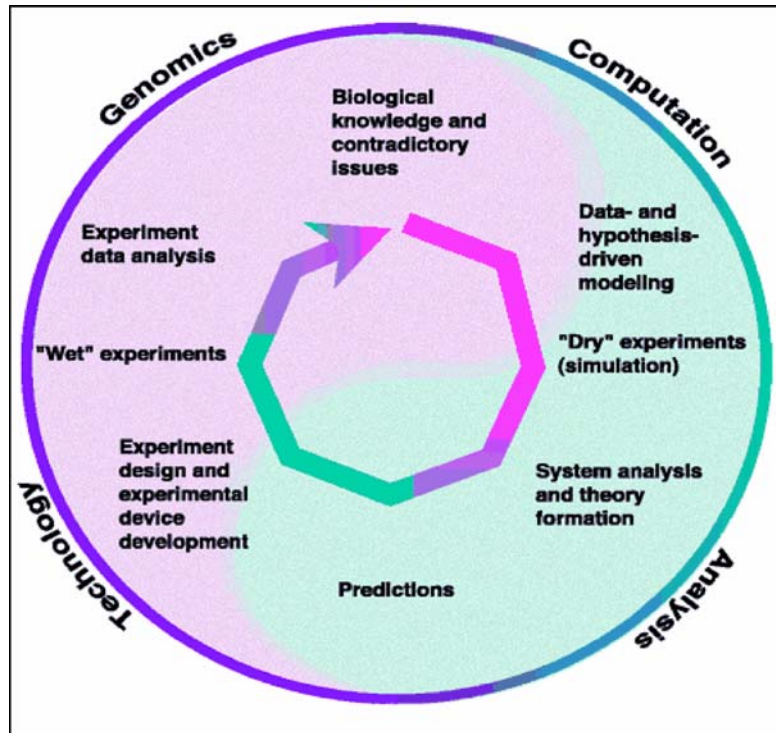


Figure 1: Bioinformatics Software Cycle

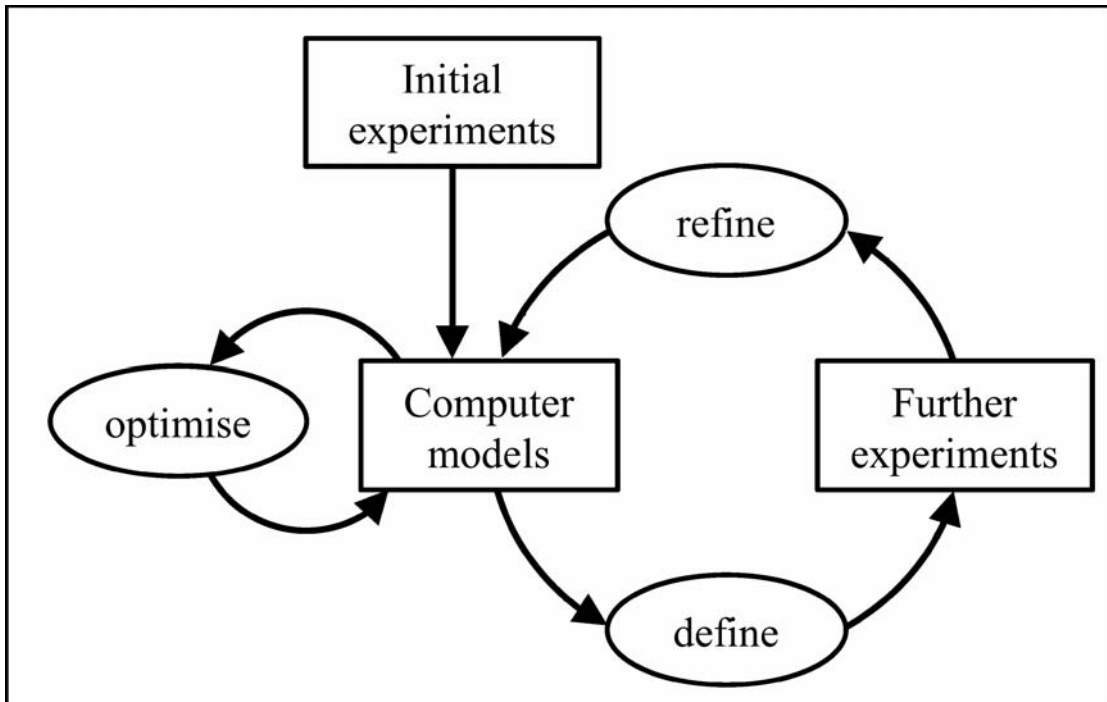
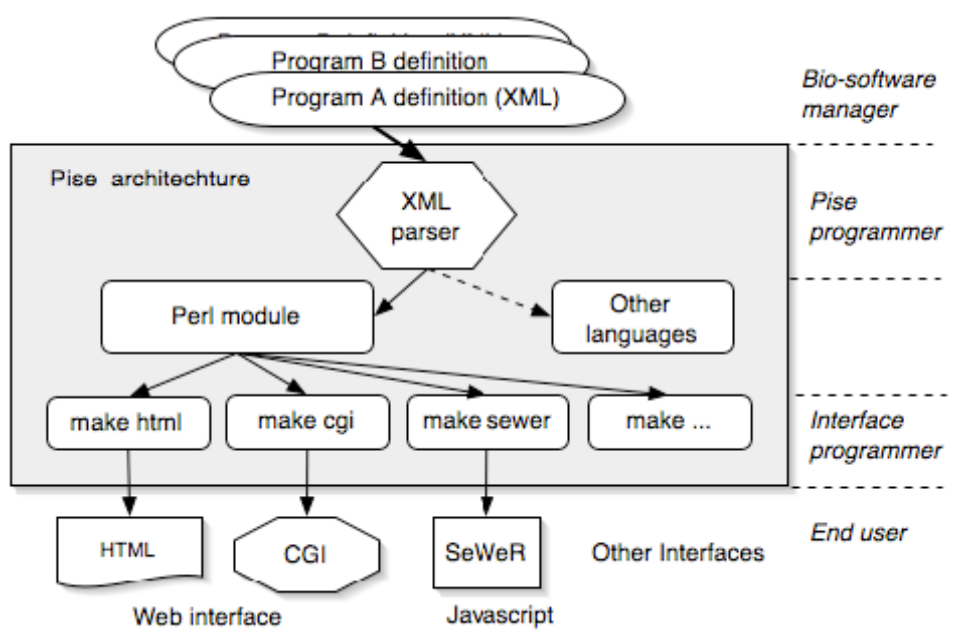


Figure 2: Cyclical Refinement of Predictive Computer Models Used to Define Further Biological Experiments

On the Internet, one can find several bioinformatics and computational biology software, but most software are poor in information technology proficiency. The following are bioinformatics and computational biology software:

### 1. Pise

Pise is interface construction software for bioinformatics applications that run by command line operations. It creates common and easy to use interfaces for the Web, or other uses. It is adaptable to new bioinformatics tools, and offers program chaining, Unix system batch and other controls, making it an attractive method for building and using your own bioinformatics web services (Gilbert, 2002), Figure 3 shows the interface architecture for Pise software

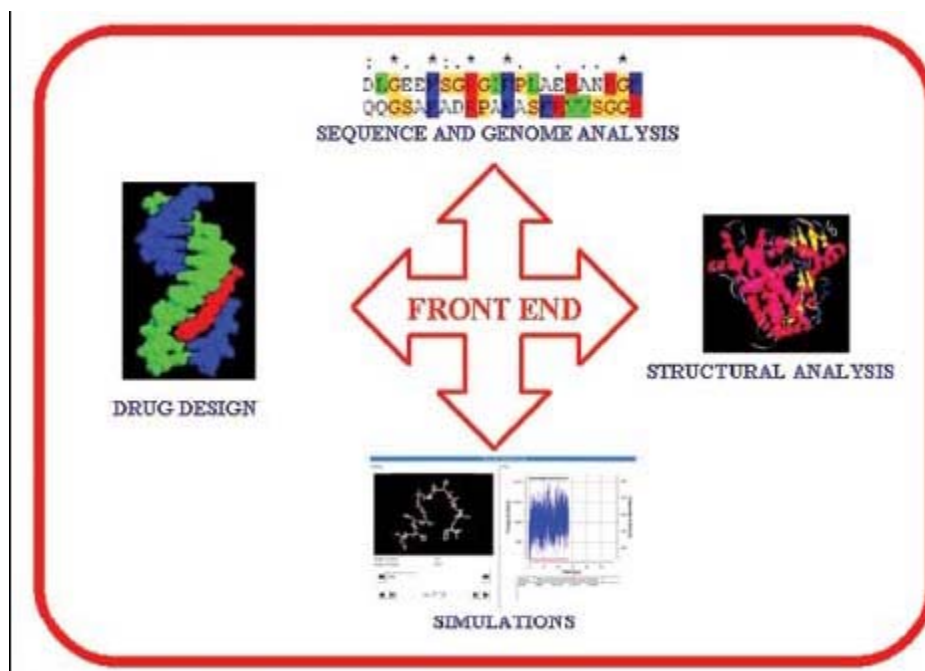


**Figure 3: Diagram of the Pise Interface Generator Architecture.**

## 2. BioSuite

BioSuite (NMITLI-BioSuite Team, 2007) is a product that integrates the functions of macromolecular sequence, structural analysis, chemoinformatics, and algorithms for aiding drug discovery. The Suite organized into four major modules, containing 79 different programs, making it one of the few comprehensive Suites that cater for a major part of the spectrum of bioinformatics applications. The four major modules are:

- (a) Genome and proteome sequence analysis.
- (b) 3-D modeling and structural analysis.
- (c) Molecular dynamics simulations.
- (d) Drug design, are made available through a convenient graphics-user interface along with adequate documentation. See Figure 4.



**Figure 4: Modular Organization of BioSuite.**



### 3. CLC bio's workbenches

This software includes several tools with different tasks (CLC bio, 2006). These tasks include the following:

- **CLC Free Workbench 2.5**, a freeware program containing a number of basic bioinformatics analyses, gathered in an integrated and user-friendly software package.
- **CLC Gene Workbench 1.0**, including advanced DNA sequence analyses such as assembly of DNA sequence data, graphically and algorithmically advanced primer design, as well as user-friendly molecular cloning tools.
- **CLC Protein Workbench 1.5**, providing a long range of advanced protein sequence analysis tools such as 3D molecular viewing, protein structure prediction, transmembrane helix prediction, Motif search, and pattern discovery.
- **CLC Combined Workbench 1.0**, aggregating all bioinformatics tools available in CLC Free Workbench, CLC Protein Workbench, and CLC Gene Workbench in a powerful and integrated bioinformatics software package (CLC bio, 2006).

### 4. Pathway

The Pathway Tools is a reusable production quality software environment for creating a Pathway/Genome Database (PGDB). A PGDB, such as EcoCyc, which integrates our evolving understanding of the genes, proteins, metabolic network, and genetic network of an organism (Karp et al, 2002). Figure 5 shows a different alternative architecture of pathway software. The configurations of alternative software architectures of the Pathway Tools(Karp et al, 2002):

- (1) Shows two Pathway Tools users accessing the same PGDBs in a single Oracle server, via a local network or the Internet.
- (2) Shows a Pathway Tools configuration in which a user accesses PGDBs in disk files.
- (3) Shows PGDBs stored in the binary program file for the Pathway Tools.

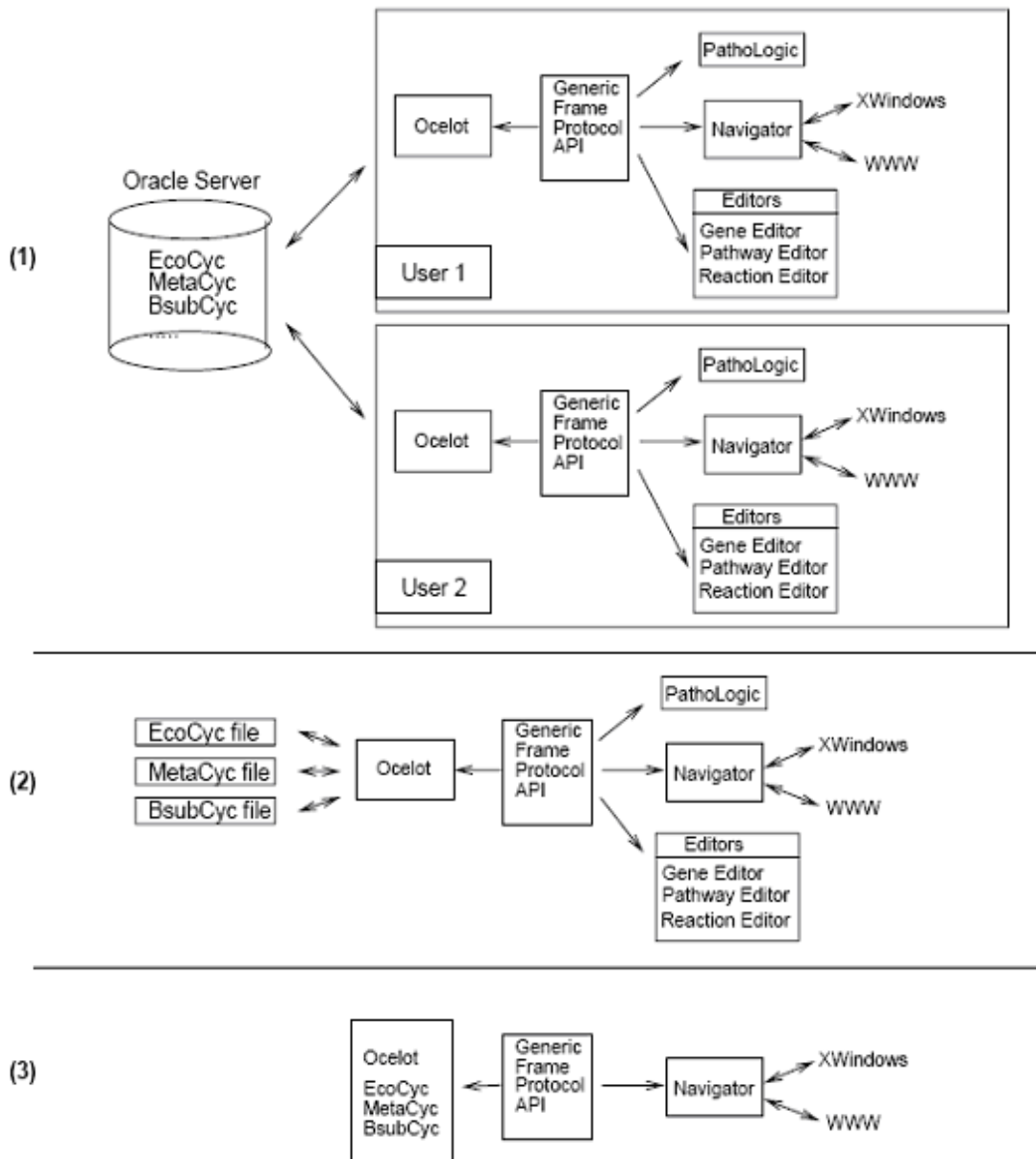


Figure 5: The alternative software architectures of the Pathway Tools.

## 5. BLAST

Basic local alignment search tool (BLAST) is a sequence similarity search program that can be used via a web interface or as a stand-alone tool to compare a user's query to a database of sequences (Ye et al, 2006). Several variants of BLAST compare all combinations of nucleotide or protein queries with nucleotide or protein databases. The BLAST is a heuristic that finds short matches between two sequences and attempts to start alignments from these 'hot spots'. In addition to performing alignments, the BLAST provides statistical information about an alignment; this is the 'expect' value, or false-positive rate. The National Center for Biotechnology Information (NCBI) maintains a BLAST server with a home page at <http://www.ncbi.nlm.nih.gov/BLAST/>. On the homepage the different BLAST searches are listed by type: nucleotide, protein, translated and genomes (Ye et al, 2006).

## 6. CLUSTALX

The CLUSTALX algorithm follows the basic form of the Feng-Doolittle (1987) algorithm for progressive alignment. Pair wise distances are calculated from a dynamic programming alignment of each sequence pair using some match/mismatch/gap scoring scheme. CLUSTALX goes a step further and uses the alignment score to approximate an evolutionary distance in terms of substitutions per site. In the Feng-Doolittle algorithm, a tree is made using the Fitch-Margoliash (1967) method while CLUSTALX builds a tree using the neighbor-joining (NJ) approach of Saitou and Nei (1987). Sequences are then added to the alignment starting with closely related sequences and working towards more distant ones. Output from CLUSTALX is examined manually and spurious alignments are edited by hand (Strain, 2006).

## 7. CFinder

CFinder is a platform-independent, stand-alone application locating overlapping groups of densely interconnected nodes in graphs and illustrate its use on the network of gene associations in the yeast genome. It was decided to maintain CFinder as an independent program (as opposed to a package plugin), because it can be employed by potential users belonging to diverse fields including, in addition to bioinformatics, economics or sociology (Adamcse et al,2006).

## 8. Cytoscape

Cytoscape is an open source program for visualizing and analyzing biological networks. The Cytoscape can be launched from the Gene Overview page to display a gene in the context of proteins and genes that interact with it or run on a list of genes. In either case, the user has the option of choosing the data sources for the interactions shown in the network. Current data sources include human protein reference database (HPRD), biomolecular interaction network database (BIND), Reactome, Molecular Interaction database (MINT) and predicted interactions from (Hulbert et al, 2006).

## 9. PAUP

PAUP is a tool for inferring and interpreting evolutionary trees. It uses parsimony, distance matrix, invariants, maximum likelihood methods and many indices and statistical tests (Cleland et al, 2004). The objective of the development of the PAUP is to provide a phylogenetics program that includes as many functions (including tree graphics) as possible in a single, platform-independent program with a menu interface.

PAUP stands for phylogenetic analysis using parsimony and contains one of the most sophisticated parsimony programs available (Catanzaro, 2003).

## 10. EMBOSS

The European Molecular Biology Open Software Suite (EMBOSS) is a new, free Open Source software analysis package specially developed for the needs of the molecular biology (e.g. EMBnet) user community. The software automatically copes with data in a variety of formats and even allows transparent retrieval of sequence data from the web. Also, as extensive libraries are provided with the package, it is a platform to allow other scientists to develop and release software in true open source spirit. EMBOSS also integrates a range of currently available packages and tools for sequence analysis into a seamless whole. EMBOSS breaks the historical trend towards commercial software packages (Retrieved February 10, 2007, from <http://www.es.embnet.org/Doc/EMBOSS/Doc/Tutorial/node1.html>).

In this study, we embarked on designing computer software specific for forensic use. The software exhibits multiple tasks and amenable for further development. It performs forensic tasks such as the calculations of the heterozygosity, power of identification, and power of discrimination required in forensic and legal settings. The software performs virtual generation of STR data which assist in assigning better STR genetic loci into forensic STR panel. The software can be improved through the addition of more important forensic parameters. Furthermore, the software can be improved through implementing other functions such as storing DNA profiles, searching and matching DNA profiles of individuals.

### (3) Materials and Methods

#### 3.1 Perl Programming Language

Computers are playing an increasingly important role in biological research and are therefore becoming an integral part of the biologist's toolbox. Computers are used in biology laboratories for manuscript preparation, data collection, database access and data analysis. Standard commercial applications, such as those available in any office package, are somewhat limited when the researcher wishes to perform detailed analyses of his/her data. Knowledge of a programming language therefore becomes an invaluable resource, as it affords the researcher almost unlimited flexibility with respect to the analyses he/she wishes to perform. Unfortunately, many programming languages are somewhat cryptic and non intuitive, and can very quickly become frustrating for the occasional programmer. Perl is becoming a standard in bioinformatics because it is less structured than traditional programming languages (Jamison, 2003). The practice of freely distributing Perl software for bioinformatics over the Internet began around 1992 (Tisdall, 2003). Gradually, Perl became more and more popular for biology applications. The release of Perl Version 5 and its support for object-oriented programming accelerated the development of reusable modules for biology at many research centers around the world.

Perl exhibits several remarkable features enabling programmers to develop biological models with ease. It is remarkably good for slicing, dicing, twisting, wringing, smoothing, summarizing and otherwise mangling text (Retrieved January 18, 2007, from [http://www.bioperl.org/wiki/How\\_Perl\\_saved\\_human\\_genome](http://www.bioperl.org/wiki/How_Perl_saved_human_genome)). Although the biological sciences do involve a good deal of numeric analysis now, most of the primary data is still text: clone names, annotations, comments, bibliographic references. Even DNA sequences are textlike. Interconverting incompatible data formats is a matter

of text mangling combined with some creative guesswork. Perl's powerful regular expression matching and string manipulation operators simplify this job in a way that isn't equalled by any other modern language.

Furthermore, biological data is sometimes incomplete, that is fields can be missing, duplicated several times or entered manually and did not quite fit the expected format. Perl does not particularly mind if a value is empty or contains odd characters. Regular expressions can be written to pick up and correct a variety of common errors in data entry. Perl encourages people to write their software in small modules, either using Perl library modules or with the classic Unix tool-oriented approach. External programs can easily be incorporated into a Perl script using a pipe, system call or socket. The dynamic loader introduced with Perl5 allows people to extend the Perl language with C routines or to make entire compiled libraries available for the Perl interpreter. Perl is easy to write and fast to develop in. The interpreter does not require you to declare all your function prototypes and data types in advance, new variables spring into existence as needed, calls to undefined functions only cause an error when the function is needed.

Moreover, Perl is a good prototyping language. It often makes sense to prototype new algorithms in Perl before moving them to a fast compiled language. Sometimes it turns out that Perl is fast enough so that the algorithm does not have to be ported; more frequently one can write a small core of the algorithm in C, compile it as a dynamically loaded module or external executable, and leave the rest of the application in Perl (Retrieved January 01, 2007, from [http://www.bioperl.org/wiki/How\\_Perl\\_saved\\_human\\_genome](http://www.bioperl.org/wiki/How_Perl_saved_human_genome)).

### 3.2 STR Genetic Loci Raw Data

The STR genetic loci raw data described in this study was compiled with permission from previously published Jordanian-STR data (Hamad et al., 2001; Salem et al., 2003; Yasin, 2002). The data comprises the types of STR genetic loci, their allelic windows, and their genotype distributions.

#### A. STR Genetic Loci and Genotypes

Tables 1 through table 17 list the seventeen genetic loci as they appeared in the sample population. These tables also comprise the observed number for each genotype of each locus. The results were used in computing the forensic parameters.

**Table 1: The CSF1PO STR Genetic Locus**

CSF1PO					
Genotype	Observed number	Genotype	Observed number	Genotype	Observed number
5,5	0	8,12	0	10,13	2
5,8	0	8,13	0	10,14	0
5,9	0	8,14	1	11,11	13
5,10	1	9,9	0	11,12	12
5,11	0	9,10	0	11,13	0
5,12	0	9,11	2	11,14	0
5,13	0	9,12	0	12,12	8
5,14	0	9,13	2	12,13	1
8,8	0	9,14	0	12,14	2
8,9	0	10,10	11	13,13	1
8,10	0	10,11	25	13,14	0
8,11	1	10,12	18	14,14	0



**Table 2: The D13S317 STR Genetic Locus**

D13S317					
Genotype	Observed number	Genotype	Observed number	Genotype	Observed number
8,8	0	9,12	5	11,13	5
8,9	2	9,13	0	11,14	3
8,10	1	9,14	1	12,12	9
8,11	7	10,10	0	12,13	8
8,12	11	10,11	2	12,14	0
8,13	5	10,12	2	13,13	2
8,14	2	10,13	1	13,14	0
9,9	1	10,14	0	14,14	0
9,10	0	11,11	9		
9,11	0	11,12	24		

**Table 3: The D16S539 STR Genetic Locus**

D16S539					
Genotype	Observed number	Genotype	Observed number	Genotype	Observed number
8,8	0	9,12	8	11,13	11
8,9	0	9,13	3	11,14	0
8,10	1	9,14	0	12,12	9
8,11	2	10,10	1	12,13	4
8,12	1	10,11	9	12,14	1
8,13	0	10,12	1	13,13	0
8,14	0	10,13	4	13,14	1
9,9	1	10,14	1	14,14	0
9,10	0	11,11	7		
9,11	10	11,12	25		

**Table 4: The D18S51 STR Genetic Locus**

D18S51					
Genotype	Observed number	Genotype	Observed number	Genotype	Observed number
10,10	0	12,17	5	14,22	0
10,11	0	12,18	4	15,15	0
10,12	1	12,19	0	15,16	3
10,13	0	12,20	1	15,17	1
10,13.2	0	12,22	0	15,18	2
10,14	0	13,13	1	15,19	1
10,15	0	13,13.2	0	15,20	0
10,16	0	13,14	3	15,22	0
10,17	0	13,15	7	16,16	1
10,18	0	13,16	5	16,17	3
10,19	0	13,17	1	16,18	1
10,20	0	13,18	2	16,19	0
10,22	0	13,19	0	16,20	0
11,11	0	13,20	3	16,22	0
11,12	0	13,22	0	17,17	0
11,13	1	13.2,13.2	0	17,18	2
11,13.2	0	13.2,14	0	17,19	0
11,14	1	13.2,15	0	17,20	0
11,15	2	13.2,16	0	17,22	0
11,16	0	13.2,17	0	18,18	0
11,17	1	13.2,18	0	18,19	1
11,18	0	13.2,19	0	18,20	1
11,19	0	13.2,20	0	18,22	1
11,20	0	13.2,22	0	19,19	0
11,22	0	14,14	3	19,20	0
12,12	6	14,15	5	19,22	0
12,13	5	14,16	5	20,20	1
12,13.2	1	14,17	4	20,22	0
12,14	6	14,18	4	22,22	0
12,15	1	14,19	3		
12,16	0	14,20	1		

**Table 5: The D21S11 STR Genetic Locus**

D21S11					
Genotype	Observed number	Genotype	Observed number	Genotype	Observed number
25,25	0	27,32.2	1	30.2,31	0
25,26	0	27,33.2	0	30.2,31.2	0
25,27	0	27,34.2	0	30.2,32	0
25,28	0	27,36	0	30.2,32.2	0
25,29	0	28,28	1	30.2,33.2	0
25,30	0	28,29	5	30.2,34.2	0
25,30.2	0	28,30	4	30.2,36	0
25,31	0	28,30.2	0	31,31	0
25,31.2	0	28,31	2	31,31.2	0
25,32	0	28,31.2	1	31,32	0
25,32.2	1	28,32	1	31,32.2	2
25,33.2	0	28,32.2	4	31,33.2	0
25,34.2	0	28,33.2	1	31,34.2	0
25,36	0	28,34.2	0	31,36	0
26,26	0	28,36	1	31.2,31.2	3
26,27	0	29,29	6	31.2,32	0
26,28	0	29,30	12	31.2,32.2	6
26,29	1	29,30.2	3	31.2,33.2	0
26,30	0	29,31	3	31.2,34.2	0
26,30.2	0	29,31.2	3	31.2,36	0
26,31	0	29,32	1	32,32	0
26,31.2	0	29,32.2	3	32,32.2	0
26,32	0	29,33.2	0	32,33.2	0
26,32.2	0	29,34.2	0	32,34.2	0
26,33.2	0	29,36	0	32,36	0
26,34.2	0	30,30	6	32.2,32.2	3
26,36	0	30,30.2	1	32.2,33.2	1
27,27	0	30,31	1	32.2,34.2	0
27,28	1	30,31.2	7	32.2,36	0
27,29	1	30,32	0	33.2,33.2	1
27,30	1	30,32.2	7	33.2,34.2	1
27,30.2	0	30,33.2	3	33.2,36	0
27,31	0	30,34.2	0	34.2,34.2	0
27,31.2	1	30,36	0	34.2,36	0
27,32	0	30.2,30.2	0	36,36	0

**Table 6: The D3S1358 STR Genetic Locus**

D3S1358					
Genotype	Observed number	Genotype	Observed number	Genotype	Observed number
12,12	0	13,17	0	15,18	9
12,13	0	13,18	0	15,19	0
12,14	0	13,19	0	16,16	5
12,15	0	14,14	0	16,17	13
12,16	0	14,15	3	16,18	4
12,17	1	14,16	1	16,19	0
12,18	0	14,17	4	17,17	5
12,19	0	14,18	2	17,18	11
13,13	0	14,19	0	17,19	0
13,14	0	15,15	4	18,18	2
13,15	0	15,16	15	18,19	1
13,16	1	15,17	19	19,19	0

**Table 7: The D5S818 STR Genetic Locus**

D5S818					
Genotype	Observed number	Genotype	Observed number	Genotype	Observed number
8,8	0	9,10	1	10,13	3
8,9	0	9,11	3	11,11	10
8,10	0	9,12	5	11,12	13
8,11	3	9,13	5	11,13	8
8,12	1	10,10	0	12,12	16
8,13	0	10,11	6	12,13	15
9,9	2	10,12	9	13,13	0

**Table 8: The D7S820 STR Genetic Locus**

D7S820					
Genotype	Observed number	Genotype	Observed number	Genotype	Observed number
7,7	0	8,11	8	10,12	11
7,8	0	8,12	4	10,13	1
7,9	0	8,13	0	11,11	8
7,10	2	9,9	0	11,12	10
7,11	1	9,10	9	11,13	1
7,12	0	9,11	2	12,12	2
7,13	0	9,12	3	12,13	0
8,8	2	9,13	3	13,13	0
8,9	4	10,10	8		
8,10	9	10,11	12		

**Table 9: The D8S1179 STR Genetic Locus**

D8S1179					
Genotype	Observed number	Genotype	Observed number	Genotype	Observed number
9,9	0	11,11	3	13,17	0
9,10	1	11,12	2	13,18	1
9,11	0	11,13	3	14,14	7
9,12	0	11,14	5	14,15	11
9,13	2	11,15	6	14,16	0
9,14	0	11,16	0	14,17	0
9,15	2	11,17	1	14,18	0
9,16	0	11,18	0	15,15	1
9,17	0	12,12	3	15,16	1
9,18	0	12,13	9	15,17	1
10,10	0	12,14	0	15,18	0
10,11	3	12,15	3	16,16	0
10,12	1	12,16	1	16,17	0
10,13	1	12,17	0	16,18	0
10,14	0	12,18	0	17,17	0
10,15	0	13,13	10	17,18	0
10,16	1	13,14	11	18,18	0
10,17	0	13,15	6		
10,18	0	13,16	4		

Table 10: The F13A1 STR Genetic Locus

F13A1					
Genotype	Observed number	Genotype	Observed number	Genotype	Observed number
3,2,3,2	3	5,11	0	8,20	0
3,2,4	1	5,12	1	9,9	0
3,2,5	12	5,13	0	9,10	0
3,2,6	7	5,16	0	9,11	1
3,2,7	1	5,20	0	9,12	0
3,2,8	2	6,6	2	9,13	0
3,2,9	0	6,7	3	9,16	0
3,2,10	0	6,8	0	9,20	0
3,2,11	0	6,9	0	10,10	0
3,2,12	0	6,10	0	10,11	0
3,2,13	0	6,11	0	10,12	0
3,2,16	0	6,12	1	10,13	0
3,2,20	0	6,13	0	10,16	0
4,4	1	6,16	1	10,20	0
4,5	10	6,20	0	11,11	0
4,6	8	7,7	4	11,12	0
4,7	1	7,8	0	11,13	0
4,8	0	7,9	0	11,16	0
4,9	0	7,10	2	11,20	0
4,10	0	7,11	0	12,12	0
4,11	0	7,12	0	12,13	0
4,12	0	7,13	1	12,16	0
4,13	0	7,16	0	12,20	0
4,16	0	7,20	0	13,13	0
4,20	0	8,8	0	13,16	0
5,5	11	8,9	0	13,20	0
5,6	14	8,10	0	16,16	0
5,7	10	8,11	0	16,20	0
5,8	2	8,12	0	20,20	1
5,9	0	8,13	0		
5,10	0	8,16	0		

**Table 11: The FES/FPS STR Genetic Locus**

FES/FPS					
Genotype	Observed number	Genotype	Observed number	Genotype	Observed number
8,8	0	9,10	14	10,13	4
8,9	1	9,11	10	11,11	17
8,10	0	9,12	2	11,12	12
8,11	2	9,13	0	11,13	2
8,12	1	10,10	7	12,12	1
8,13	0	10,11	20	12,13	1
9,9	1	10,12	5	13,13	0

**Table 12: The FGA STR Genetic Locus**

FGA					
Genotype	Observed number	Genotype	Observed number	Genotype	Observed number
18,18	0	20,21	6	22,28	0
18,19	0	20,22	0	23,23	3
18,20	0	20,23	1	23,24	7
18,21	1	20,24	3	23,25	3
18,22	0	20,25	1	23,26	1
18,23	0	20,26	0	23,27	0
18,24	0	20,27	0	23,28	1
18,25	0	20,28	0	24,24	1
18,26	0	21,21	4	24,25	4
18,27	0	21,22	8	24,26	0
18,28	0	21,23	7	24,27	2
19,19	1	21,24	8	24,28	0
19,20	3	21,25	1	25,25	0
19,21	4	21,26	0	25,26	1
19,22	1	21,27	0	25,27	0
19,23	2	21,28	0	25,28	1
19,24	0	22,22	5	26,26	0
19,25	3	22,23	5	26,27	0
19,26	1	22,24	4	26,28	0
19,27	0	22,25	5	27,27	0
19,28	0	22,26	0	27,28	0
20,20	2	22,27	0	28,28	0

**Table 13: The Penta D STR Genetic Locus**

Penta D					
Genotype	Observed number	Genotype	Observed number	Genotype	Observed number
2,2,2,2	1	5,11.2	0	9,15	2
2,2,3,2	0	5,12	1	10,10	1
2,2,5	0	5,13	0	10,11	5
2,2,7	0	5,14	0	10,11.2	0
2,2,8	0	5,15	0	10,12	5
2,2,9	0	7,7	0	10,13	6
2,2,10	0	7,8	0	10,14	4
2,2,11	1	7,9	0	10,15	1
2,2,11.2	0	7,10	1	11,11	3
2,2,12	0	7,11	0	11,11.2	0
2,2,13	0	7,11.2	0	11,12	5
2,2,14	0	7,12	0	11,13	8
2,2,15	0	7,13	0	11,14	0
3,2,3,2	0	7,14	0	11,15	2
3,2,5	0	7,15	0	11.2,11.2	0
3,2,7	0	8,8	0	11.2,12	0
3,2,8	0	8,9	1	11.2,13	0
3,2,9	0	8,10	0	11.2,14	0
3,2,10	1	8,11	2	11.2,15	0
3,2,11	0	8,11.2	0	12,12	1
3,2,11.2	0	8,12	0	12,13	2
3,2,12	0	8,13	1	12,14	1
3,2,13	0	8,14	1	12,15	3
3,2,14	0	8,15	0	13,13	5
3,2,15	0	9,9	2	13,14	4
5,5	0	9,10	9	13,15	1
5,7	0	9,11	8	14,14	0
5,8	0	9,11.2	0	14,15	0
5,9	0	9,12	6	15,15	0
5,10	1	9,13	5		
5,11	0	9,14	0		



Table 14: The Penta E STR Genetic Locus

Penta E					
Genotype	Observed number	Genotype	Observed number	Genotype	Observed number
5,5	1	8,19	0	12,17	0
5,7	2	8,20	0	12,18	1
5,8	0	9,9	1	12,19	3
5,9	0	9,10	0	12,20	1
5,10	1	9,11	0	13,13	1
5,11	2	9,12	0	13,14	3
5,12	5	9,13	0	13,15	0
5,13	1	9,14	0	13,16	0
5,14	1	9,15	1	13,17	2
5,15	1	9,16	0	13,18	1
5,16	0	9,17	0	13,19	1
5,17	2	9,18	0	13,20	1
5,18	0	9,19	0	14,14	1
5,19	0	9,20	0	14,15	0
5,20	0	10,10	3	14,16	0
7,7	0	10,11	2	14,17	0
7,8	1	10,12	2	14,18	0
7,9	0	10,13	1	14,19	0
7,10	0	10,14	1	14,20	0
7,11	2	10,15	1	15,15	2
7,12	3	10,16	0	15,16	1
7,13	3	10,17	1	15,17	0
7,14	1	10,18	2	15,18	0
7,15	0	10,19	0	15,19	1
7,16	1	10,20	0	15,20	2
7,17	0	11,11	1	16,16	1
7,18	0	11,12	3	16,17	0
7,19	0	11,13	2	16,18	0
7,20	0	11,14	2	16,19	0
8,8	4	11,15	0	16,20	0
8,9	1	11,16	1	17,17	3
8,10	0	11,17	1	17,18	0
8,11	2	11,18	0	17,19	0
8,12	0	11,19	1	17,20	0
8,13	1	11,20	0	18,18	1
8,14	1	12,12	6	18,19	0
8,15	0	12,13	2	18,20	0
8,16	0	12,14	0	19,19	2
8,17	0	12,15	2	19,20	0
8,18	0	12,16	0	20,20	0

**Table 15: The TH01 STR Genetic Locus**

TH01					
Genotype	Observed number	Genotype	Observed number	Genotype	Observed number
5,5	5	6,9	7	8,9,3	1
5,6	5	6,9,3	1	8,10	2
5,7	3	6,10	3	9,9	6
5,8	2	7,7	2	9,9,3	3
5,9	4	7,8	6	9,10	4
5,9,3	0	7,9	10	9,3,9,3	1
5,10	0	7,9,3	4	9,3,10	0
6,6	7	7,10	2	10,10	1
6,7	2	8,8	3		
6,8	10	8,9	6		

**Table 16: The TPOX STR Genetic Locus**

TPOX					
Genotype	Observed number	Genotype	Observed number	Genotype	Observed number
7,7	0	8,9	7	9,12	0
7,8	1	8,10	6	10,10	4
7,9	0	8,11	17	10,11	2
7,10	0	8,12	5	10,12	0
7,11	0	9,9	4	11,11	13
7,12	0	9,10	2	11,12	1
8,8	33	9,11	4	12,12	1

**Table 17: The vWA STR Genetic Locus**

vWA					
Genotype	Observed number	Genotype	Observed number	Genotype	Observed number
13,13	0	14,18	4	16,19	3
13,14	0	14,19	0	16,20	1
13,15	1	14,20	0	17,17	5
13,16	0	15,15	3	17,18	17
13,17	0	15,16	2	17,19	1
13,18	0	15,17	12	17,20	1
13,19	0	15,18	3	18,18	2
13,20	0	15,19	2	18,19	3
14,14	0	15,20	0	18,20	0
14,15	1	16,16	4	19,19	2
14,16	2	16,17	16	19,20	0
14,17	7	16,18	8	20,20	0

## B. The STR Allelic Windows

Table 18 explores the allelic window for each locus that is used to generate all combinations of genotypes.

**Table 18: STR Allelic Windows**

Locus	Alleles
TPOX	6,7,8,9,10,11,12,13,14,15
D16S539	5,8,9,10,11,12,13,13.3,14,15
Penta D	2.2,3.2,5,6,7,8,9,9.3,10,11,11.2,12,13,13.2,14,15,16,17
Penta E	5,6,7,8,9,10,11,12,13,13.2,14,15,16,17,18,19, 20,20.3,21,22,23,24,25
vWA	10,11,12,13,14,15,16,17,18,19,20,21,22
FGA	14,16,17,17.2,18,18.2,19,19.2,19.3,20,20.2,21,21.2,22,22.2, 23,23.2,24,24.2,25,25.2,26,26.1,27,28,29,30,30.2,31,31.2, 32,34,42.2,43.2,44.2,45.2,46.2
CSF1PO	5,6,7,8,9,10,11,11.1,12,13,14,15
TH01	4,5,6,7,8,8.3,9,9.3,10,11,13.3
D21S11	24,24.2,24.3,25,25.2,26,27,28,28.2,29,29.2,30,30.2,31,31.2, 32,32.1,32.2,33,33.1,33.2,34,34.1,34.2,35,35.2,36,37,38
D18S51	8,9,10,10.2,11,12,13,13.2,14,14.2,15,15.2,16,17,17.2, 18,18.2,19,20,20.2,21,22,22.2,23,23.2,24,25,26,27
D13S317	6,7,8,9,10,11,12,13,14,15
D8S1179	7,8,9,9.2,10,10.2,11,11.3,12,13,14,15,16,17,18,19,20,21,22
D7S820	6,7,8,9,9.1,10,10.3,11,12,13,14
D5S818	7,8,9,10,11,12,13,14,15,16
D3S1358	11,12,13,14,15,16,16.2,17,18,19,20,21
F13A1	3.2,4,5,6,7,8,9,10,11,12,13,16,20
FES/FPS	8,9,10,11,12,13

### 3.3 Biostatistics of Forensic Parameters

The observed genotypic frequencies at a specific locus were calculated by counting the number of individuals with one particular genotype and dividing this number by the total number of individuals in the sample. The observed allelic frequencies at each locus were determined from the numbers of each genotype in the sample set (Yasin *et al.*, 1999), (Hamad *et al.*, 2001), (Yasin, 2002).

Estimates for expected homozygosity and heterozygosity were calculated based on the Hardy-Weinberg Equilibrium (HWE). Percentage genotype representation (PGR) was calculated as the number of genotypes present in the population sample divided by the total number of possible genotypes for the specific locus (Hamad *et al.*, 2001; Salem *et al.*, 2003; Yasin *et al.*, 2002). The total number of possible genotypes was calculated using the formula  $n(n+1)/2$ . The  $n$  is the total number of possible alleles found at the locus (Tracey, 2001). Similarly, the percentage allele representation (PAR) was calculated as the number of possible alleles present in the population sample divided by the total number of possible alleles for the locus (Hamad *et al.*, 2001), (Yasin, 2002).

The determination of some parameters of forensic interest was performed for each locus as indicators of their discrimination potential in human identification. The power of discrimination ( $P_D$ ) and the power of identity ( $P_I$ ) were calculated following Jones's method (Jones, 1972); as in Equation(1).

$$P_D = 1 - P_I \dots\dots\dots(1)$$

where the  $P_I$  value can be calculated using Equation (2).

$$P_I = \sum x_i^2 \dots\dots\dots(2)$$

where  $x_i$  is the frequency of  $i$ th phenotype.

The heterozygosity value (H) was estimated as suggested by Nei (1978), where:

$$\text{heterozygosity} = 1 - \text{homozygosity}.$$

The Homozygosity (Homo) can be computed using Equation(3):

$$\mathbf{Homo} = \sum P_j^2 \dots\dots\dots(3)$$

The  $P_1, P_2, \dots, P_k$  represent the allele frequency of K alleles at a particular locus.

The polymorphism information content (PIC) was calculated as described by Botstein and coworkers (1980), see Equation (4).

$$\mathbf{PIC} = 1 - \sum_{i=1}^n P_i^2 - \left( \sum_{i=1}^n P_i^2 \right)^2 + \sum_{i=1}^n P_i^4 \dots\dots\dots(4)$$

The  $P_i$  is the frequency of  $i$ th allele.

The Number of Impossible Genotype was calculated according to the Equation (5).

$$\mathbf{I_G} = n.y + \frac{1}{2}y - \frac{1}{2}y^2 \dots\dots\dots (5)$$

Where  $n$  is the total number of alleles in a STR allelic window and the  $y$  is the number of alleles absent from the population.

Statistical analysis including the difference between two percentages, linear regression and exponential regression was carried out using the STATISTICA for windows (StatSoft, OK, USA).

### 3.4 Model Flowchart

A flowchart is the graphic representation of all the major steps within a process. The flowchart helps in understanding the complete process, identifying data gathering points and the critical stages of a process, locating potential problem areas, identifying duplication of efforts, and show relationships between different steps in a process.

The flowchart in Figure 6 represents the experimental process to calculate the forensic parameters including expected heterozygosity, expected homozygosity, observed heterozygosity, observed homozygosity, power of identification, power of discrimination, the polymorphic information content, allelic representation, genotype representation, and the impossibility (these formulas illustrated in 3.3) from observed genotypes numbers for a locus.

The process starts with inserting observed genotypes numbers, followed by extracting alleles from inserted genotypes and computing the observed number for each one. After that it calculates for every genotype the allele frequency, the observed allele frequency and the expected allele frequency which depends on heterogeneous or homogeneous of the genotype. The expected allele frequency and the sample size are used in computing the expected numbers for each allele which is used in calculating the main ten forensic parameters (expected heterozygosity, expected homozygosity, observed heterozygosity, observed homozygosity, PI, PD, PIC, AR, GR, I). This procedure is applied to real and virtual data, therefore reports and charts including the data and comparison between both will be shown as results for this process.

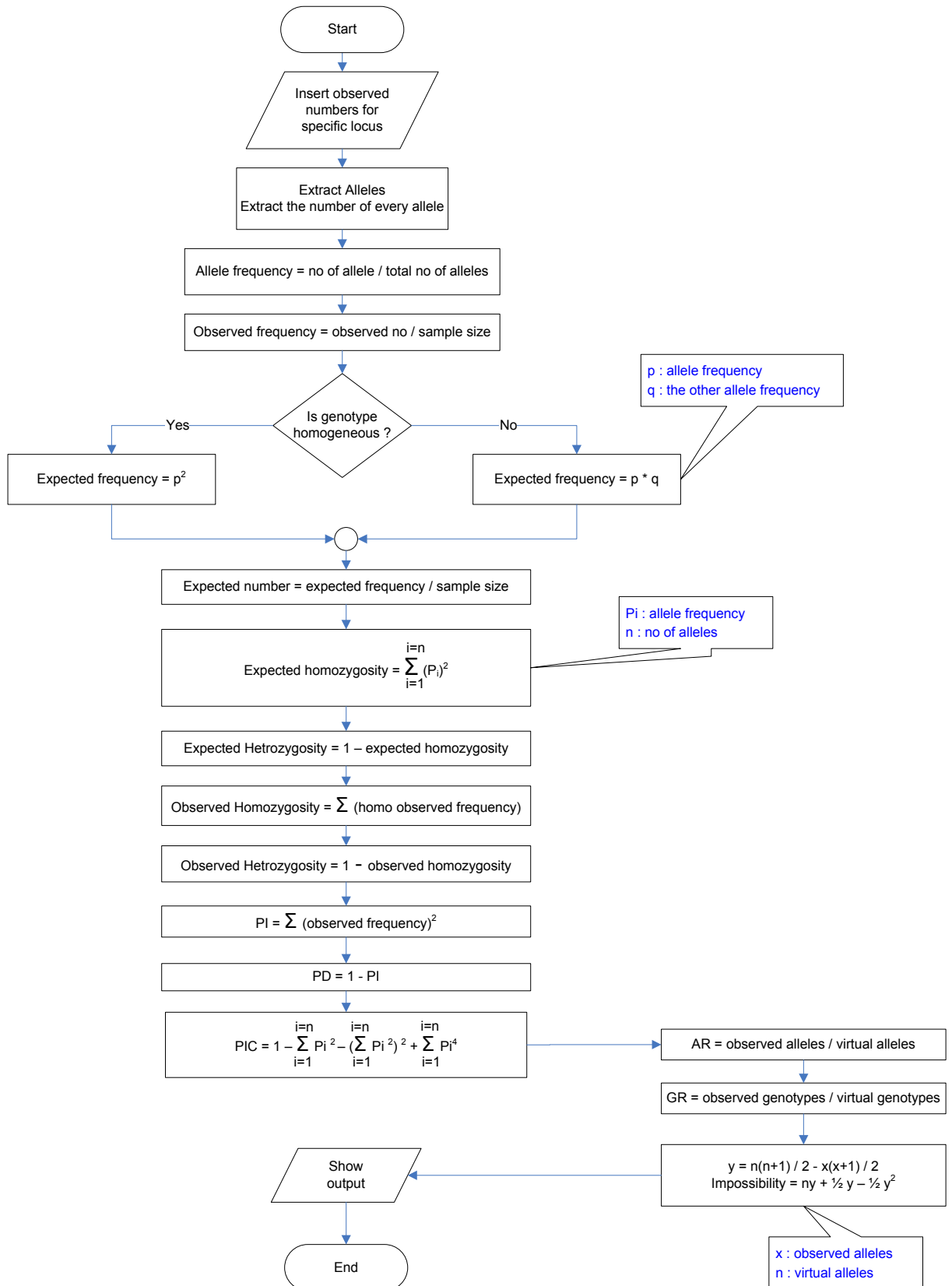


Figure 6: Forensic Parameters Model Flowchart



### 3.5 Use Case Diagram

The Use Case Model describes the proposed functionality of the new system. A Use Case represents a discrete unit of interaction between a user (human or machine) and the system. A Use Case is a single unit of meaningful work; for example login to system, register with system and create order are all Use Cases. Each Use Case has a description which describes the functionality that will be built in the proposed system. The Use Case Diagram in Figure 7 describes the functionality for the implementation of software, who could use the system, and for what.

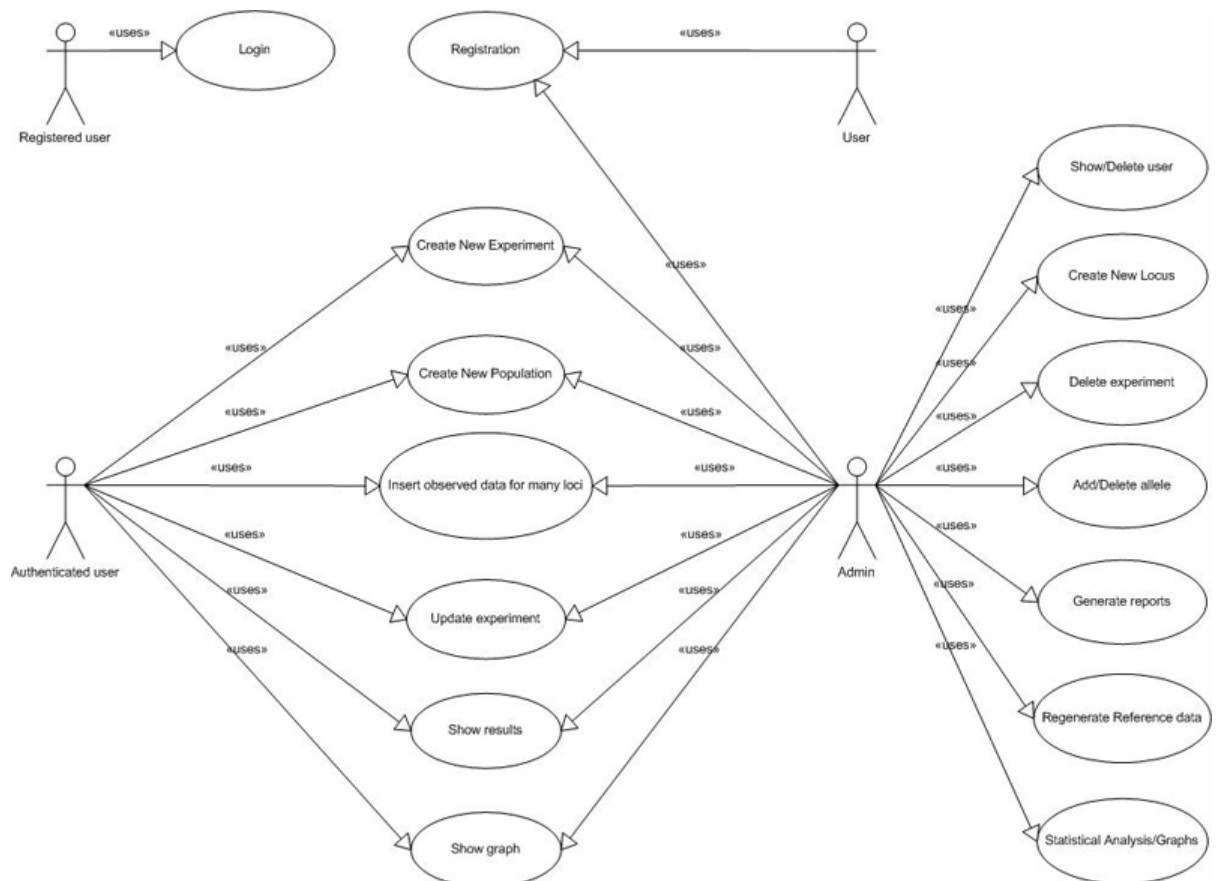


Figure 7: Use Case Diagram

### 3.6 Web Diagram

A web diagram is a visual representation of application components and flow (Lowery, 2006). Because of the levels of indirection involved in a Struts application, being able to visually see the application's flow can help the user to better understand the application. The web diagram in Figure 8 represents the pages and its functionality in the implementation of software.

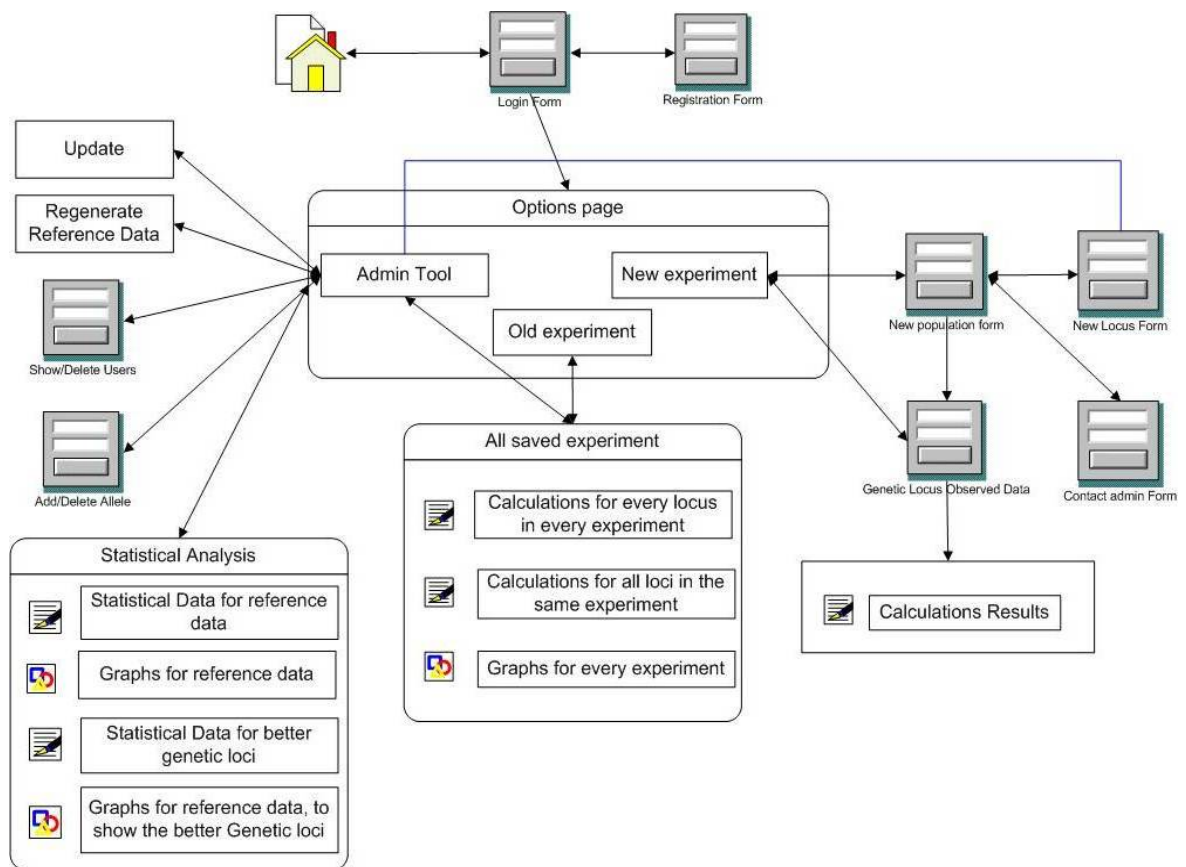


Figure 8: Web Diagram for computed forensic system

### 3.7 The Computed System User's Guide

Figures 9 through 18 describe the procedural process that is required to use the computed system efficiently.

- 1- For using the implementation, you should be authenticated, if not you should register as a **New User**. Fill all required field then click **Register**.

Home > Login > Register

Fields marked with an asterisk \* are required.

\* First name: Raed

\* Last name: Khalil

\* User name: raed

\* Password: Six characters or more.

\* Re-type password:

\* E-mail: raed\_email@yahoo.com

Company: BAU

Register

Figure 9: Registration Form

- 2- Login with your **Username** and **Password**.

Human Identification Using Forensic Parameters

Home > Login

Sign in to insert new experiment or show old one !

User Name: raed

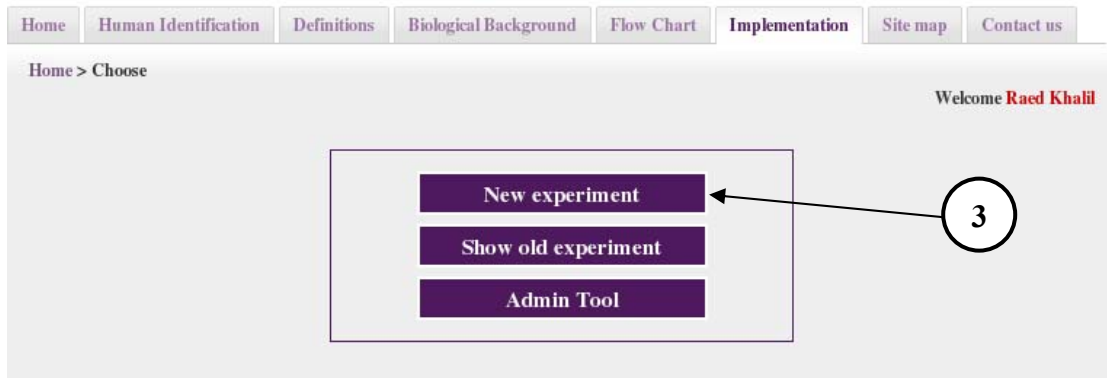
Password:

login

New users [register here!](#)

Figure 10: Login Form

3- Click on **New Experiment**.



**Figure 11: Options Menu**

4- Fill the **New Experiment** data:

- a. Choose a population from the existing list or add new population name.
- b. Enter the population size.
- c. Enter the sample size.
- d. Choose the experimental STR loci.
- e. You can add a **New Locus**.
- f. Click **Next**.

The screenshot shows the 'New Population' form with the following elements and callouts:

- 4-a**: Points to the 'Population name' dropdown menu.
- 4-b**: Points to the 'Add new population name' button.
- 4-c**: Points to the 'Population size' input field.
- 4-d**: Points to the 'Sample population' input field.
- 4-e**: Points to the 'New Loci' button.
- 4-f**: Points to the 'Next >>' button.

The form includes a navigation bar with 'Home', 'Human Identification', 'Definitions', 'Biological Background', 'Implementation', 'Site map', and 'Contact us'. The main content area has a breadcrumb 'Home > Choose > New Population' and a welcome message 'Welcome Raed Khalil'. The 'Population name' dropdown is set to 'Jordanian'. The 'Population size' is 6000000 and 'Sample population' is 100. The 'Appear Loci' list contains 'Penta D', 'Penta E', and 'CSF1PO'. The 'Add' and 'Remove' buttons are visible. The 'New Loci' button is at the bottom left, and the 'Next >>' button is at the bottom right.

Figure 12: New Population & Experiment Menu

5- Fill the data for each locus:

- Choose the STR locus from the menu.
- All possible genotypes will appear. Choose the experimental genotypes for this locus.
- Click **Done**.

The screenshot shows the 'Fill Data' form with the following elements and callouts:

- 5-a**: Points to the 'Genotype locus' dropdown menu.
- 5-b**: Points to the 'Possible genotype' table.
- 5-c**: Points to the 'Done' button.

The form includes a navigation bar with 'Home', 'Human Identification', 'Definitions', 'Biological Background', 'Flow Chart', 'Implementation', 'Site map', and 'Contact us'. The main content area has a breadcrumb 'Home > Choose > Fill Data' and a welcome message 'Welcome Raed Khalil'. The 'Genotype locus' dropdown is set to 'TPOX' with '(55 genotype)' next to it. The 'Possible genotype' table is shown below:

<input type="checkbox"/> 6,6	<input type="checkbox"/> 6,7	<input type="checkbox"/> 6,8	<input type="checkbox"/> 6,9	<input type="checkbox"/> 6,10	<input type="checkbox"/> 6,11	<input type="checkbox"/> 6,12	<input type="checkbox"/> 6,13	<input type="checkbox"/> 6,14
<input type="checkbox"/> 6,15	<input checked="" type="checkbox"/> 7,7	<input checked="" type="checkbox"/> 7,8	<input checked="" type="checkbox"/> 7,9	<input checked="" type="checkbox"/> 7,10	<input checked="" type="checkbox"/> 7,11	<input checked="" type="checkbox"/> 7,12	<input type="checkbox"/> 7,13	<input type="checkbox"/> 7,14
<input type="checkbox"/> 7,15	<input checked="" type="checkbox"/> 8,8	<input checked="" type="checkbox"/> 8,9	<input checked="" type="checkbox"/> 8,10	<input checked="" type="checkbox"/> 8,11	<input checked="" type="checkbox"/> 8,12	<input type="checkbox"/> 8,13	<input type="checkbox"/> 8,14	<input type="checkbox"/> 8,15
<input checked="" type="checkbox"/> 9,9	<input checked="" type="checkbox"/> 9,10	<input checked="" type="checkbox"/> 9,11	<input checked="" type="checkbox"/> 9,12	<input type="checkbox"/> 9,13	<input type="checkbox"/> 9,14	<input type="checkbox"/> 9,15	<input checked="" type="checkbox"/> 10,10	<input checked="" type="checkbox"/> 10,11
<input checked="" type="checkbox"/> 10,12	<input type="checkbox"/> 10,13	<input type="checkbox"/> 10,14	<input type="checkbox"/> 10,15	<input checked="" type="checkbox"/> 11,11	<input checked="" type="checkbox"/> 11,12	<input type="checkbox"/> 11,13	<input type="checkbox"/> 11,14	<input type="checkbox"/> 11,15
<input checked="" type="checkbox"/> 12,12	<input type="checkbox"/> 12,13	<input type="checkbox"/> 12,14	<input type="checkbox"/> 12,15	<input type="checkbox"/> 13,13	<input type="checkbox"/> 13,14	<input type="checkbox"/> 13,15	<input type="checkbox"/> 14,14	<input type="checkbox"/> 14,15
<input type="checkbox"/> 15,15								

The 'Done' button is at the bottom right.

Figure 13: New Experiment Data Form

- d. After click **Done**, a table with all selected genotypes and a blank text will be created to enter all observed data.
- e. Click **Save** to save the data and skip to the next locus, or **Show Results** to have a report for the selected locus.

Home > Choose > Fill Data

Welcome **Raed Khalil**

Genotype locus: TPOX (55 genotype)

Possible genotype:

<input type="checkbox"/> 6,6	<input type="checkbox"/> 6,7	<input type="checkbox"/> 6,8	<input type="checkbox"/> 6,9	<input type="checkbox"/> 6,10	<input type="checkbox"/> 6,11	<input type="checkbox"/> 6,12	<input type="checkbox"/> 6,13	<input type="checkbox"/> 6,14
<input type="checkbox"/> 6,15	<input checked="" type="checkbox"/> 7,7	<input checked="" type="checkbox"/> 7,8	<input checked="" type="checkbox"/> 7,9	<input checked="" type="checkbox"/> 7,10	<input checked="" type="checkbox"/> 7,11	<input checked="" type="checkbox"/> 7,12	<input type="checkbox"/> 7,13	<input type="checkbox"/> 7,14
<input type="checkbox"/> 7,15	<input checked="" type="checkbox"/> 8,8	<input checked="" type="checkbox"/> 8,9	<input checked="" type="checkbox"/> 8,10	<input checked="" type="checkbox"/> 8,11	<input checked="" type="checkbox"/> 8,12	<input type="checkbox"/> 8,13	<input type="checkbox"/> 8,14	<input type="checkbox"/> 8,15
<input checked="" type="checkbox"/> 9,9	<input checked="" type="checkbox"/> 9,10	<input checked="" type="checkbox"/> 9,11	<input checked="" type="checkbox"/> 9,12	<input type="checkbox"/> 9,13	<input type="checkbox"/> 9,14	<input type="checkbox"/> 9,15	<input checked="" type="checkbox"/> 10,10	<input checked="" type="checkbox"/> 10,11
<input checked="" type="checkbox"/> 10,12	<input type="checkbox"/> 10,13	<input type="checkbox"/> 10,14	<input type="checkbox"/> 10,15	<input checked="" type="checkbox"/> 11,11	<input checked="" type="checkbox"/> 11,12	<input type="checkbox"/> 11,13	<input type="checkbox"/> 11,14	<input type="checkbox"/> 11,15
<input checked="" type="checkbox"/> 12,12	<input type="checkbox"/> 12,13	<input type="checkbox"/> 12,14	<input type="checkbox"/> 12,15	<input type="checkbox"/> 13,13	<input type="checkbox"/> 13,14	<input type="checkbox"/> 13,15	<input type="checkbox"/> 14,14	<input type="checkbox"/> 14,15
<input type="checkbox"/> 15,15								

**Done**

Provide your experiment:( 21 selected genotype)

7,7	7,8	7,9	7,10	7,11	7,12	8,8	8,9	8,10	8,11	8,12
0	1	0	0	0	0	33	7	6	17	5
9,9	9,10	9,11	9,12	10,10	10,11	10,12	11,11	11,12	12,12	
4	2	4	0	4	2	0	13	1	1	

**Save** **Show results**

Figure 14: New Experiment Data-Continued

6- Back to the main menu, by click on **Choose** link.

7- Click on **Admin Tool**.

Home > Choose

Welcome **Raed Khalil**

**New experiment**

**Show old experiment**

**Admin Tool**

Figure 15: Options Menu

8- Click on **Statistical Analysis**.

Home > Choose > Admin Tool

Welcome Raed Khalil

New locus Add/Delete Allele Update Show Users

Show Experiments Regenerate Reference Data **Statistical Analysis**

Locus	Allels	PD	Homo	Hetro	PI	PIC
TPOX						
D16S539						
Penta D						
Penta E						
VWA						
FGA						
CSF1PO						
TH01						
D21S11						

Figure 16: Admin Tools

9- Click on the **Population** link.

Home > Choose > Admin > Statistical Analysis

Welcome Raed Khalil

Reference Data - Population

Locus: TPOX Charts Reports

Figure 17: Statistical Analysis

10- Choose the population that your experiment belongs to from the menu, and click

**Show.**

Home > Choose > Admin > Statistical Analysis

Welcome Raed Khalil

Reference Data - Population

Population: Jordanian Show

Figure 18: Statistical Analysis for Population

## (4) RESULTS

We have implemented our computer software to regenerate previously published Jordanian forensic STR-database and generate the virtual or theoretical STR forensic parameters. Thus, this section includes the following two categories of data:

### A. Published Jordanian STR Database (Real Data)

The real data is an output of real research projects. The computer software generate the observed genotypes of the seventeen STR genetic loci within the Jordanian sample size of 100 individuals. The tables 19 to 120 describe the results obtained for each STR genetic locus. They include the allelic frequency distributions, the observed and expected genotypic frequency distributions, and the resultant real and virtual forensic parameters values for all of the seventeen STR genetic loci.

#### 1. The CSF1PO STR Genetic Locus

This locus includes twelve alleles; of which eight were observed in reality.

**Table 19 : The Observed and Expected Genotypic Frequency Distributions of the CSF1PO STR Genetic Locus in Jordanian Population**

```
*****
**   Observed and Expected Genotypic Frequency Distribution **
**           at CSF1PO in 100 Unrelated Jordanian           **
*****
```

CSF1PO Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
5,5	0	0	0.0025	0.00003
5,8	0	0	0.01	0.00010
5,9	0	0	0.02	0.00020
5,10	1	0.01	0.34	0.00340
5,11	0	0	0.33	0.00330
5,12	0	0	0.245	0.00245
5,13	0	0	0.035	0.00035
5,14	0	0	0.015	0.00015
8,8	0	0	0.01	0.00010
8,9	0	0	0.04	0.00040
8,10	0	0	0.68	0.00680
8,11	1	0.01	0.66	0.00660
8,12	0	0	0.49	0.00490
8,13	0	0	0.07	0.00070
8,14	1	0.01	0.03	0.00030



9,9	0	0	0.04	0.00040
9,10	0	0	1.36	0.01360
9,11	2	0.02	1.32	0.01320
9,12	0	0	0.98	0.00980
9,13	2	0.02	0.14	0.00140
9,14	0	0	0.06	0.00060
10,10	11	0.11	11.56	0.11560
10,11	25	0.25	22.44	0.22440
10,12	18	0.18	16.66	0.16660
10,13	2	0.02	2.38	0.02380
10,14	0	0	1.02	0.01020
11,11	13	0.13	10.89	0.10890
11,12	12	0.12	16.17	0.16170
11,13	0	0	2.31	0.02310
11,14	0	0	0.99	0.00990
12,12	8	0.08	6.0025	0.06002
12,13	1	0.01	1.715	0.01715
12,14	2	0.02	0.735	0.00735
13,13	1	0.01	0.1225	0.00123
13,14	0	0	0.105	0.00105
14,14	0	0	0.0225	0.00022
Total	100	1	100	1.00

**Table 20 : The CSF1PO Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of CSF1PO in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
5	1	0.005
8	2	0.010
9	4	0.020
10	68	0.340
11	66	0.330
12	49	0.245
13	7	0.035
14	3	0.015
Total	200	1

**Table 21 : The Forensic Parameters for the CSF1PO STR Genetic Locus**

Results				
	Real Data	Reference		
		Min	AVG	MAX
Expected homozygosity	0.28650			
Expected hetrozygosity	0.71350			
Observed Homozygosity	0.33000	0.11700	0.15373	0.18900
Observed Hetrozygosity	0.67000	0.81100	0.84627	0.88300
Power of Identity	0.14680	0.01330	0.01373	0.01423
Power of Discrimination	0.85320	0.98577	0.98627	0.98670
PIC	0.83729	0.98558	0.98608	0.98652
Impossible Genotype	42.00000			0.00000
Allelic Representation	0.66667			
Genotype Representation	0.46154			

## 2. The D3S1358 STR Genetic Locus

This locus includes twelve alleles; of which eight were observed in reality.

**Table 22 : The Observed and Expected Genotypic Frequency Distributions of the D3S1358 STR Genetic Locus in Jordanian Population**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at D3S1358 in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

D3S1358 Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
12,12	0	0	0.0025	0.00003
12,13	0	0	0.005	0.00005
12,14	0	0	0.05	0.00050
12,15	0	0	0.27	0.00270
12,16	0	0	0.22	0.00220
12,17	1	0.01	0.29	0.00290
12,18	0	0	0.155	0.00155
12,19	0	0	0.005	0.00005
13,13	0	0	0.0025	0.00003
13,14	0	0	0.05	0.00050
13,15	0	0	0.27	0.00270
13,16	1	0.01	0.22	0.00220
13,17	0	0	0.29	0.00290
13,18	0	0	0.155	0.00155
13,19	0	0	0.005	0.00005
14,14	0	0	0.25	0.00250
14,15	3	0.03	2.7	0.02700
14,16	1	0.01	2.2	0.02200
14,17	4	0.04	2.9	0.02900
14,18	2	0.02	1.55	0.01550
14,19	0	0	0.05	0.00050
15,15	4	0.04	7.29	0.07290
15,16	15	0.15	11.88	0.11880
15,17	19	0.19	15.66	0.15660
15,18	9	0.09	8.37	0.08370

15,19	0	0	0.27	0.00270
16,16	5	0.05	4.84	0.04840
16,17	13	0.13	12.76	0.12760
16,18	4	0.04	6.82	0.06820
16,19	0	0	0.22	0.00220
17,17	5	0.05	8.41	0.08410
17,18	11	0.11	8.99	0.08990
17,19	0	0	0.29	0.00290
18,18	2	0.02	2.4025	0.02403
18,19	1	0.01	0.155	0.00155
19,19	0	0	0.0025	0.00003
Total	100	1	100	1.00

**Table 23 : The D3S1358 Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of D3S1358 in 100 Unrelated Jordanian\*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
12	1	0.005
13	1	0.005
14	10	0.050
15	54	0.270
16	44	0.220
17	58	0.290
18	31	0.155
19	1	0.005
Total	200	1

**Table 24 : The Forensic Parameters for the D3S1358 STR Genetic Locus**

Results				
	Real Data	Reference		
		Min	AVG	MAX
Expected homozygosity	0.23200			
Expected hetrozygosity	0.76800			
Observed Homozygosity	0.16000	0.12400	0.15396	0.19200
Observed Hetrozygosity	0.84000	0.80800	0.84604	0.87600
Power of Identity	0.10760	0.01336	0.01373	0.01430
Power of Discrimination	0.89240	0.98570	0.98627	0.98664
PIC	0.88315	0.98550	0.98608	0.98647
Impossible Genotype	42.00000			0.00000
Allelic Representation	0.66667			
Genotype Representation	0.46154			

### 3. The D5S818 STR Genetic Locus

This locus includes ten alleles; of which six were observed in reality.

**Table 25 : The Observed and Expected Genotypic Frequency Distributions of the D5S818 STR Genetic Locus in Jordanian Population**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at D5S818 in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

D5S818 Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
8,8	0	0	0.04	0.00040
8,9	0	0	0.36	0.00360
8,10	0	0	0.38	0.00380
8,11	3	0.03	1.06	0.01060
8,12	1	0.01	1.5	0.01500
8,13	0	0	0.62	0.00620
9,9	2	0.02	0.81	0.00810
9,10	1	0.01	1.71	0.01710
9,11	3	0.03	4.77	0.04770
9,12	5	0.05	6.75	0.06750
9,13	5	0.05	2.79	0.02790
10,10	0	0	0.9025	0.00903
10,11	6	0.06	5.035	0.05035
10,12	9	0.09	7.125	0.07125
10,13	3	0.03	2.945	0.02945
11,11	10	0.1	7.0225	0.07023
11,12	13	0.13	19.875	0.19875
11,13	8	0.08	8.215	0.08215
12,12	16	0.16	14.0625	0.14062
12,13	15	0.15	11.625	0.11625
13,13	0	0	2.4025	0.02403
Total	100	1	100	1.00

**Table 26 : The D5S818 Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of D5S818 in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
8	4	0.020
9	18	0.090
10	19	0.095
11	53	0.265
12	75	0.375
13	31	0.155
Total	200	1

**Table 27 : The Forensic Parameters for the D5S818 STR Genetic Locus**

Results				
	Real Data	Reference		
		Min	AVG	MAX
Expected homozygosity	0.25240			
Expected hetrozygosity	0.74760			
Observed Homozygosity	0.28000	0.14200	0.18221	0.23000
Observed Hetrozygosity	0.72000	0.77000	0.81779	0.85800
Power of Identity	0.10140	0.01865	0.01911	0.01982
Power of Discrimination	0.89860	0.98018	0.98089	0.98135
PIC	0.89000	0.97980	0.98053	0.98101
Impossible Genotype	34.00000			0.00000
Allelic Representation	0.60000			
Genotype Representation	0.38182			

#### 4. The D7S820 STR Genetic Locus

This locus includes eleven alleles; of which seven were observed in reality.

**Table 28 : The Observed and Expected Genotypic Frequency Distributions of the D7S820 Genetic Locus in Jordanian Population**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at D7S820 in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

D7S820 Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
7,7	0	0	0.0225	0.00022
7,8	0	0	0.435	0.00435
7,9	0	0	0.315	0.00315
7,10	2	0.02	0.9	0.00900
7,11	1	0.01	0.75	0.00750
7,12	0	0	0.48	0.00480
7,13	0	0	0.075	0.00075
8,8	2	0.02	2.1025	0.02102
8,9	4	0.04	3.045	0.03045
8,10	9	0.09	8.7	0.08700
8,11	8	0.08	7.25	0.07250
8,12	4	0.04	4.64	0.04640
8,13	0	0	0.725	0.00725
9,9	0	0	1.1025	0.01102
9,10	9	0.09	6.3	0.06300
9,11	2	0.02	5.25	0.05250
9,12	3	0.03	3.36	0.03360
9,13	3	0.03	0.525	0.00525
10,10	8	0.08	9	0.09000
10,11	12	0.12	15	0.15000
10,12	11	0.11	9.6	0.09600
10,13	1	0.01	1.5	0.01500
11,11	8	0.08	6.25	0.06250
11,12	10	0.1	8	0.08000
11,13	1	0.01	1.25	0.01250
12,12	2	0.02	2.56	0.02560
12,13	0	0	0.8	0.00800
13,13	0	0	0.0625	0.00063
Total	100	1	100	1.00

**Table 29 : The D7S820 Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of D7S820 in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
7	3	0.015
8	29	0.145
9	21	0.105
10	60	0.300
11	50	0.250
12	32	0.160
13	5	0.025
Total	200	1

**Table 30 : The forensic Parameters for the D7S820 STR Genetic Locus**

Results				
	Real Data	Reference		
		Min	AVG	MAX
Expected homozygosity	0.21100			
Expected hetrozygosity	0.78900			
Observed Homozygosity	0.20000	0.12600	0.16635	0.20200
Observed Hetrozygosity	0.80000	0.79800	0.83365	0.87400
Power of Identity	0.07880	0.01563	0.01607	0.01661
Power of Discrimination	0.92120	0.98339	0.98393	0.98437
PIC	0.91571	0.98312	0.98368	0.98413
Impossible Genotype	38.00000			0.00000
Allelic Representation	0.63636			
Genotype Representation	0.42424			

## 5. The D8S1179 STR Genetic Locus

This locus includes nineteen alleles; of which ten were observed in reality.

**Table 31 : The Observed and Expected Genotypic Frequency Distributions of the D8S1179 STR Genetic Locus in Jordanian Population**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at D8S1179 in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

D8S1179 Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
9,9	0	0	0.0625	0.00063
9,10	1	0.01	0.175	0.00175
9,11	0	0	0.65	0.00650
9,12	0	0	0.55	0.00550
9,13	2	0.02	1.425	0.01425
9,14	0	0	1.025	0.01025
9,15	2	0.02	0.8	0.00800
9,16	0	0	0.175	0.00175
9,17	0	0	0.05	0.00050
9,18	0	0	0.025	0.00025
10,10	0	0	0.1225	0.00123
10,11	3	0.03	0.91	0.00910
10,12	1	0.01	0.77	0.00770
10,13	1	0.01	1.995	0.01995
10,14	0	0	1.435	0.01435
10,15	0	0	1.12	0.01120
10,16	1	0.01	0.245	0.00245
10,17	0	0	0.07	0.00070
10,18	0	0	0.035	0.00035
11,11	3	0.03	1.69	0.01690
11,12	2	0.02	2.86	0.02860
11,13	3	0.03	7.41	0.07410
11,14	5	0.05	5.33	0.05330
11,15	6	0.06	4.16	0.04160
11,16	0	0	0.91	0.00910
11,17	1	0.01	0.26	0.00260
11,18	0	0	0.13	0.00130
12,12	3	0.03	1.21	0.01210
12,13	9	0.09	6.27	0.06270
12,14	0	0	4.51	0.04510
12,15	3	0.03	3.52	0.03520
12,16	1	0.01	0.77	0.00770
12,17	0	0	0.22	0.00220
12,18	0	0	0.11	0.00110
13,13	10	0.1	8.1225	0.08122
13,14	11	0.11	11.685	0.11685
13,15	6	0.06	9.12	0.09120
13,16	4	0.04	1.995	0.01995
13,17	0	0	0.57	0.00570
13,18	1	0.01	0.285	0.00285
14,14	7	0.07	4.2025	0.04202
14,15	11	0.11	6.56	0.06560
14,16	0	0	1.435	0.01435
14,17	0	0	0.41	0.00410
14,18	0	0	0.205	0.00205
15,15	1	0.01	2.56	0.02560



15,16	1	0.01	1.12	0.01120
15,17	1	0.01	0.32	0.00320
15,18	0	0	0.16	0.00160
16,16	0	0	0.1225	0.00123
16,17	0	0	0.07	0.00070
16,18	0	0	0.035	0.00035
17,17	0	0	0.01	0.00010
17,18	0	0	0.01	0.00010
18,18	0	0	0.0025	0.00003
Total	100	1	100	1.00

**Table 32 : The D8S1179 Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\*Alleles Frequencies of D8S1179 in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
9	5	0.025
10	7	0.035
11	26	0.130
12	22	0.110
13	57	0.285
14	41	0.205
15	32	0.160
16	7	0.035
17	2	0.010
18	1	0.005
Total	200	1

**Table 33 : The Forensic Parameters for the D8S1179 STR Genetic Locus**

Results				
	Real Data	Reference		
		Min	AVG	MAX
Expected homozygosity	0.18105			
Expected hetrozygosity	0.81895			
Observed Homozygosity	0.24000	0.07600	0.09978	0.13200
Observed Hetrozygosity	0.76000	0.86800	0.90022	0.92400
Power of Identity	0.06520	0.00584	0.00607	0.00633
Power of Discrimination	0.93480	0.99367	0.99393	0.99416
PIC	0.93107	0.99363	0.99389	0.99413
Impossible Genotype	135.00000			0.00000
Allelic Representation	0.52632			
Genotype Representation	0.28947			

## 6. The D13S317 STR Genetic Locus

This locus includes ten alleles; of which seven were observed in reality.

**Table 34 : The Observed and Expected Genotypic Frequency Distributions of the D13S317 STR Genetic Locus in Jordanian Population**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at D13S317 in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

D13S317 Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
8,8	0	0	1.96	0.01960
8,9	2	0.02	1.4	0.01400
8,10	1	0.01	0.84	0.00840
8,11	7	0.07	8.26	0.08260
8,12	11	0.11	9.52	0.09520
8,13	5	0.05	3.22	0.03220
8,14	2	0.02	0.84	0.00840
9,9	1	0.01	0.25	0.00250
9,10	0	0	0.3	0.00300
9,11	0	0	2.95	0.02950
9,12	5	0.05	3.4	0.03400
9,13	0	0	1.15	0.01150
9,14	1	0.01	0.3	0.00300
10,10	0	0	0.09	0.00090
10,11	2	0.02	1.77	0.01770
10,12	2	0.02	2.04	0.02040
10,13	1	0.01	0.69	0.00690
10,14	0	0	0.18	0.00180
11,11	9	0.09	8.7025	0.08702
11,12	24	0.24	20.06	0.20060
11,13	5	0.05	6.785	0.06785
11,14	3	0.03	1.77	0.01770
12,12	9	0.09	11.56	0.11560
12,13	8	0.08	7.82	0.07820

12,14	0	0	2.04	0.02040
13,13	2	0.02	1.3225	0.01323
13,14	0	0	0.69	0.00690
14,14	0	0	0.09	0.00090
Total	100	1	100	1.00

**Table 35 : The D13S317 Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\*Alleles Frequencies of D13S317 in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
8	28	0.140
9	10	0.050
10	6	0.030
11	59	0.295
12	68	0.340
13	23	0.115
14	6	0.030
Total	200	1

**Table 36 : The Forensic Parameters for the D13S317 STR Genetic Locus**

Results				
	Real Data	Reference		
		Min	AVG	MAX
Expected homozygosity	0.23975			
Expected hetrozygosity	0.76025			
Observed Homozygosity	0.21000	0.14600	0.18169	0.22100
Observed Hetrozygosity	0.79000	0.77900	0.81831	0.85400
Power of Identity	0.10800	0.01869	0.01910	0.01974
Power of Discrimination	0.89200	0.98026	0.98090	0.98131
PIC	0.88402	0.97988	0.98054	0.98097
Impossible Genotype	27.00000			0.00000
Allelic Representation	0.70000			
Genotype Representation	0.50909			

## 7. D16S539

This locus includes ten alleles; of which seven were observed in reality.

**Table 37 : The Observed and Expected Genotypic Frequency Distributions of the D16S539 STR Genetic Locus in Jordanian Population**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at D16S539 in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

D16S539 Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
8,8	0	0	0.04	0.00040
8,9	0	0	0.46	0.00460
8,10	1	0.01	0.36	0.00360
8,11	2	0.02	1.42	0.01420
8,12	1	0.01	1.16	0.01160
8,13	0	0	0.46	0.00460
8,14	0	0	0.06	0.00060
9,9	1	0.01	1.3225	0.01323
9,10	0	0	2.07	0.02070
9,11	10	0.1	8.165	0.08165
9,12	8	0.08	6.67	0.06670
9,13	3	0.03	2.645	0.02645
9,14	0	0	0.345	0.00345
10,10	1	0.01	0.81	0.00810
10,11	9	0.09	6.39	0.06390
10,12	1	0.01	5.22	0.05220
10,13	4	0.04	2.07	0.02070
10,14	1	0.01	0.27	0.00270
11,11	7	0.07	12.6025	0.12602
11,12	25	0.25	20.59	0.20590
11,13	11	0.11	8.165	0.08165
11,14	0	0	1.065	0.01065
12,12	9	0.09	8.41	0.08410
12,13	4	0.04	6.67	0.06670
12,14	1	0.01	0.87	0.00870
13,13	0	0	1.3225	0.01323
13,14	1	0.01	0.345	0.00345
14,14	0	0	0.0225	0.00022
Total	100	1	100	1.00

**Table 38 : The D16S539 Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\*Alleles Frequencies of D16S539 in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
8	4	0.020
9	23	0.115
10	18	0.090
11	71	0.355
12	58	0.290
13	23	0.115
14	3	0.015
Total	200	1

**Table 39 : The Forensic Parameters for the D16S539 STR Genetic Locus**

Results				
	Real Data	Reference		
		Min	AVG	MAX
Expected homozygosity	0.24530			
Expected hetrozygosity	0.75470			
Observed Homozygosity	0.18000	0.13800	0.18167	0.21900
Observed Hetrozygosity	0.82000	0.78100	0.81833	0.86200
Power of Identity	0.11740	0.01863	0.01911	0.01977
Power of Discrimination	0.88260	0.98023	0.98089	0.98137
PIC	0.87317	0.97985	0.98054	0.98103
Impossible Genotype	27.00000			0.00000
Allelic Representation	0.70000			
Genotype Representation	0.50909			

## 8. The D18S51 STR Genetic Locus

This locus includes twenty nine alleles; of which thirteen were observed in reality.

**Table 40 : The Observed and Expected Genotypic Frequency Distributions of the D18S51 STR Genetic Locus in Jordanian Population**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at D18S51 in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

D18S51 Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
10,10	0	0	0.0025	0.00003
10,11	0	0	0.025	0.00025
10,12	1	0.01	0.18	0.00180
10,13	0	0	0.145	0.00145
10,13.2	0	0	0.005	0.00005
10,14	0	0	0.19	0.00190
10,15	0	0	0.11	0.00110
10,16	0	0	0.095	0.00095
10,17	0	0	0.085	0.00085
10,18	0	0	0.09	0.00090
10,19	0	0	0.025	0.00025
10,20	0	0	0.04	0.00040
10,22	0	0	0.005	0.00005
11,11	0	0	0.0625	0.00063
11,12	0	0	0.9	0.00900
11,13	1	0.01	0.725	0.00725
11,13.2	0	0	0.025	0.00025
11,14	1	0.01	0.95	0.00950
11,15	2	0.02	0.55	0.00550
11,16	0	0	0.475	0.00475
11,17	1	0.01	0.425	0.00425
11,18	0	0	0.45	0.00450
11,19	0	0	0.125	0.00125
11,20	0	0	0.2	0.00200
11,22	0	0	0.025	0.00025
12,12	6	0.06	3.24	0.03240
12,13	5	0.05	5.22	0.05220
12,13.2	1	0.01	0.18	0.00180
12,14	6	0.06	6.84	0.06840
12,15	1	0.01	3.96	0.03960
12,16	0	0	3.42	0.03420
12,17	5	0.05	3.06	0.03060
12,18	4	0.04	3.24	0.03240
12,19	0	0	0.9	0.00900
12,20	1	0.01	1.44	0.01440
12,22	0	0	0.18	0.00180
13,13	1	0.01	2.1025	0.02102
13,13.2	0	0	0.145	0.00145
13,14	3	0.03	5.51	0.05510
13,15	7	0.07	3.19	0.03190
13,16	5	0.05	2.755	0.02755
13,17	1	0.01	2.465	0.02465
13,18	2	0.02	2.61	0.02610
13,19	0	0	0.725	0.00725
13,20	3	0.03	1.16	0.01160
13,22	0	0	0.145	0.00145

13.2,13.2	0	0	0.0025	0.00003
13.2,14	0	0	0.19	0.00190
13.2,15	0	0	0.11	0.00110
13.2,16	0	0	0.095	0.00095
13.2,17	0	0	0.085	0.00085
13.2,18	0	0	0.09	0.00090
13.2,19	0	0	0.025	0.00025
13.2,20	0	0	0.04	0.00040
13.2,22	0	0	0.005	0.00005
14,14	3	0.03	3.61	0.03610
14,15	5	0.05	4.18	0.04180
14,16	5	0.05	3.61	0.03610
14,17	4	0.04	3.23	0.03230
14,18	4	0.04	3.42	0.03420
14,19	3	0.03	0.95	0.00950
14,20	1	0.01	1.52	0.01520
14,22	0	0	0.19	0.00190
15,15	0	0	1.21	0.01210
15,16	3	0.03	2.09	0.02090
15,17	1	0.01	1.87	0.01870
15,18	2	0.02	1.98	0.01980
15,19	1	0.01	0.55	0.00550
15,20	0	0	0.88	0.00880
15,22	0	0	0.11	0.00110
16,16	1	0.01	0.9025	0.00903
16,17	3	0.03	1.615	0.01615
16,18	1	0.01	1.71	0.01710
16,19	0	0	0.475	0.00475
16,20	0	0	0.76	0.00760
16,22	0	0	0.095	0.00095
17,17	0	0	0.7225	0.00723
17,18	2	0.02	1.53	0.01530
17,19	0	0	0.425	0.00425
17,20	0	0	0.68	0.00680
17,22	0	0	0.085	0.00085
18,18	0	0	0.81	0.00810
18,19	1	0.01	0.45	0.00450
18,20	1	0.01	0.72	0.00720
18,22	1	0.01	0.09	0.00090
19,19	0	0	0.0625	0.00063
19,20	0	0	0.2	0.00200
19,22	0	0	0.025	0.00025
20,20	1	0.01	0.16	0.00160
20,22	0	0	0.04	0.00040
22,22	0	0	0.0025	0.00003
Total	100	1	100	1.00

**Table 41 : The D18S51 Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of D18S51 in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
10	1	0.005
11	5	0.025
12	36	0.180
13	29	0.145
13.2	1	0.005
14	38	0.190
15	22	0.110
16	19	0.095
17	17	0.085
18	18	0.090
19	5	0.025
20	8	0.040
22	1	0.005
Total	200	1

**Table 42 : The Forensic Parameters for the D18S51 STR Genetic Locus**

Results				
	Real Data	Reference		
		Min	AVG	MAX
Expected homozygosity	0.12890			
Expected hetrozygosity	0.87110			
Observed Homozygosity	0.12000	0.04900	0.06644	0.08800
Observed Hetrozygosity	0.88000	0.91200	0.93357	0.95100
Power of Identity	0.03820	0.00273	0.00286	0.00298
Power of Discrimination	0.96180	0.99702	0.99714	0.99727
PIC	0.96044	0.99702	0.99713	0.99726
Impossible Genotype	344.00000			0.00000
Allelic Representation	0.44828			
Genotype Representation	0.20920			



## 9. The D21S11 STR Genetic Locus

This locus includes twenty nine alleles; of which fourteen were observed in reality.

**Table 43 : The Observed and Expected Genotypic Frequency Distributions of the D21S11 STR Genetic Locus in Jordanian Population**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at D21S11 in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

D21S11 Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
25, 25	0	0	0.0025	0.00003
25, 26	0	0	0.005	0.00005
25, 27	0	0	0.025	0.00025
25, 28	0	0	0.11	0.00110
25, 29	0	0	0.22	0.00220
25, 30	0	0	0.24	0.00240
25, 30.2	0	0	0.02	0.00020
25, 31	0	0	0.04	0.00040
25, 31.2	0	0	0.12	0.00120
25, 32	0	0	0.01	0.00010
25, 32.2	1	0.01	0.155	0.00155
25, 33.2	0	0	0.04	0.00040
25, 34.2	0	0	0.005	0.00005
25, 36	0	0	0.005	0.00005
26, 26	0	0	0.0025	0.00003
26, 27	0	0	0.025	0.00025
26, 28	0	0	0.11	0.00110
26, 29	1	0.01	0.22	0.00220
26, 30	0	0	0.24	0.00240
26, 30.2	0	0	0.02	0.00020
26, 31	0	0	0.04	0.00040
26, 31.2	0	0	0.12	0.00120
26, 32	0	0	0.01	0.00010
26, 32.2	0	0	0.155	0.00155
26, 33.2	0	0	0.04	0.00040
26, 34.2	0	0	0.005	0.00005
26, 36	0	0	0.005	0.00005
27, 27	0	0	0.0625	0.00063
27, 28	1	0.01	0.55	0.00550
27, 29	1	0.01	1.1	0.01100
27, 30	1	0.01	1.2	0.01200
27, 30.2	0	0	0.1	0.00100
27, 31	0	0	0.2	0.00200
27, 31.2	1	0.01	0.6	0.00600
27, 32	0	0	0.05	0.00050
27, 32.2	1	0.01	0.775	0.00775
27, 33.2	0	0	0.2	0.00200
27, 34.2	0	0	0.025	0.00025
27, 36	0	0	0.025	0.00025
28, 28	1	0.01	1.21	0.01210
28, 29	5	0.05	4.84	0.04840
28, 30	4	0.04	5.28	0.05280
28, 30.2	0	0	0.44	0.00440
28, 31	2	0.02	0.88	0.00880
28, 31.2	1	0.01	2.64	0.02640
28, 32	1	0.01	0.22	0.00220

28,32.2	4	0.04	3.41	0.03410
28,33.2	1	0.01	0.88	0.00880
28,34.2	0	0	0.11	0.00110
28,36	1	0.01	0.11	0.00110
29,29	6	0.06	4.84	0.04840
29,30	12	0.12	10.56	0.10560
29,30.2	3	0.03	0.88	0.00880
29,31	3	0.03	1.76	0.01760
29,31.2	3	0.03	5.28	0.05280
29,32	1	0.01	0.44	0.00440
29,32.2	3	0.03	6.82	0.06820
29,33.2	0	0	1.76	0.01760
29,34.2	0	0	0.22	0.00220
29,36	0	0	0.22	0.00220
30,30	6	0.06	5.76	0.05760
30,30.2	1	0.01	0.96	0.00960
30,31	1	0.01	1.92	0.01920
30,31.2	7	0.07	5.76	0.05760
30,32	0	0	0.48	0.00480
30,32.2	7	0.07	7.44	0.07440
30,33.2	3	0.03	1.92	0.01920
30,34.2	0	0	0.24	0.00240
30,36	0	0	0.24	0.00240
30.2,30.2	0	0	0.04	0.00040
30.2,31	0	0	0.16	0.00160
30.2,31.2	0	0	0.48	0.00480
30.2,32	0	0	0.04	0.00040
30.2,32.2	0	0	0.62	0.00620
30.2,33.2	0	0	0.16	0.00160
30.2,34.2	0	0	0.02	0.00020
30.2,36	0	0	0.02	0.00020
31,31	0	0	0.16	0.00160
31,31.2	0	0	0.96	0.00960
31,32	0	0	0.08	0.00080
31,32.2	2	0.02	1.24	0.01240
31,33.2	0	0	0.32	0.00320
31,34.2	0	0	0.04	0.00040
31,36	0	0	0.04	0.00040
31.2,31.2	3	0.03	1.44	0.01440
31.2,32	0	0	0.24	0.00240
31.2,32.2	6	0.06	3.72	0.03720
31.2,33.2	0	0	0.96	0.00960
31.2,34.2	0	0	0.12	0.00120
31.2,36	0	0	0.12	0.00120
32,32	0	0	0.01	0.00010
32,32.2	0	0	0.31	0.00310
32,33.2	0	0	0.08	0.00080
32,34.2	0	0	0.01	0.00010
32,36	0	0	0.01	0.00010
32.2,32.2	3	0.03	2.4025	0.02403
32.2,33.2	1	0.01	1.24	0.01240
32.2,34.2	0	0	0.155	0.00155
32.2,36	0	0	0.155	0.00155
33.2,33.2	1	0.01	0.16	0.00160
33.2,34.2	1	0.01	0.04	0.00040
33.2,36	0	0	0.04	0.00040
34.2,34.2	0	0	0.0025	0.00003
34.2,36	0	0	0.005	0.00005
36,36	0	0	0.0025	0.00003
Total	100	1	100	1.00

**Table 44 : The D21S11 Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of D21S11 in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
25	1	0.005
26	1	0.005
27	5	0.025
28	22	0.110
29	44	0.220
30	48	0.240
30.2	4	0.020
31	8	0.040
31.2	24	0.120
32	2	0.010
32.2	31	0.155
33.2	8	0.040
34.2	1	0.005
36	1	0.005
Total	200	1

**Table 45: The Forensic Parameters for the D21S11 STR Genetic Locus**

Results				
	Real Data	Reference		
		Min	AVG	MAX
Expected homozygosity	0.16095			
Expected hetrozygosity	0.83905			
Observed Homozygosity	0.20000	0.04800	0.06658	0.08800
Observed Hetrozygosity	0.80000	0.91200	0.93342	0.95200
Power of Identity	0.04960	0.00274	0.00286	0.00297
Power of Discrimination	0.95040	0.99703	0.99714	0.99726
PIC	0.94825	0.99702	0.99713	0.99725
Impossible Genotype	330.00000			0.00000
Allelic Representation	0.48276			
Genotype Representation	0.24138			

## 10. The F13A1STR Genetic Locus

This locus includes thirteen alleles; of which were thirteen observed in reality.

**Table 46: The Observed and Expected Genotypic Frequency Distributions of the F13A1 STR Genetic Locus in Jordanian Population**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at F13A1 in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

F13A1 Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
3.2,3.2	3	0.03	2.1025	0.02102
3.2,4	1	0.01	3.19	0.03190
3.2,5	12	0.12	10.295	0.10295
3.2,6	7	0.07	5.51	0.05510
3.2,7	1	0.01	3.77	0.03770
3.2,8	2	0.02	0.58	0.00580
3.2,9	0	0	0.145	0.00145
3.2,10	0	0	0.29	0.00290
3.2,11	0	0	0.145	0.00145
3.2,12	0	0	0.29	0.00290
3.2,13	0	0	0.145	0.00145
3.2,16	0	0	0.145	0.00145
3.2,20	0	0	0.29	0.00290
4,4	1	0.01	1.21	0.01210
4,5	10	0.1	7.81	0.07810
4,6	8	0.08	4.18	0.04180
4,7	1	0.01	2.86	0.02860
4,8	0	0	0.44	0.00440
4,9	0	0	0.11	0.00110
4,10	0	0	0.22	0.00220
4,11	0	0	0.11	0.00110
4,12	0	0	0.22	0.00220
4,13	0	0	0.11	0.00110
4,16	0	0	0.11	0.00110
4,20	0	0	0.22	0.00220
5,5	11	0.11	12.6025	0.12602
5,6	14	0.14	13.49	0.13490
5,7	10	0.1	9.23	0.09230
5,8	2	0.02	1.42	0.01420
5,9	0	0	0.355	0.00355
5,10	0	0	0.71	0.00710
5,11	0	0	0.355	0.00355
5,12	1	0.01	0.71	0.00710
5,13	0	0	0.355	0.00355
5,16	0	0	0.355	0.00355
5,20	0	0	0.71	0.00710
6,6	2	0.02	3.61	0.03610
6,7	3	0.03	4.94	0.04940
6,8	0	0	0.76	0.00760
6,9	0	0	0.19	0.00190
6,10	0	0	0.38	0.00380
6,11	0	0	0.19	0.00190
6,12	1	0.01	0.38	0.00380
6,13	0	0	0.19	0.00190
6,16	1	0.01	0.19	0.00190
6,20	0	0	0.38	0.00380

7,7	4	0.04	1.69	0.01690
7,8	0	0	0.52	0.00520
7,9	0	0	0.13	0.00130
7,10	2	0.02	0.26	0.00260
7,11	0	0	0.13	0.00130
7,12	0	0	0.26	0.00260
7,13	1	0.01	0.13	0.00130
7,16	0	0	0.13	0.00130
7,20	0	0	0.26	0.00260
8,8	0	0	0.04	0.00040
8,9	0	0	0.02	0.00020
8,10	0	0	0.04	0.00040
8,11	0	0	0.02	0.00020
8,12	0	0	0.04	0.00040
8,13	0	0	0.02	0.00020
8,16	0	0	0.02	0.00020
8,20	0	0	0.04	0.00040
9,9	0	0	0.0025	0.00003
9,10	0	0	0.01	0.00010
9,11	1	0.01	0.005	0.00005
9,12	0	0	0.01	0.00010
9,13	0	0	0.005	0.00005
9,16	0	0	0.005	0.00005
9,20	0	0	0.01	0.00010
10,10	0	0	0.01	0.00010
10,11	0	0	0.01	0.00010
10,12	0	0	0.02	0.00020
10,13	0	0	0.01	0.00010
10,16	0	0	0.01	0.00010
10,20	0	0	0.02	0.00020
11,11	0	0	0.0025	0.00003
11,12	0	0	0.01	0.00010
11,13	0	0	0.005	0.00005
11,16	0	0	0.005	0.00005
11,20	0	0	0.01	0.00010
12,12	0	0	0.01	0.00010
12,13	0	0	0.01	0.00010
12,16	0	0	0.01	0.00010
12,20	0	0	0.02	0.00020
13,13	0	0	0.0025	0.00003
13,16	0	0	0.005	0.00005
13,20	0	0	0.01	0.00010
16,16	0	0	0.0025	0.00003
16,20	0	0	0.01	0.00010
20,20	1	0.01	0.01	0.00010
Total	100	0.97	100	1.00

**Table 47: The F13A1 Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of F13A1 in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
3.2	29	0.145
4	22	0.110
5	71	0.355
6	38	0.190
7	26	0.130
8	4	0.020
9	1	0.005
10	2	0.010
11	1	0.005
12	2	0.010
13	1	0.005
16	1	0.005
20	2	0.010
Total	200	1

**Table 48: The Forensic Parameters for the F13A1 STR Genetic Locus**

Results				
	Real Data	Reference		
		Min	AVG	MAX
Expected homozygosity	0.21295			
Expected hetrozygosity	0.78705			
Observed Homozygosity	0.22000	0.10800	0.14295	0.18100
Observed Hetrozygosity	0.78000	0.81900	0.85705	0.89200
Power of Identity	0.08340	0.01152	0.01189	0.01232
Power of Discrimination	0.91660	0.98768	0.98811	0.98848
PIC	0.91065	0.98753	0.98797	0.98834
Impossible Genotype	0.00000			0.00000
Allelic Representation	1.00000			
Genotype Representation	1.00000			

## 11. The FES/FPS STR Genetic Locus

This locus includes six alleles; all were observed in reality.

**Table 49: The Observed and Expected Genotypic Frequency Distributions of the FES/FPS STR Genetic Locus in Jordanian Population**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at FES/FPS in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

FES/FPS Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
8,8	0	0	0.04	0.00040
8,9	1	0.01	0.58	0.00580
8,10	0	0	1.14	0.01140
8,11	2	0.02	1.6	0.01600
8,12	1	0.01	0.46	0.00460
8,13	0	0	0.14	0.00140
9,9	1	0.01	2.1025	0.02102
9,10	14	0.14	8.265	0.08265
9,11	10	0.1	11.6	0.11600
9,12	2	0.02	3.335	0.03335
9,13	0	0	1.015	0.01015
10,10	7	0.07	8.1225	0.08122
10,11	20	0.2	22.8	0.22800
10,12	5	0.05	6.555	0.06555
10,13	4	0.04	1.995	0.01995
11,11	17	0.17	16	0.16000
11,12	12	0.12	9.2	0.09200
11,13	2	0.02	2.8	0.02800
12,12	1	0.01	1.3225	0.01323
12,13	1	0.01	0.805	0.00805
13,13	0	0	0.1225	0.00123
Total	100	1	100	1.00

**Table 50: The FES/FPS Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\*Alleles Frequencies of FES/FPS in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
8	4	0.020
9	29	0.145
10	57	0.285
11	80	0.400
12	23	0.115
13	7	0.035
Total	200	1

**Table 51: The Forensic Parameters for the FES/FPS STR Genetic Locus**

Results				
	Real Data	Reference		
		Min	AVG	MAX
Expected homozygosity	0.27710			
Expected hetrozygosity	0.72290			
Observed Homozygosity	0.26000	0.24600	0.28603	0.33300
Observed Hetrozygosity	0.74000	0.66700	0.71397	0.75400
Power of Identity	0.12360	0.04787	0.04856	0.04967
Power of Discrimination	0.87640	0.95033	0.95144	0.95213
PIC	0.86428	0.94799	0.94921	0.94995
Impossible Genotype	0.00000			0.00000
Allelic Representation	1.00000			
Genotype Representation	1.00000			

## 12. The FGA STR Genetic Locus

This locus includes thirty seven alleles; of which eleven were observed in reality.

**Table 52: The Observed and Expected Genotypic Frequency Distributions of the FGA STR Genetic Locus in Jordanian Population**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at FGA in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

FGA Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
18,18	0	0	0.0025	0.00003
18,19	0	0	0.08	0.00080
18,20	0	0	0.09	0.00090
18,21	1	0.01	0.215	0.00215
18,22	0	0	0.165	0.00165
18,23	0	0	0.165	0.00165
18,24	0	0	0.15	0.00150
18,25	0	0	0.095	0.00095
18,26	0	0	0.015	0.00015
18,27	0	0	0.01	0.00010
18,28	0	0	0.01	0.00010
19,19	1	0.01	0.64	0.00640
19,20	3	0.03	1.44	0.01440
19,21	4	0.04	3.44	0.03440
19,22	1	0.01	2.64	0.02640
19,23	2	0.02	2.64	0.02640
19,24	0	0	2.4	0.02400
19,25	3	0.03	1.52	0.01520
19,26	1	0.01	0.24	0.00240
19,27	0	0	0.16	0.00160
19,28	0	0	0.16	0.00160
20,20	2	0.02	0.81	0.00810
20,21	6	0.06	3.87	0.03870
20,22	0	0	2.97	0.02970
20,23	1	0.01	2.97	0.02970
20,24	3	0.03	2.7	0.02700



20,25	1	0.01	1.71	0.01710
20,26	0	0	0.27	0.00270
20,27	0	0	0.18	0.00180
20,28	0	0	0.18	0.00180
21,21	4	0.04	4.6225	0.04622
21,22	8	0.08	7.095	0.07095
21,23	7	0.07	7.095	0.07095
21,24	8	0.08	6.45	0.06450
21,25	1	0.01	4.085	0.04085
21,26	0	0	0.645	0.00645
21,27	0	0	0.43	0.00430
21,28	0	0	0.43	0.00430
22,22	5	0.05	2.7225	0.02723
22,23	5	0.05	5.445	0.05445
22,24	4	0.04	4.95	0.04950
22,25	5	0.05	3.135	0.03135
22,26	0	0	0.495	0.00495
22,27	0	0	0.33	0.00330
22,28	0	0	0.33	0.00330
23,23	3	0.03	2.7225	0.02723
23,24	7	0.07	4.95	0.04950
23,25	3	0.03	3.135	0.03135
23,26	1	0.01	0.495	0.00495
23,27	0	0	0.33	0.00330
23,28	1	0.01	0.33	0.00330
24,24	1	0.01	2.25	0.02250
24,25	4	0.04	2.85	0.02850
24,26	0	0	0.45	0.00450
24,27	2	0.02	0.3	0.00300
24,28	0	0	0.3	0.00300
25,25	0	0	0.9025	0.00903
25,26	1	0.01	0.285	0.00285
25,27	0	0	0.19	0.00190
25,28	1	0.01	0.19	0.00190
26,26	0	0	0.0225	0.00022
26,27	0	0	0.03	0.00030
26,28	0	0	0.03	0.00030
27,27	0	0	0.01	0.00010
27,28	0	0	0.02	0.00020
28,28	0	0	0.01	0.00010
Total	100	1	100	1.00

**Table 53: The FGA Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of FGA in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
18	1	0.005
19	16	0.080
20	18	0.090
21	43	0.215
22	33	0.165
23	33	0.165
24	30	0.150
25	19	0.095
26	3	0.015
27	2	0.010
28	2	0.010
Total	200	1

**Table 54: The Forensic Parameters for the FGA STR Genetic Locus**

	Results			
	Real Data	Reference		
		Min	AVG	MAX
Expected homozygosity	0.14715			
Expected hetrozygosity	0.85285			
Observed Homozygosity	0.16000	0.04300	0.05254	0.06900
Observed Hetrozygosity	0.84000	0.93100	0.94746	0.95700
Power of Identity	0.04700	0.00167	0.00172	0.00177
Power of Discrimination	0.95300	0.99823	0.99828	0.99833
PIC	0.95097	0.99823	0.99828	0.99833
Impossible Genotype	637.00000			0.00000
Allelic Representation	0.29730			
Genotype Representation	0.09388			

### 13. The Penta D STR Genetic Locus

This locus includes eighteen alleles; of which thirteen were observed in reality.

**Table 55: The Observed and Expected Genotypic Frequency Distributions of the Penta D STR Genetic Locus in Jordanian Population**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at Penta D in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

Penta D Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
2.2,2.2	1	0.01	0.0225	0.00022
2.2,3.2	0	0	0.015	0.00015
2.2,5	0	0	0.03	0.00030
2.2,7	0	0	0.015	0.00015
2.2,8	0	0	0.075	0.00075
2.2,9	0	0	0.525	0.00525
2.2,10	0	0	0.525	0.00525
2.2,11	1	0.01	0.555	0.00555
2.2,11.2	0	0	0	0.00000
2.2,12	0	0	0.375	0.00375
2.2,13	0	0	0.555	0.00555
2.2,14	0	0	0.15	0.00150
2.2,15	0	0	0.135	0.00135
3.2,3.2	0	0	0.0025	0.00003
3.2,5	0	0	0.01	0.00010
3.2,7	0	0	0.005	0.00005
3.2,8	0	0	0.025	0.00025
3.2,9	0	0	0.175	0.00175
3.2,10	1	0.01	0.175	0.00175
3.2,11	0	0	0.185	0.00185
3.2,11.2	0	0	0	0.00000
3.2,12	0	0	0.125	0.00125
3.2,13	0	0	0.185	0.00185
3.2,14	0	0	0.05	0.00050
3.2,15	0	0	0.045	0.00045
5,5	0	0	0.01	0.00010
5,7	0	0	0.01	0.00010
5,8	0	0	0.05	0.00050
5,9	0	0	0.35	0.00350
5,10	1	0.01	0.35	0.00350
5,11	0	0	0.37	0.00370
5,11.2	0	0	0	0.00000
5,12	1	0.01	0.25	0.00250
5,13	0	0	0.37	0.00370
5,14	0	0	0.1	0.00100
5,15	0	0	0.09	0.00090
7,7	0	0	0.0025	0.00003
7,8	0	0	0.025	0.00025
7,9	0	0	0.175	0.00175
7,10	1	0.01	0.175	0.00175
7,11	0	0	0.185	0.00185
7,11.2	0	0	0	0.00000
7,12	0	0	0.125	0.00125
7,13	0	0	0.185	0.00185
7,14	0	0	0.05	0.00050
7,15	0	0	0.045	0.00045

8,8	0	0	0.0625	0.00063
8,9	1	0.01	0.875	0.00875
8,10	0	0	0.875	0.00875
8,11	2	0.02	0.925	0.00925
8,11.2	0	0	0	0.00000
8,12	0	0	0.625	0.00625
8,13	1	0.01	0.925	0.00925
8,14	1	0.01	0.25	0.00250
8,15	0	0	0.225	0.00225
9,9	2	0.02	3.0625	0.03062
9,10	9	0.09	6.125	0.06125
9,11	8	0.08	6.475	0.06475
9,11.2	0	0	0	0.00000
9,12	6	0.06	4.375	0.04375
9,13	5	0.05	6.475	0.06475
9,14	0	0	1.75	0.01750
9,15	2	0.02	1.575	0.01575
10,10	1	0.01	3.0625	0.03062
10,11	5	0.05	6.475	0.06475
10,11.2	0	0	0	0.00000
10,12	5	0.05	4.375	0.04375
10,13	6	0.06	6.475	0.06475
10,14	4	0.04	1.75	0.01750
10,15	1	0.01	1.575	0.01575
11,11	3	0.03	3.4225	0.03422
11,11.2	0	0	0	0.00000
11,12	5	0.05	4.625	0.04625
11,13	8	0.08	6.845	0.06845
11,14	0	0	1.85	0.01850
11,15	2	0.02	1.665	0.01665
11.2,11.2	0	0	0	0.00000
11.2,12	0	0	0	0.00000
11.2,13	0	0	0	0.00000
11.2,14	0	0	0	0.00000
11.2,15	0	0	0	0.00000
12,12	1	0.01	1.5625	0.01562
12,13	2	0.02	4.625	0.04625
12,14	1	0.01	1.25	0.01250
12,15	3	0.03	1.125	0.01125
13,13	5	0.05	3.4225	0.03422
13,14	4	0.04	1.85	0.01850
13,15	1	0.01	1.665	0.01665
14,14	0	0	0.25	0.00250
14,15	0	0	0.45	0.00450
15,15	0	0	0.2025	0.00202
Total	100	0.99	100	1.00

**Table 56: The Penta D Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\*Alleles Frequencies of Penta D in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
2.2	3	0.015
3.2	1	0.005
5	2	0.010
7	1	0.005
8	5	0.025
9	35	0.175
10	35	0.175
11	37	0.185
11.2	0	0.000
12	25	0.125
13	37	0.185
14	10	0.050
15	9	0.045
Total	200	1

**Table 57: The Forensic Parameters for the Penta D STR Genetic Locus**

Results				
	Real Data	Reference		
		Min	AVG	MAX
Expected homozygosity	0.15085			
Expected hetrozygosity	0.84915			
Observed Homozygosity	0.13000	0.07800	0.10493	0.13600
Observed Hetrozygosity	0.87000	0.86400	0.89507	0.92200
Power of Identity	0.04900	0.00640	0.00667	0.00697
Power of Discrimination	0.95100	0.99303	0.99333	0.99360
PIC	0.94881	0.99299	0.99328	0.99356
Impossible Genotype	80.00000			0.00000
Allelic Representation	0.72222			
Genotype Representation	0.53216			

#### 14. The Penta E STR Genetic Locus

This locus includes twenty three alleles; of which fifteen were observed in reality.

**Table 58: The Observed and Expected Genotypic Frequency Distributions of the Penta E STR Genetic Locus in Jordanian Population**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at Penta E in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

Penta E Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
5,5	1	0.01	0.7225	0.00723
5,7	2	0.02	1.105	0.01105
5,8	0	0	1.19	0.01190
5,9	0	0	0.34	0.00340
5,10	1	0.01	1.445	0.01445
5,11	2	0.02	1.7	0.01700
5,12	5	0.05	2.89	0.02890
5,13	1	0.01	1.7	0.01700
5,14	1	0.01	0.935	0.00935
5,15	1	0.01	1.105	0.01105
5,16	0	0	0.425	0.00425
5,17	2	0.02	1.02	0.01020
5,18	0	0	0.51	0.00510
5,19	0	0	0.85	0.00850
5,20	0	0	0.34	0.00340
7,7	0	0	0.4225	0.00423
7,8	1	0.01	0.91	0.00910
7,9	0	0	0.26	0.00260
7,10	0	0	1.105	0.01105
7,11	2	0.02	1.3	0.01300
7,12	3	0.03	2.21	0.02210
7,13	3	0.03	1.3	0.01300
7,14	1	0.01	0.715	0.00715
7,15	0	0	0.845	0.00845
7,16	1	0.01	0.325	0.00325
7,17	0	0	0.78	0.00780
7,18	0	0	0.39	0.00390
7,19	0	0	0.65	0.00650
7,20	0	0	0.26	0.00260
8,8	4	0.04	0.49	0.00490
8,9	1	0.01	0.28	0.00280
8,10	0	0	1.19	0.01190
8,11	2	0.02	1.4	0.01400
8,12	0	0	2.38	0.02380
8,13	1	0.01	1.4	0.01400
8,14	1	0.01	0.77	0.00770
8,15	0	0	0.91	0.00910
8,16	0	0	0.35	0.00350
8,17	0	0	0.84	0.00840
8,18	0	0	0.42	0.00420
8,19	0	0	0.7	0.00700
8,20	0	0	0.28	0.00280
9,9	1	0.01	0.04	0.00040
9,10	0	0	0.34	0.00340
9,11	0	0	0.4	0.00400
9,12	0	0	0.68	0.00680

9,13	0	0	0.4	0.00400
9,14	0	0	0.22	0.00220
9,15	1	0.01	0.26	0.00260
9,16	0	0	0.1	0.00100
9,17	0	0	0.24	0.00240
9,18	0	0	0.12	0.00120
9,19	0	0	0.2	0.00200
9,20	0	0	0.08	0.00080
10,10	3	0.03	0.7225	0.00723
10,11	2	0.02	1.7	0.01700
10,12	2	0.02	2.89	0.02890
10,13	1	0.01	1.7	0.01700
10,14	1	0.01	0.935	0.00935
10,15	1	0.01	1.105	0.01105
10,16	0	0	0.425	0.00425
10,17	1	0.01	1.02	0.01020
10,18	2	0.02	0.51	0.00510
10,19	0	0	0.85	0.00850
10,20	0	0	0.34	0.00340
11,11	1	0.01	1	0.01000
11,12	3	0.03	3.4	0.03400
11,13	2	0.02	2	0.02000
11,14	2	0.02	1.1	0.01100
11,15	0	0	1.3	0.01300
11,16	1	0.01	0.5	0.00500
11,17	1	0.01	1.2	0.01200
11,18	0	0	0.6	0.00600
11,19	1	0.01	1	0.01000
11,20	0	0	0.4	0.00400
12,12	6	0.06	2.89	0.02890
12,13	2	0.02	3.4	0.03400
12,14	0	0	1.87	0.01870
12,15	2	0.02	2.21	0.02210
12,16	0	0	0.85	0.00850
12,17	0	0	2.04	0.02040
12,18	1	0.01	1.02	0.01020
12,19	3	0.03	1.7	0.01700
12,20	1	0.01	0.68	0.00680
13,13	1	0.01	1	0.01000
13,14	3	0.03	1.1	0.01100
13,15	0	0	1.3	0.01300
13,16	0	0	0.5	0.00500
13,17	2	0.02	1.2	0.01200
13,18	1	0.01	0.6	0.00600
13,19	1	0.01	1	0.01000
13,20	1	0.01	0.4	0.00400
14,14	1	0.01	0.3025	0.00302
14,15	0	0	0.715	0.00715
14,16	0	0	0.275	0.00275
14,17	0	0	0.66	0.00660
14,18	0	0	0.33	0.00330
14,19	0	0	0.55	0.00550
14,20	0	0	0.22	0.00220
15,15	2	0.02	0.4225	0.00423
15,16	1	0.01	0.325	0.00325
15,17	0	0	0.78	0.00780
15,18	0	0	0.39	0.00390
15,19	1	0.01	0.65	0.00650
15,20	2	0.02	0.26	0.00260
16,16	1	0.01	0.0625	0.00063
16,17	0	0	0.3	0.00300

16,18	0	0	0.15	0.00150
16,19	0	0	0.25	0.00250
16,20	0	0	0.1	0.00100
17,17	3	0.03	0.36	0.00360
17,18	0	0	0.36	0.00360
17,19	0	0	0.6	0.00600
17,20	0	0	0.24	0.00240
18,18	1	0.01	0.09	0.00090
18,19	0	0	0.3	0.00300
18,20	0	0	0.12	0.00120
19,19	2	0.02	0.25	0.00250
19,20	0	0	0.2	0.00200
20,20	0	0	0.04	0.00040
Total	100	0.99	100	1.00

**Table 59: The Penta E Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of Penta E in 100 Unrelated Jordanian\*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
5	17	0.085
7	13	0.065
8	14	0.070
9	4	0.020
10	17	0.085
11	20	0.100
12	34	0.170
13	20	0.100
14	11	0.055
15	13	0.065
16	5	0.025
17	12	0.060
18	6	0.030
19	10	0.050
20	4	0.020
Total	200	1



**Table 60: The Forensic Parameters for the Penta E STR Genetic Locus**

Results				
	Real Data	Reference		
		Min	AVG	MAX
Expected homozygosity	0.08815			
Expected hetrozygosity	0.91185			
Observed Homozygosity	0.27000	0.06100	0.08350	0.11000
Observed Hetrozygosity	0.73000	0.89000	0.91650	0.93900
Power of Identity	0.02360	0.00417	0.00434	0.00458
Power of Discrimination	0.97640	0.99542	0.99566	0.99583
PIC	0.97587	0.99540	0.99564	0.99581
Impossible Genotype	156.00000			0.00000
Allelic Representation	0.65217			
Genotype Representation	0.43478			

### 15. The TH01 STR Genetic Locus

This locus includes eleven alleles; of which seven were observed in reality.

**Table 61: The Observed and Expected Genotypic Frequency Distributions of the TH01 STR Genetic Locus in Jordanian Population**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at TH01 in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

TH01 Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
5,5	5	0.05	1.44	0.01440
5,6	5	0.05	5.04	0.05040
5,7	3	0.03	3.72	0.03720
5,8	2	0.02	3.96	0.03960
5,9	4	0.04	5.52	0.05520
5,9.3	0	0	1.32	0.01320
5,10	0	0	1.56	0.01560
6,6	7	0.07	4.41	0.04410
6,7	2	0.02	6.51	0.06510
6,8	10	0.1	6.93	0.06930
6,9	7	0.07	9.66	0.09660
6,9.3	1	0.01	2.31	0.02310
6,10	3	0.03	2.73	0.02730
7,7	2	0.02	2.4025	0.02403
7,8	6	0.06	5.115	0.05115
7,9	10	0.1	7.13	0.07130
7,9.3	4	0.04	1.705	0.01705
7,10	2	0.02	2.015	0.02015
8,8	3	0.03	2.7225	0.02723
8,9	6	0.06	7.59	0.07590
8,9.3	1	0.01	1.815	0.01815
8,10	2	0.02	2.145	0.02145
9,9	6	0.06	5.29	0.05290

9,9.3	3	0.03	2.53	0.02530
9,10	4	0.04	2.99	0.02990
9.3,9.3	1	0.01	0.3025	0.00302
9.3,10	0	0	0.715	0.00715
10,10	1	0.01	0.4225	0.00423
Total	100	0.95	100	1.00

**Table 62 : The TH01 Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of TH01 in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
5	24	0.120
6	42	0.210
7	31	0.155
8	33	0.165
9	46	0.230
9.3	11	0.055
10	13	0.065
Total	200	1

**Table 63 : The Forensic Parameters for the TH01 STR Genetic Locus**

	Results			
	Real Data	Reference		
		Min	AVG	MAX
Expected homozygosity	0.16990			
Expected hetrozygosity	0.83010			
Observed Homozygosity	0.25000	0.13400	0.16631	0.20100
Observed Hetrozygosity	0.75000	0.79900	0.83369	0.86600
Power of Identity	0.05640	0.01563	0.01607	0.01663
Power of Discrimination	0.94360	0.98337	0.98393	0.98437
PIC	0.94073	0.98310	0.98367	0.98413
Impossible Genotype	38.00000			0.00000
Allelic Representation	0.63636			
Genotype Representation	0.42424			

## 16. The TPOX STR Genetic Locus

This locus includes ten alleles; of which six were observed in reality.

**Table 64: The Observed and Expected Genotypic Frequency Distributions of the TPOX STR Genetic Locus in Jordanian Population**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at TPOX in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

TPOX Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
7,7	0	0	0.0025	0.00003
7,8	1	0.01	0.51	0.00510
7,9	0	0	0.105	0.00105
7,10	0	0	0.09	0.00090
7,11	0	0	0.25	0.00250
7,12	0	0	0.04	0.00040
8,8	33	0.33	26.01	0.26010
8,9	7	0.07	10.71	0.10710
8,10	6	0.06	9.18	0.09180
8,11	17	0.17	25.5	0.25500
8,12	5	0.05	4.08	0.04080
9,9	4	0.04	1.1025	0.01102
9,10	2	0.02	1.89	0.01890
9,11	4	0.04	5.25	0.05250
9,12	0	0	0.84	0.00840
10,10	4	0.04	0.81	0.00810
10,11	2	0.02	4.5	0.04500
10,12	0	0	0.72	0.00720
11,11	13	0.13	6.25	0.06250
11,12	1	0.01	2	0.02000
12,12	1	0.01	0.16	0.00160
Total	100	1	100	1.00

**Table 65: The TPOX Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of TPOX in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
7	1	0.005
8	102	0.510
9	21	0.105
10	18	0.090
11	50	0.250
12	8	0.040
Total	200	1

**Table 66: The Forensic Parameters for the TPOX STR Genetic Locus**

Results				
	Real Data	Reference		
		Min	AVG	MAX
Expected homozygosity	0.34335			
Expected hetrozygosity	0.65665			
Observed Homozygosity	0.55000	0.14300	0.18186	0.21800
Observed Hetrozygosity	0.45000	0.78200	0.81814	0.85700
Power of Identity	0.17160	0.01862	0.01910	0.01996
Power of Discrimination	0.82840	0.98004	0.98090	0.98138
PIC	0.81198	0.97966	0.98054	0.98104
Impossible Genotype	34.00000			0.00000
Allelic Representation	0.60000			
Genotype Representation	0.38182			

## 17. The vWA STR Genetic Locus

This locus includes thirteen alleles; of which eight were observed in reality.

**Table 67: The Observed and Expected Genotypic Frequency Distributions of the vWA STR Genetic Locus in Jordanian Population**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at VWA in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

VWA Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
13,13	0	0	0.0025	0.00003
13,14	0	0	0.07	0.00070
13,15	1	0.01	0.135	0.00135
13,16	0	0	0.2	0.00200
13,17	0	0	0.32	0.00320
13,18	0	0	0.195	0.00195
13,19	0	0	0.065	0.00065
13,20	0	0	0.01	0.00010
14,14	0	0	0.49	0.00490
14,15	1	0.01	1.89	0.01890
14,16	2	0.02	2.8	0.02800
14,17	7	0.07	4.48	0.04480
14,18	4	0.04	2.73	0.02730
14,19	0	0	0.91	0.00910
14,20	0	0	0.14	0.00140
15,15	3	0.03	1.8225	0.01823
15,16	2	0.02	5.4	0.05400
15,17	12	0.12	8.64	0.08640
15,18	3	0.03	5.265	0.05265
15,19	2	0.02	1.755	0.01755
15,20	0	0	0.27	0.00270
16,16	4	0.04	4	0.04000
16,17	16	0.16	12.8	0.12800
16,18	8	0.08	7.8	0.07800
16,19	3	0.03	2.6	0.02600
16,20	1	0.01	0.4	0.00400
17,17	5	0.05	10.24	0.10240
17,18	17	0.17	12.48	0.12480
17,19	1	0.01	4.16	0.04160
17,20	1	0.01	0.64	0.00640
18,18	2	0.02	3.8025	0.03803
18,19	3	0.03	2.535	0.02535
18,20	0	0	0.39	0.00390
19,19	2	0.02	0.4225	0.00423
19,20	0	0	0.13	0.00130
20,20	0	0	0.01	0.00010
Total	100	1	100	1.00

**Table 68: The vWA Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of VWA in 100 Unrelated Jordanian \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
13	1	0.005
14	14	0.070
15	27	0.135
16	40	0.200
17	64	0.320
18	39	0.195
19	13	0.065
20	2	0.010
Total	200	1

**Table 69: The Forensic Parameters for the vWA STR Genetic Locus**

Results				
	Real Data	Reference		
		Min	AVG	MAX
Expected homozygosity	0.20790			
Expected hetrozygosity	0.79210			
Observed Homozygosity	0.16000	0.11000	0.14316	0.18200
Observed Hetrozygosity	0.84000	0.81800	0.85684	0.89000
Power of Identity	0.09200	0.01155	0.01189	0.01242
Power of Discrimination	0.90800	0.98758	0.98811	0.98845
PIC	0.90131	0.98743	0.98797	0.98832
Impossible Genotype	55.00000			0.00000
Allelic Representation	0.61538			
Genotype Representation	0.39560			

## B. Virtual STR Database

Unlike the real data, virtual data is not for any specific population. The data was generated randomly using special algorithm distributed between all genotypes, and all genotypes are supposed to exist. Virtual data is used as a reference data for the Jordanian-population data.

The implementation of the computer software repeats the generation data process and calculations different times depending on the administrator's input. For technical reasons, the run times reaches only for 1000 times only and this is more than enough to achieve the target. The default value for the population sample size was considered at 1000 individuals. The maximum obtained values for the forensic parameters such as heterozygosity  $(VH_{obs})_{max}$  and the power of discrimination  $(VTP_D)_{max}$  were selected and stored. The tables 70 to 120 show the various virtual forensic parameter values.

### 1. The CSF1PO STR Genetic Locus

**Table 70: Virtual Observed and Expected Genotypic Frequency Distributions for the CSF1PO STR Genetic Locus**

```
*****
**   Observed and Expected Genotypic Frequency Distribution   **
**           at CSF1PO in 1000 Unrelated                       **
*****
```

CSF1PO Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
5,5	14	0.014	8.464	0.00846
5,6	22	0.022	16.836	0.01684
5,7	18	0.018	15.364	0.01536
5,8	14	0.014	14.444	0.01444
5,9	10	0.01	15.64	0.01564
5,10	14	0.014	16.284	0.01628
5,11	4	0.004	14.26	0.01426
5,11.1	20	0.02	16.008	0.01601
5,12	19	0.019	16.56	0.01656
5,13	14	0.014	14.904	0.01490
5,14	11	0.011	12.328	0.01233
5,15	10	0.01	14.444	0.01444
6,6	16	0.016	8.37225	0.00837
6,7	13	0.013	15.2805	0.01528
6,8	8	0.008	14.3655	0.01437
6,9	13	0.013	15.555	0.01556
6,10	10	0.01	16.1955	0.01620
6,11	11	0.011	14.1825	0.01418
6,11.1	12	0.012	15.921	0.01592

6,12	18	0.018	16.47	0.01647
6,13	21	0.021	14.823	0.01482
6,14	12	0.012	12.261	0.01226
6,15	11	0.011	14.3655	0.01437
7,7	10	0.01	6.97225	0.00697
7,8	12	0.012	13.1095	0.01311
7,9	15	0.015	14.195	0.01420
7,10	17	0.017	14.7795	0.01478
7,11	16	0.016	12.9425	0.01294
7,11.1	14	0.014	14.529	0.01453
7,12	14	0.014	15.03	0.01503
7,13	10	0.01	13.527	0.01353
7,14	5	0.005	11.189	0.01119
7,15	13	0.013	13.1095	0.01311
8,8	12	0.012	6.16225	0.00616
8,9	13	0.013	13.345	0.01335
8,10	18	0.018	13.8945	0.01389
8,11	14	0.014	12.1675	0.01217
8,11.1	8	0.008	13.659	0.01366
8,12	17	0.017	14.13	0.01413
8,13	9	0.009	12.717	0.01272
8,14	8	0.008	10.519	0.01052
8,15	12	0.012	12.3245	0.01232
9,9	16	0.016	7.225	0.00723
9,10	14	0.014	15.045	0.01505
9,11	12	0.012	13.175	0.01318
9,11.1	11	0.011	14.79	0.01479
9,12	14	0.014	15.3	0.01530
9,13	8	0.008	13.77	0.01377
9,14	10	0.01	11.39	0.01139
9,15	18	0.018	13.345	0.01335
10,10	13	0.013	7.83225	0.00783
10,11	15	0.015	13.7175	0.01372
10,11.1	13	0.013	15.399	0.01540
10,12	13	0.013	15.93	0.01593
10,13	13	0.013	14.337	0.01434
10,14	12	0.012	11.859	0.01186
10,15	12	0.012	13.8945	0.01389
11,11	8	0.008	6.00625	0.00601
11,11.1	16	0.016	13.485	0.01348
11,12	13	0.013	13.95	0.01395
11,13	13	0.013	12.555	0.01256
11,14	15	0.015	10.385	0.01039
11,15	10	0.01	12.1675	0.01217
11.1,11.1	15	0.015	7.569	0.00757
11.1,12	11	0.011	15.66	0.01566
11.1,13	13	0.013	14.094	0.01409
11.1,14	14	0.014	11.658	0.01166
11.1,15	12	0.012	13.659	0.01366
12,12	16	0.016	8.1	0.00810
12,13	10	0.01	14.58	0.01458
12,14	7	0.007	12.06	0.01206
12,15	12	0.012	14.13	0.01413
13,13	13	0.013	6.561	0.00656
13,14	11	0.011	10.854	0.01085
13,15	14	0.014	12.717	0.01272
14,14	9	0.009	4.489	0.00449
14,15	11	0.011	10.519	0.01052
15,15	11	0.011	6.16225	0.00616
Total	1000	1	1000	1.00



**Table 71: Virtual CSF1PO Allelic Frequency Distributions**

```

*****
**      Alleles Frequencies of CSF1PO in 1000 Unrelated      **
*****

```

Allele	Number of Alleles	Allele Frequency
5	184	0.092
6	183	0.091
7	167	0.084
8	157	0.079
9	170	0.085
10	177	0.088
11	155	0.077
11.1	174	0.087
12	180	0.090
13	162	0.081
14	134	0.067
15	157	0.079
Total	2000	1

**Table 72: Virtual CSF1PO Forensic Parameters**

Results	
Expected homozygosity	0.08392
Expected hetrozygosity	0.91608
Observed Homozygosity	0.15300
Observed Hetrozygosity	0.84700
Power of Identity	0.01370
Power of Discrimination	0.98630
PIC	0.98611
Impossible Genotype	0.00000
Allelic Representation	1.00000
Genotype Representation	1.00000

## 2. The D3S1358 STR Genetic Locus

**Table 73: Virtual Observed and Expected Genotypic Frequency Distributions for the D3S1358 STR Genetic Locus**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at D3S1358 in 1000 Unrelated \*\*  
 \*\*\*\*\*

D3S1358 Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
11,11	10	0.01	6.16225	0.00616
11,12	13	0.013	13.1095	0.01311
11,13	20	0.02	13.188	0.01319
11,14	18	0.018	13.659	0.01366
11,15	8	0.008	13.7375	0.01374
11,16	8	0.008	10.5975	0.01060
11,16.2	9	0.009	12.089	0.01209
11,17	12	0.012	14.444	0.01444
11,18	10	0.01	13.345	0.01335
11,19	14	0.014	14.444	0.01444
11,20	16	0.016	13.502	0.01350
11,21	9	0.009	12.56	0.01256
12,12	13	0.013	6.97225	0.00697
12,13	9	0.009	14.028	0.01403
12,14	11	0.011	14.529	0.01453
12,15	18	0.018	14.6125	0.01461
12,16	12	0.012	11.2725	0.01127
12,16.2	12	0.012	12.859	0.01286
12,17	16	0.016	15.364	0.01536
12,18	11	0.011	14.195	0.01420
12,19	15	0.015	15.364	0.01536
12,20	11	0.011	14.362	0.01436
12,21	13	0.013	13.36	0.01336
13,13	12	0.012	7.056	0.00706
13,14	13	0.013	14.616	0.01462
13,15	15	0.015	14.7	0.01470
13,16	9	0.009	11.34	0.01134
13,16.2	9	0.009	12.936	0.01294
13,17	15	0.015	15.456	0.01546
13,18	12	0.012	14.28	0.01428
13,19	17	0.017	15.456	0.01546
13,20	11	0.011	14.448	0.01445
13,21	14	0.014	13.44	0.01344
14,14	17	0.017	7.569	0.00757
14,15	9	0.009	15.225	0.01522
14,16	9	0.009	11.745	0.01175
14,16.2	13	0.013	13.398	0.01340
14,17	14	0.014	16.008	0.01601
14,18	10	0.01	14.79	0.01479
14,19	16	0.016	16.008	0.01601
14,20	11	0.011	14.964	0.01496
14,21	16	0.016	13.92	0.01392
15,15	11	0.011	7.65625	0.00766
15,16	13	0.013	11.8125	0.01181
15,16.2	15	0.015	13.475	0.01347
15,17	14	0.014	16.1	0.01610
15,18	14	0.014	14.875	0.01487
15,19	13	0.013	16.1	0.01610

15,20	19	0.019	15.05	0.01505
15,21	15	0.015	14	0.01400
16,16	9	0.009	4.55625	0.00456
16,16.2	11	0.011	10.395	0.01039
16,17	16	0.016	12.42	0.01242
16,18	13	0.013	11.475	0.01148
16,19	14	0.014	12.42	0.01242
16,20	3	0.003	11.61	0.01161
16,21	9	0.009	10.8	0.01080
16.2,16.2	7	0.007	5.929	0.00593
16.2,17	14	0.014	14.168	0.01417
16.2,18	15	0.015	13.09	0.01309
16.2,19	20	0.02	14.168	0.01417
16.2,20	13	0.013	13.244	0.01324
16.2,21	9	0.009	12.32	0.01232
17,17	13	0.013	8.464	0.00846
17,18	17	0.017	15.64	0.01564
17,19	16	0.016	16.928	0.01693
17,20	13	0.013	15.824	0.01582
17,21	11	0.011	14.72	0.01472
18,18	14	0.014	7.225	0.00723
18,19	14	0.014	15.64	0.01564
18,20	14	0.014	14.62	0.01462
18,21	12	0.012	13.6	0.01360
19,19	14	0.014	8.464	0.00846
19,20	8	0.008	15.824	0.01582
19,21	9	0.009	14.72	0.01472
20,20	17	0.017	7.396	0.00740
20,21	19	0.019	13.76	0.01376
21,21	12	0.012	6.4	0.00640
Total	1000	1	1000	1.00

**Table 74: Virtual D3S1358 Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of D3S1358 in 1000 Unrelated \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
11	157	0.079
12	167	0.084
13	168	0.084
14	174	0.087
15	175	0.087
16	135	0.068
16.2	154	0.077
17	184	0.092
18	170	0.085
19	184	0.092

20	172	0.086
21	160	0.080
Total	2000	1

**Table 75: Virtual D3S1358 Forensic Parameters**

Results	
Expected homozygosity	0.08385
Expected hetrozygosity	0.91615
Observed Homozygosity	0.14900
Observed Hetrozygosity	0.85100
Power of Identity	0.01364
Power of Discrimination	0.98636
PIC	0.98617
Impossible Genotype	0.00000
Allelic Representation	1.00000
Genotype Representation	1.00000

### 3. The D5S818 STR Genetic Locus

**Table 76: Virtual Observed and Expected Genotypic Frequency Distributions for the D5S818 STR Genetic Locus**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at D5S818 in 1000 Unrelated \*\*  
 \*\*\*\*\*

D5S818 Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
7,7	14	0.014	8.01025	0.00801
7,8	14	0.014	18.437	0.01844
7,9	19	0.019	17.0945	0.01709
7,10	23	0.023	18.258	0.01826
7,11	20	0.02	18.258	0.01826
7,12	14	0.014	19.0635	0.01906
7,13	14	0.014	17.9	0.01790
7,14	17	0.017	15.3045	0.01530
7,15	15	0.015	19.511	0.01951
7,16	15	0.015	19.153	0.01915
8,8	22	0.022	10.609	0.01061
8,9	23	0.023	19.673	0.01967
8,10	18	0.018	21.012	0.02101
8,11	19	0.019	21.012	0.02101
8,12	17	0.017	21.939	0.02194
8,13	21	0.021	20.6	0.02060
8,14	13	0.013	17.613	0.01761
8,15	18	0.018	22.454	0.02245
8,16	19	0.019	22.042	0.02204

9,9	10	0.01	9.12025	0.00912
9,10	19	0.019	19.482	0.01948
9,11	22	0.022	19.482	0.01948
9,12	18	0.018	20.3415	0.02034
9,13	15	0.015	19.1	0.01910
9,14	16	0.016	16.3305	0.01633
9,15	23	0.023	20.819	0.02082
9,16	16	0.016	20.437	0.02044
10,10	28	0.028	10.404	0.01040
10,11	10	0.01	20.808	0.02081
10,12	17	0.017	21.726	0.02173
10,13	20	0.02	20.4	0.02040
10,14	9	0.009	17.442	0.01744
10,15	17	0.017	22.236	0.02224
10,16	15	0.015	21.828	0.02183
11,11	15	0.015	10.404	0.01040
11,12	23	0.023	21.726	0.02173
11,13	25	0.025	20.4	0.02040
11,14	17	0.017	17.442	0.01744
11,15	15	0.015	22.236	0.02224
11,16	23	0.023	21.828	0.02183
12,12	21	0.021	11.34225	0.01134
12,13	15	0.015	21.3	0.02130
12,14	23	0.023	18.2115	0.01821
12,15	27	0.027	23.217	0.02322
12,16	17	0.017	22.791	0.02279
13,13	17	0.017	10	0.01000
13,14	18	0.018	17.1	0.01710
13,15	17	0.017	21.8	0.02180
13,16	21	0.021	21.4	0.02140
14,14	10	0.01	7.31025	0.00731
14,15	20	0.02	18.639	0.01864
14,16	18	0.018	18.297	0.01830
15,15	23	0.023	11.881	0.01188
15,16	20	0.02	23.326	0.02333
16,16	25	0.025	11.449	0.01145
Total	1000	1	1000	1.00

**Table 77: Virtual D5S818 Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of D5S818 in 1000 Unrelated \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
7	179	0.089
8	206	0.103
9	191	0.096
10	204	0.102
11	204	0.102
12	213	0.106
13	200	0.100

14	171	0.086
15	218	0.109
16	214	0.107
Total	2000	1

**Table 78: Virtual D5S818 Forensic Parameters**

Results	
Expected homozygosity	0.10053
Expected hetrozygosity	0.89947
Observed Homozygosity	0.18500
Observed Hetrozygosity	0.81500
Power of Identity	0.01915
Power of Discrimination	0.98085
PIC	0.98049
Impossible Genotype	0.00000
Allelic Representation	1.00000
Genotype Representation	1.00000

#### 4. The D7S820 STR Genetic Locus

**Table 79: Virtual Observed and Expected Genotypic Frequency Distributions for the D7S820 STR Genetic Locus**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at D7S820 in 1000 Unrelated \*\*  
 \*\*\*\*\*

D7S820 Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
6,6	15	0.015	7.396	0.00740
6,7	12	0.012	14.792	0.01479
6,8	16	0.016	16.168	0.01617
6,9	15	0.015	16.082	0.01608
6,9.1	14	0.014	15.996	0.01600
6,10	17	0.017	18.06	0.01806
6,10.3	11	0.011	15.824	0.01582
6,11	14	0.014	14.62	0.01462
6,12	13	0.013	14.792	0.01479
6,13	16	0.016	15.91	0.01591
6,14	14	0.014	14.964	0.01496
7,7	9	0.009	7.396	0.00740
7,8	21	0.021	16.168	0.01617
7,9	15	0.015	16.082	0.01608
7,9.1	10	0.01	15.996	0.01600
7,10	18	0.018	18.06	0.01806

7,10.3	17	0.017	15.824	0.01582
7,11	15	0.015	14.62	0.01462
7,12	11	0.011	14.792	0.01479
7,13	17	0.017	15.91	0.01591
7,14	18	0.018	14.964	0.01496
8,8	14	0.014	8.836	0.00884
8,9	19	0.019	17.578	0.01758
8,9.1	17	0.017	17.484	0.01748
8,10	17	0.017	19.74	0.01974
8,10.3	12	0.012	17.296	0.01730
8,11	9	0.009	15.98	0.01598
8,12	18	0.018	16.168	0.01617
8,13	17	0.017	17.39	0.01739
8,14	14	0.014	16.356	0.01636
9,9	18	0.018	8.74225	0.00874
9,9.1	18	0.018	17.391	0.01739
9,10	17	0.017	19.635	0.01963
9,10.3	18	0.018	17.204	0.01720
9,11	12	0.012	15.895	0.01589
9,12	14	0.014	16.082	0.01608
9,13	9	0.009	17.2975	0.01730
9,14	14	0.014	16.269	0.01627
9.1,9.1	13	0.013	8.649	0.00865
9.1,10	16	0.016	19.53	0.01953
9.1,10.3	14	0.014	17.112	0.01711
9.1,11	22	0.022	15.81	0.01581
9.1,12	15	0.015	15.996	0.01600
9.1,13	11	0.011	17.205	0.01720
9.1,14	23	0.023	16.182	0.01618
10,10	19	0.019	11.025	0.01102
10,10.3	20	0.02	19.32	0.01932
10,11	14	0.014	17.85	0.01785
10,12	10	0.01	18.06	0.01806
10,13	22	0.022	19.425	0.01942
10,14	21	0.021	18.27	0.01827
10.3,10.3	13	0.013	8.464	0.00846
10.3,11	24	0.024	15.64	0.01564
10.3,12	11	0.011	15.824	0.01582
10.3,13	16	0.016	17.02	0.01702
10.3,14	15	0.015	16.008	0.01601
11,11	8	0.008	7.225	0.00723
11,12	15	0.015	14.62	0.01462
11,13	17	0.017	15.725	0.01572
11,14	12	0.012	14.79	0.01479
12,12	17	0.017	7.396	0.00740
12,13	16	0.016	15.91	0.01591
12,14	15	0.015	14.964	0.01496
13,13	15	0.015	8.55625	0.00856
13,14	14	0.014	16.095	0.01609
14,14	7	0.007	7.569	0.00757
Total	1000	1	1000	1.00

**Table 80: Virtual D7S820 Allelic Frequency Distributions**

```

*****
**      Alleles Frequencies of D7S820 in 1000 Unrelated      **
*****

```

Allele	Number of Alleles	Allele Frequency
6	172	0.086
7	172	0.086
8	188	0.094
9	187	0.093
9.1	186	0.093
10	210	0.105
10.3	184	0.092
11	170	0.085
12	172	0.086
13	185	0.092
14	174	0.087
Total	2000	1

**Table 81: Virtual D7S820 Forensic Parameters**

Results	
Expected homozygosity	0.09125
Expected hetrozygosity	0.90875
Observed Homozygosity	0.14800
Observed Hetrozygosity	0.85200
Power of Identity	0.01601
Power of Discrimination	0.98399
PIC	0.98374
Impossible Genotype	0.00000
Allelic Representation	1.00000
Genotype Representation	1.00000



## 5. The D8S1179 STR Genetic Locus

**Table 82: Virtual Observed and Expected Genotypic Frequency Distributions for the D8S1179 STR Genetic Locus**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at D8S1179 in 1000 Unrelated \*\*  
 \*\*\*\*\*

D8S1179 Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
7,7	3	0.003	2.401	0.00240
7,8	6	0.006	5.439	0.00544
7,9	6	0.006	5.537	0.00554
7,9.2	7	0.007	5.194	0.00519
7,10	6	0.006	4.9	0.00490
7,10.2	3	0.003	4.802	0.00480
7,11	3	0.003	5.586	0.00559
7,11.3	4	0.004	5.586	0.00559
7,12	6	0.006	5.488	0.00549
7,13	3	0.003	4.998	0.00500
7,14	1	0.001	4.704	0.00470
7,15	5	0.005	5.439	0.00544
7,16	5	0.005	4.655	0.00466
7,17	7	0.007	5.39	0.00539
7,18	8	0.008	5.096	0.00510
7,19	9	0.009	4.998	0.00500
7,20	4	0.004	4.704	0.00470
7,21	2	0.002	5.145	0.00515
7,22	7	0.007	5.537	0.00554
8,8	8	0.008	3.08025	0.00308
8,9	7	0.007	6.2715	0.00627
8,9.2	4	0.004	5.883	0.00588
8,10	3	0.003	5.55	0.00555
8,10.2	3	0.003	5.439	0.00544
8,11	7	0.007	6.327	0.00633
8,11.3	5	0.005	6.327	0.00633
8,12	5	0.005	6.216	0.00622
8,13	6	0.006	5.661	0.00566
8,14	6	0.006	5.328	0.00533
8,15	7	0.007	6.1605	0.00616
8,16	6	0.006	5.2725	0.00527
8,17	3	0.003	6.105	0.00611
8,18	9	0.009	5.772	0.00577
8,19	3	0.003	5.661	0.00566
8,20	7	0.007	5.328	0.00533
8,21	4	0.004	5.8275	0.00583
8,22	4	0.004	6.2715	0.00627
9,9	8	0.008	3.19225	0.00319
9,9.2	4	0.004	5.989	0.00599
9,10	6	0.006	5.65	0.00565
9,10.2	5	0.005	5.537	0.00554
9,11	8	0.008	6.441	0.00644
9,11.3	5	0.005	6.441	0.00644
9,12	6	0.006	6.328	0.00633
9,13	4	0.004	5.763	0.00576
9,14	5	0.005	5.424	0.00542
9,15	6	0.006	6.2715	0.00627
9,16	6	0.006	5.3675	0.00537

9,17	8	0.008	6.215	0.00622
9,18	4	0.004	5.876	0.00588
9,19	4	0.004	5.763	0.00576
9,20	7	0.007	5.424	0.00542
9,21	3	0.003	5.9325	0.00593
9,22	3	0.003	6.3845	0.00638
9.2,9.2	4	0.004	2.809	0.00281
9.2,10	9	0.009	5.3	0.00530
9.2,10.2	3	0.003	5.194	0.00519
9.2,11	3	0.003	6.042	0.00604
9.2,11.3	8	0.008	6.042	0.00604
9.2,12	8	0.008	5.936	0.00594
9.2,13	4	0.004	5.406	0.00541
9.2,14	6	0.006	5.088	0.00509
9.2,15	6	0.006	5.883	0.00588
9.2,16	4	0.004	5.035	0.00503
9.2,17	5	0.005	5.83	0.00583
9.2,18	2	0.002	5.512	0.00551
9.2,19	5	0.005	5.406	0.00541
9.2,20	5	0.005	5.088	0.00509
9.2,21	7	0.007	5.565	0.00556
9.2,22	8	0.008	5.989	0.00599
10,10	5	0.005	2.5	0.00250
10,10.2	6	0.006	4.9	0.00490
10,11	5	0.005	5.7	0.00570
10,11.3	6	0.006	5.7	0.00570
10,12	3	0.003	5.6	0.00560
10,13	8	0.008	5.1	0.00510
10,14	3	0.003	4.8	0.00480
10,15	2	0.002	5.55	0.00555
10,16	5	0.005	4.75	0.00475
10,17	1	0.001	5.5	0.00550
10,18	1	0.001	5.2	0.00520
10,19	5	0.005	5.1	0.00510
10,20	8	0.008	4.8	0.00480
10,21	8	0.008	5.25	0.00525
10,22	5	0.005	5.65	0.00565
10.2,10.2	5	0.005	2.401	0.00240
10.2,11	4	0.004	5.586	0.00559
10.2,11.3	5	0.005	5.586	0.00559
10.2,12	8	0.008	5.488	0.00549
10.2,13	2	0.002	4.998	0.00500
10.2,14	6	0.006	4.704	0.00470
10.2,15	6	0.006	5.439	0.00544
10.2,16	4	0.004	4.655	0.00466
10.2,17	4	0.004	5.39	0.00539
10.2,18	6	0.006	5.096	0.00510
10.2,19	4	0.004	4.998	0.00500
10.2,20	8	0.008	4.704	0.00470
10.2,21	4	0.004	5.145	0.00515
10.2,22	7	0.007	5.537	0.00554
11,11	10	0.01	3.249	0.00325
11,11.3	4	0.004	6.498	0.00650
11,12	5	0.005	6.384	0.00638
11,13	6	0.006	5.814	0.00581
11,14	4	0.004	5.472	0.00547
11,15	4	0.004	6.327	0.00633
11,16	3	0.003	5.415	0.00542
11,17	7	0.007	6.27	0.00627
11,18	8	0.008	5.928	0.00593
11,19	6	0.006	5.814	0.00581

11,20	4	0.004	5.472	0.00547
11,21	4	0.004	5.985	0.00598
11,22	9	0.009	6.441	0.00644
11.3,11.3	8	0.008	3.249	0.00325
11.3,12	2	0.002	6.384	0.00638
11.3,13	4	0.004	5.814	0.00581
11.3,14	8	0.008	5.472	0.00547
11.3,15	8	0.008	6.327	0.00633
11.3,16	7	0.007	5.415	0.00542
11.3,17	6	0.006	6.27	0.00627
11.3,18	8	0.008	5.928	0.00593
11.3,19	4	0.004	5.814	0.00581
11.3,20	1	0.001	5.472	0.00547
11.3,21	7	0.007	5.985	0.00598
11.3,22	6	0.006	6.441	0.00644
12,12	8	0.008	3.136	0.00314
12,13	8	0.008	5.712	0.00571
12,14	2	0.002	5.376	0.00538
12,15	9	0.009	6.216	0.00622
12,16	7	0.007	5.32	0.00532
12,17	2	0.002	6.16	0.00616
12,18	7	0.007	5.824	0.00582
12,19	7	0.007	5.712	0.00571
12,20	3	0.003	5.376	0.00538
12,21	3	0.003	5.88	0.00588
12,22	5	0.005	6.328	0.00633
13,13	3	0.003	2.601	0.00260
13,14	6	0.006	4.896	0.00490
13,15	6	0.006	5.661	0.00566
13,16	7	0.007	4.845	0.00484
13,17	5	0.005	5.61	0.00561
13,18	6	0.006	5.304	0.00530
13,19	6	0.006	5.202	0.00520
13,20	3	0.003	4.896	0.00490
13,21	6	0.006	5.355	0.00535
13,22	6	0.006	5.763	0.00576
14,14	1	0.001	2.304	0.00230
14,15	6	0.006	5.328	0.00533
14,16	5	0.005	4.56	0.00456
14,17	10	0.01	5.28	0.00528
14,18	2	0.002	4.992	0.00499
14,19	6	0.006	4.896	0.00490
14,20	2	0.002	4.608	0.00461
14,21	11	0.011	5.04	0.00504
14,22	5	0.005	5.424	0.00542
15,15	3	0.003	3.08025	0.00308
15,16	4	0.004	5.2725	0.00527
15,17	8	0.008	6.105	0.00611
15,18	7	0.007	5.772	0.00577
15,19	8	0.008	5.661	0.00566
15,20	5	0.005	5.328	0.00533
15,21	3	0.003	5.8275	0.00583
15,22	5	0.005	6.2715	0.00627
16,16	4	0.004	2.25625	0.00226
16,17	4	0.004	5.225	0.00523
16,18	4	0.004	4.94	0.00494
16,19	3	0.003	4.845	0.00484
16,20	4	0.004	4.56	0.00456
16,21	5	0.005	4.9875	0.00499
16,22	4	0.004	5.3675	0.00537
17,17	6	0.006	3.025	0.00302

17,18	5	0.005	5.72	0.00572
17,19	2	0.002	5.61	0.00561
17,20	9	0.009	5.28	0.00528
17,21	7	0.007	5.775	0.00577
17,22	5	0.005	6.215	0.00622
18,18	4	0.004	2.704	0.00270
18,19	5	0.005	5.304	0.00530
18,20	4	0.004	4.992	0.00499
18,21	6	0.006	5.46	0.00546
18,22	4	0.004	5.876	0.00588
19,19	5	0.005	2.601	0.00260
19,20	3	0.003	4.896	0.00490
19,21	5	0.005	5.355	0.00535
19,22	7	0.007	5.763	0.00576
20,20	6	0.006	2.304	0.00230
20,21	3	0.003	5.04	0.00504
20,22	4	0.004	5.424	0.00542
21,21	5	0.005	2.75625	0.00276
21,22	7	0.007	5.9325	0.00593
22,22	6	0.006	3.19225	0.00319
Total	1000	1	999.99999999	1.00

**Table 83: Virtual D8S1179 Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of D8S1179 in 1000 Unrelated \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
7	98	0.049
8	111	0.056
9	113	0.057
9.2	106	0.053
10	100	0.050
10.2	98	0.049
11	114	0.057
11.3	114	0.057
12	112	0.056
13	102	0.051
14	96	0.048
15	111	0.056
16	95	0.048
17	110	0.055
18	104	0.052

19	102	0.051
20	96	0.048
21	105	0.052
22	113	0.057
Total	2000	1

**Table 84: Virtual D8S1179 Forensic Parameters**

Results	
Expected homozygosity	0.05284
Expected hetrozygosity	0.94716
Observed Homozygosity	0.10200
Observed Hetrozygosity	0.89800
Power of Identity	0.00605
Power of Discrimination	0.99395
PIC	0.99392
Impossible Genotype	0.00000
Allelic Representation	1.00000
Genotype Representation	1.00000

## 6. The D13S317 STR Genetic Locus

**Table 85: Virtual Observed and Expected Genotypic Frequency Distributions for the D13S317 STR Genetic Locus**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at D13S317 in 1000 Unrelated \*\*  
 \*\*\*\*\*

D13S317 Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
6,6	11	0.011	7.48225	0.00748
6,7	16	0.016	18.165	0.01816
6,8	20	0.02	17.2135	0.01721
6,9	18	0.018	17.3865	0.01739
6,10	13	0.013	14.359	0.01436
6,11	14	0.014	19.2895	0.01929
6,12	17	0.017	17.9055	0.01791
6,13	14	0.014	18.4245	0.01842
6,14	17	0.017	16.0025	0.01600
6,15	22	0.022	19.2895	0.01929
7,7	16	0.016	11.025	0.01102
7,8	24	0.024	20.895	0.02090
7,9	16	0.016	21.105	0.02110
7,10	16	0.016	17.43	0.01743
7,11	23	0.023	23.415	0.02341

7,12	22	0.022	21.735	0.02173
7,13	19	0.019	22.365	0.02236
7,14	20	0.02	19.425	0.01942
7,15	22	0.022	23.415	0.02341
8,8	16	0.016	9.90025	0.00990
8,9	22	0.022	19.9995	0.02000
8,10	14	0.014	16.517	0.01652
8,11	19	0.019	22.1885	0.02219
8,12	16	0.016	20.5965	0.02060
8,13	22	0.022	21.1935	0.02119
8,14	14	0.014	18.4075	0.01841
8,15	16	0.016	22.1885	0.02219
9,9	19	0.019	10.10025	0.01010
9,10	11	0.011	16.683	0.01668
9,11	22	0.022	22.4115	0.02241
9,12	21	0.021	20.8035	0.02080
9,13	19	0.019	21.4065	0.02141
9,14	17	0.017	18.5925	0.01859
9,15	17	0.017	22.4115	0.02241
10,10	19	0.019	6.889	0.00689
10,11	14	0.014	18.509	0.01851
10,12	13	0.013	17.181	0.01718
10,13	18	0.018	17.679	0.01768
10,14	19	0.019	15.355	0.01536
10,15	10	0.01	18.509	0.01851
11,11	22	0.022	12.43225	0.01243
11,12	22	0.022	23.0805	0.02308
11,13	21	0.021	23.7495	0.02375
11,14	22	0.022	20.6275	0.02063
11,15	22	0.022	24.8645	0.02486
12,12	22	0.022	10.71225	0.01071
12,13	19	0.019	22.0455	0.02205
12,14	16	0.016	19.1475	0.01915
12,15	17	0.017	23.0805	0.02308
13,13	22	0.022	11.34225	0.01134
13,14	17	0.017	19.7025	0.01970
13,15	20	0.02	23.7495	0.02375
14,14	7	0.007	8.55625	0.00856
14,15	29	0.029	20.6275	0.02063
15,15	24	0.024	12.43225	0.01243
Total	1000	1	1000	1.00

**Table 86: Virtual D13S317 Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of D13S317 in 1000 Unrelated \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
6	173	0.086
7	210	0.105
8	199	0.100
9	201	0.101
10	166	0.083

11	223	0.112
12	207	0.103
13	213	0.106
14	185	0.092
15	223	0.112
Total	2000	1

**Table 87: Virtual D13S317 Forensic Parameters**

Results	
Expected homozygosity	0.10087
Expected hetrozygosity	0.89913
Observed Homozygosity	0.17800
Observed Hetrozygosity	0.82200
Power of Identity	0.01908
Power of Discrimination	0.98092
PIC	0.98057
Impossible Genotype	0.00000
Allelic Representation	1.00000
Genotype Representation	1.00000

## 7. The D16S539 STR Genetic Locus

**Table 88: Virtual Observed and Expected Genotypic Frequency Distributions for the D16S539 STR Genetic Locus**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at D16S539 in 1000 Unrelated \*\*  
 \*\*\*\*\*

D16S539 Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
5,5	23	0.023	10.92025	0.01092
5,8	19	0.019	22.154	0.02215
5,9	18	0.018	20.1685	0.02017
5,10	14	0.014	20.1685	0.02017
5,11	18	0.018	23.5125	0.02351
5,12	25	0.025	21.945	0.02194
5,13	19	0.019	21.318	0.02132
5,13.3	10	0.01	19.437	0.01944
5,14	19	0.019	15.7795	0.01578
5,15	21	0.021	22.6765	0.02268
8,8	20	0.02	11.236	0.01124
8,9	19	0.019	20.458	0.02046
8,10	21	0.021	20.458	0.02046

8,11	20	0.02	23.85	0.02385
8,12	17	0.017	22.26	0.02226
8,13	20	0.02	21.624	0.02162
8,13.3	22	0.022	19.716	0.01972
8,14	16	0.016	16.006	0.01601
8,15	18	0.018	23.002	0.02300
9,9	12	0.012	9.31225	0.00931
9,10	18	0.018	18.6245	0.01862
9,11	20	0.02	21.7125	0.02171
9,12	16	0.016	20.265	0.02026
9,13	22	0.022	19.686	0.01969
9,13.3	18	0.018	17.949	0.01795
9,14	13	0.013	14.5715	0.01457
9,15	25	0.025	20.9405	0.02094
10,10	17	0.017	9.31225	0.00931
10,11	19	0.019	21.7125	0.02171
10,12	20	0.02	20.265	0.02026
10,13	19	0.019	19.686	0.01969
10,13.3	22	0.022	17.949	0.01795
10,14	8	0.008	14.5715	0.01457
10,15	18	0.018	20.9405	0.02094
11,11	26	0.026	12.65625	0.01266
11,12	20	0.02	23.625	0.02363
11,13	20	0.02	22.95	0.02295
11,13.3	17	0.017	20.925	0.02092
11,14	14	0.014	16.9875	0.01699
11,15	25	0.025	24.4125	0.02441
12,12	18	0.018	11.025	0.01102
12,13	24	0.024	21.42	0.02142
12,13.3	16	0.016	19.53	0.01953
12,14	11	0.011	15.855	0.01585
12,15	25	0.025	22.785	0.02278
13,13	16	0.016	10.404	0.01040
13,13.3	15	0.015	18.972	0.01897
13,14	12	0.012	15.402	0.01540
13,15	21	0.021	22.134	0.02213
13.3,13.3	17	0.017	8.649	0.00865
13.3,14	16	0.016	14.043	0.01404
13.3,15	16	0.016	20.181	0.02018
14,14	12	0.012	5.70025	0.00570
14,15	18	0.018	16.3835	0.01638
15,15	15	0.015	11.77225	0.01177
Total	1000	1	1000	1.00

**Table 89: Virtual D16S539 Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of D16S539 in 1000 Unrelated \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
5	209	0.104
8	212	0.106
9	193	0.097
10	193	0.097



11	225	0.113
12	210	0.105
13	204	0.102
13.3	186	0.093
14	151	0.075
15	217	0.108
Total	2000	1

**Table 90: Virtual D16S539 Forensic Parameters**

Results	
Expected homozygosity	0.10099
Expected hetrozygosity	0.89901
Observed Homozygosity	0.17600
Observed Hetrozygosity	0.82400
Power of Identity	0.01903
Power of Discrimination	0.98097
PIC	0.98061
Impossible Genotype	0.00000
Allelic Representation	1.00000
Genotype Representation	1.00000

## 8. The D18S51 STR Genetic Locus

**Table 91: Virtual Observed and Expected Genotypic Frequency Distributions for the D18S51 STR Genetic Locus**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at D18S51 in 1000 Unrelated \*\*  
 \*\*\*\*\*

D18S51 Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
8,8	2	0.002	1.089	0.00109
8,9	3	0.003	2.409	0.00241
8,10	2	0.002	2.541	0.00254
8,10.2	3	0.003	2.475	0.00248
8,11	2	0.002	2.409	0.00241
8,12	1	0.001	2.376	0.00238
8,13	2	0.002	2.277	0.00228
8,13.2	1	0.001	2.079	0.00208
8,14	2	0.002	2.475	0.00248
8,14.2	2	0.002	2.475	0.00248
8,15	1	0.001	2.046	0.00205

8,15.2	2	0.002	2.211	0.00221
8,16	2	0.002	2.409	0.00241
8,17	3	0.003	2.244	0.00224
8,17.2	2	0.002	2.211	0.00221
8,18	5	0.005	2.277	0.00228
8,18.2	2	0.002	2.013	0.00201
8,19	3	0.003	2.508	0.00251
8,20	2	0.002	2.772	0.00277
8,20.2	2	0.002	2.277	0.00228
8,21	3	0.003	2.475	0.00248
8,22	2	0.002	2.277	0.00228
8,22.2	3	0.003	1.815	0.00181
8,23	1	0.001	2.046	0.00205
8,23.2	2	0.002	2.277	0.00228
8,24	1	0.001	2.145	0.00215
8,25	3	0.003	2.376	0.00238
8,26	3	0.003	1.98	0.00198
8,27	2	0.002	1.947	0.00195
9,9	2	0.002	1.33225	0.00133
9,10	5	0.005	2.8105	0.00281
9,10.2	2	0.002	2.7375	0.00274
9,11	3	0.003	2.6645	0.00266
9,12	3	0.003	2.628	0.00263
9,13	1	0.001	2.5185	0.00252
9,13.2	3	0.003	2.2995	0.00230
9,14	4	0.004	2.7375	0.00274
9,14.2	4	0.004	2.7375	0.00274
9,15	2	0.002	2.263	0.00226
9,15.2	1	0.001	2.4455	0.00245
9,16	2	0.002	2.6645	0.00266
9,17	1	0.001	2.482	0.00248
9,17.2	4	0.004	2.4455	0.00245
9,18	2	0.002	2.5185	0.00252
9,18.2	2	0.002	2.2265	0.00223
9,19	2	0.002	2.774	0.00277
9,20	4	0.004	3.066	0.00307
9,20.2	2	0.002	2.5185	0.00252
9,21	2	0.002	2.7375	0.00274
9,22	4	0.004	2.5185	0.00252
9,22.2	2	0.002	2.0075	0.00201
9,23	1	0.001	2.263	0.00226
9,23.2	3	0.003	2.5185	0.00252
9,24	2	0.002	2.3725	0.00237
9,25	1	0.001	2.628	0.00263
9,26	1	0.001	2.19	0.00219
9,27	3	0.003	2.1535	0.00215
10,10	3	0.003	1.48225	0.00148
10,10.2	1	0.001	2.8875	0.00289
10,11	2	0.002	2.8105	0.00281
10,12	3	0.003	2.772	0.00277
10,13	1	0.001	2.6565	0.00266
10,13.2	3	0.003	2.4255	0.00243
10,14	5	0.005	2.8875	0.00289
10,14.2	4	0.004	2.8875	0.00289
10,15	3	0.003	2.387	0.00239
10,15.2	2	0.002	2.5795	0.00258
10,16	2	0.002	2.8105	0.00281
10,17	2	0.002	2.618	0.00262
10,17.2	5	0.005	2.5795	0.00258
10,18	3	0.003	2.6565	0.00266
10,18.2	2	0.002	2.3485	0.00235

10,19	3	0.003	2.926	0.00293
10,20	3	0.003	3.234	0.00323
10,20.2	3	0.003	2.6565	0.00266
10,21	3	0.003	2.8875	0.00289
10,22	2	0.002	2.6565	0.00266
10,22.2	2	0.002	2.1175	0.00212
10,23	2	0.002	2.387	0.00239
10,23.2	1	0.001	2.6565	0.00266
10,24	2	0.002	2.5025	0.00250
10,25	3	0.003	2.772	0.00277
10,26	1	0.001	2.31	0.00231
10,27	1	0.001	2.2715	0.00227
10.2,10.2	3	0.003	1.40625	0.00141
10.2,11	1	0.001	2.7375	0.00274
10.2,12	2	0.002	2.7	0.00270
10.2,13	4	0.004	2.5875	0.00259
10.2,13.2	2	0.002	2.3625	0.00236
10.2,14	5	0.005	2.8125	0.00281
10.2,14.2	3	0.003	2.8125	0.00281
10.2,15	1	0.001	2.325	0.00232
10.2,15.2	4	0.004	2.5125	0.00251
10.2,16	2	0.002	2.7375	0.00274
10.2,17	2	0.002	2.55	0.00255
10.2,17.2	3	0.003	2.5125	0.00251
10.2,18	2	0.002	2.5875	0.00259
10.2,18.2	4	0.004	2.2875	0.00229
10.2,19	3	0.003	2.85	0.00285
10.2,20	2	0.002	3.15	0.00315
10.2,20.2	5	0.005	2.5875	0.00259
10.2,21	3	0.003	2.8125	0.00281
10.2,22	1	0.001	2.5875	0.00259
10.2,22.2	2	0.002	2.0625	0.00206
10.2,23	1	0.001	2.325	0.00232
10.2,23.2	2	0.002	2.5875	0.00259
10.2,24	5	0.005	2.4375	0.00244
10.2,25	1	0.001	2.7	0.00270
10.2,26	1	0.001	2.25	0.00225
10.2,27	2	0.002	2.2125	0.00221
11,11	2	0.002	1.33225	0.00133
11,12	4	0.004	2.628	0.00263
11,13	2	0.002	2.5185	0.00252
11,13.2	4	0.004	2.2995	0.00230
11,14	1	0.001	2.7375	0.00274
11,14.2	2	0.002	2.7375	0.00274
11,15	2	0.002	2.263	0.00226
11,15.2	3	0.003	2.4455	0.00245
11,16	3	0.003	2.6645	0.00266
11,17	3	0.003	2.482	0.00248
11,17.2	4	0.004	2.4455	0.00245
11,18	4	0.004	2.5185	0.00252
11,18.2	3	0.003	2.2265	0.00223
11,19	3	0.003	2.774	0.00277
11,20	3	0.003	3.066	0.00307
11,20.2	3	0.003	2.5185	0.00252
11,21	3	0.003	2.7375	0.00274
11,22	2	0.002	2.5185	0.00252
11,22.2	1	0.001	2.0075	0.00201
11,23	1	0.001	2.263	0.00226
11,23.2	2	0.002	2.5185	0.00252
11,24	1	0.001	2.3725	0.00237
11,25	3	0.003	2.628	0.00263

11,26	2	0.002	2.19	0.00219
11,27	2	0.002	2.1535	0.00215
12,12	3	0.003	1.296	0.00130
12,13	4	0.004	2.484	0.00248
12,13.2	1	0.001	2.268	0.00227
12,14	2	0.002	2.7	0.00270
12,14.2	3	0.003	2.7	0.00270
12,15	3	0.003	2.232	0.00223
12,15.2	3	0.003	2.412	0.00241
12,16	2	0.002	2.628	0.00263
12,17	3	0.003	2.448	0.00245
12,17.2	1	0.001	2.412	0.00241
12,18	3	0.003	2.484	0.00248
12,18.2	2	0.002	2.196	0.00220
12,19	3	0.003	2.736	0.00274
12,20	4	0.004	3.024	0.00302
12,20.2	2	0.002	2.484	0.00248
12,21	2	0.002	2.7	0.00270
12,22	2	0.002	2.484	0.00248
12,22.2	2	0.002	1.98	0.00198
12,23	1	0.001	2.232	0.00223
12,23.2	2	0.002	2.484	0.00248
12,24	1	0.001	2.34	0.00234
12,25	3	0.003	2.592	0.00259
12,26	1	0.001	2.16	0.00216
12,27	3	0.003	2.124	0.00212
13,13	3	0.003	1.19025	0.00119
13,13.2	5	0.005	2.1735	0.00217
13,14	4	0.004	2.5875	0.00259
13,14.2	2	0.002	2.5875	0.00259
13,15	1	0.001	2.139	0.00214
13,15.2	3	0.003	2.3115	0.00231
13,16	2	0.002	2.5185	0.00252
13,17	1	0.001	2.346	0.00235
13,17.2	3	0.003	2.3115	0.00231
13,18	2	0.002	2.3805	0.00238
13,18.2	1	0.001	2.1045	0.00210
13,19	2	0.002	2.622	0.00262
13,20	1	0.001	2.898	0.00290
13,20.2	2	0.002	2.3805	0.00238
13,21	2	0.002	2.5875	0.00259
13,22	1	0.001	2.3805	0.00238
13,22.2	1	0.001	1.8975	0.00190
13,23	2	0.002	2.139	0.00214
13,23.2	2	0.002	2.3805	0.00238
13,24	2	0.002	2.2425	0.00224
13,25	4	0.004	2.484	0.00248
13,26	3	0.003	2.07	0.00207
13,27	3	0.003	2.0355	0.00204
13.2,13.2	1	0.001	0.99225	0.00099
13.2,14	1	0.001	2.3625	0.00236
13.2,14.2	1	0.001	2.3625	0.00236
13.2,15	2	0.002	1.953	0.00195
13.2,15.2	3	0.003	2.1105	0.00211
13.2,16	3	0.003	2.2995	0.00230
13.2,17	3	0.003	2.142	0.00214
13.2,17.2	1	0.001	2.1105	0.00211
13.2,18	2	0.002	2.1735	0.00217
13.2,18.2	1	0.001	1.9215	0.00192
13.2,19	2	0.002	2.394	0.00239
13.2,20	3	0.003	2.646	0.00265

13.2,20.2	1	0.001	2.1735	0.00217
13.2,21	1	0.001	2.3625	0.00236
13.2,22	3	0.003	2.1735	0.00217
13.2,22.2	2	0.002	1.7325	0.00173
13.2,23	4	0.004	1.953	0.00195
13.2,23.2	1	0.001	2.1735	0.00217
13.2,24	3	0.003	2.0475	0.00205
13.2,25	2	0.002	2.268	0.00227
13.2,26	1	0.001	1.89	0.00189
13.2,27	2	0.002	1.8585	0.00186
14,14	3	0.003	1.40625	0.00141
14,14.2	2	0.002	2.8125	0.00281
14,15	4	0.004	2.325	0.00232
14,15.2	1	0.001	2.5125	0.00251
14,16	3	0.003	2.7375	0.00274
14,17	1	0.001	2.55	0.00255
14,17.2	4	0.004	2.5125	0.00251
14,18	1	0.001	2.5875	0.00259
14,18.2	3	0.003	2.2875	0.00229
14,19	2	0.002	2.85	0.00285
14,20	2	0.002	3.15	0.00315
14,20.2	1	0.001	2.5875	0.00259
14,21	1	0.001	2.8125	0.00281
14,22	3	0.003	2.5875	0.00259
14,22.2	2	0.002	2.0625	0.00206
14,23	1	0.001	2.325	0.00232
14,23.2	3	0.003	2.5875	0.00259
14,24	4	0.004	2.4375	0.00244
14,25	1	0.001	2.7	0.00270
14,26	4	0.004	2.25	0.00225
14,27	2	0.002	2.2125	0.00221
14.2,14.2	2	0.002	1.40625	0.00141
14.2,15	2	0.002	2.325	0.00232
14.2,15.2	2	0.002	2.5125	0.00251
14.2,16	5	0.005	2.7375	0.00274
14.2,17	1	0.001	2.55	0.00255
14.2,17.2	1	0.001	2.5125	0.00251
14.2,18	1	0.001	2.5875	0.00259
14.2,18.2	2	0.002	2.2875	0.00229
14.2,19	2	0.002	2.85	0.00285
14.2,20	5	0.005	3.15	0.00315
14.2,20.2	1	0.001	2.5875	0.00259
14.2,21	3	0.003	2.8125	0.00281
14.2,22	4	0.004	2.5875	0.00259
14.2,22.2	2	0.002	2.0625	0.00206
14.2,23	2	0.002	2.325	0.00232
14.2,23.2	3	0.003	2.5875	0.00259
14.2,24	4	0.004	2.4375	0.00244
14.2,25	2	0.002	2.7	0.00270
14.2,26	3	0.003	2.25	0.00225
14.2,27	3	0.003	2.2125	0.00221
15,15	2	0.002	0.961	0.00096
15,15.2	3	0.003	2.077	0.00208
15,16	2	0.002	2.263	0.00226
15,17	1	0.001	2.108	0.00211
15,17.2	2	0.002	2.077	0.00208
15,18	1	0.001	2.139	0.00214
15,18.2	2	0.002	1.891	0.00189
15,19	2	0.002	2.356	0.00236
15,20	3	0.003	2.604	0.00260
15,20.2	3	0.003	2.139	0.00214

15,21	2	0.002	2.325	0.00232
15,22	1	0.001	2.139	0.00214
15,22.2	1	0.001	1.705	0.00170
15,23	3	0.003	1.922	0.00192
15,23.2	2	0.002	2.139	0.00214
15,24	2	0.002	2.015	0.00201
15,25	3	0.003	2.232	0.00223
15,26	2	0.002	1.86	0.00186
15,27	2	0.002	1.829	0.00183
15.2,15.2	2	0.002	1.12225	0.00112
15.2,16	1	0.001	2.4455	0.00245
15.2,17	1	0.001	2.278	0.00228
15.2,17.2	2	0.002	2.2445	0.00224
15.2,18	3	0.003	2.3115	0.00231
15.2,18.2	3	0.003	2.0435	0.00204
15.2,19	3	0.003	2.546	0.00255
15.2,20	2	0.002	2.814	0.00281
15.2,20.2	3	0.003	2.3115	0.00231
15.2,21	2	0.002	2.5125	0.00251
15.2,22	2	0.002	2.3115	0.00231
15.2,22.2	2	0.002	1.8425	0.00184
15.2,23	2	0.002	2.077	0.00208
15.2,23.2	3	0.003	2.3115	0.00231
15.2,24	1	0.001	2.1775	0.00218
15.2,25	3	0.003	2.412	0.00241
15.2,26	1	0.001	2.01	0.00201
15.2,27	2	0.002	1.9765	0.00198
16,16	2	0.002	1.33225	0.00133
16,17	2	0.002	2.482	0.00248
16,17.2	5	0.005	2.4455	0.00245
16,18	2	0.002	2.5185	0.00252
16,18.2	3	0.003	2.2265	0.00223
16,19	2	0.002	2.774	0.00277
16,20	3	0.003	3.066	0.00307
16,20.2	2	0.002	2.5185	0.00252
16,21	2	0.002	2.7375	0.00274
16,22	2	0.002	2.5185	0.00252
16,22.2	3	0.003	2.0075	0.00201
16,23	2	0.002	2.263	0.00226
16,23.2	3	0.003	2.5185	0.00252
16,24	2	0.002	2.3725	0.00237
16,25	4	0.004	2.628	0.00263
16,26	1	0.001	2.19	0.00219
16,27	2	0.002	2.1535	0.00215
17,17	2	0.002	1.156	0.00116
17,17.2	1	0.001	2.278	0.00228
17,18	5	0.005	2.346	0.00235
17,18.2	2	0.002	2.074	0.00207
17,19	2	0.002	2.584	0.00258
17,20	6	0.006	2.856	0.00286
17,20.2	2	0.002	2.346	0.00235
17,21	2	0.002	2.55	0.00255
17,22	4	0.004	2.346	0.00235
17,22.2	1	0.001	1.87	0.00187
17,23	4	0.004	2.108	0.00211
17,23.2	1	0.001	2.346	0.00235
17,24	3	0.003	2.21	0.00221
17,25	1	0.001	2.448	0.00245
17,26	3	0.003	2.04	0.00204
17,27	3	0.003	2.006	0.00201
17.2,17.2	1	0.001	1.12225	0.00112

17.2,18	1	0.001	2.3115	0.00231
17.2,18.2	3	0.003	2.0435	0.00204
17.2,19	1	0.001	2.546	0.00255
17.2,20	4	0.004	2.814	0.00281
17.2,20.2	1	0.001	2.3115	0.00231
17.2,21	2	0.002	2.5125	0.00251
17.2,22	1	0.001	2.3115	0.00231
17.2,22.2	1	0.001	1.8425	0.00184
17.2,23	4	0.004	2.077	0.00208
17.2,23.2	2	0.002	2.3115	0.00231
17.2,24	3	0.003	2.1775	0.00218
17.2,25	2	0.002	2.412	0.00241
17.2,26	1	0.001	2.01	0.00201
17.2,27	1	0.001	1.9765	0.00198
18,18	3	0.003	1.19025	0.00119
18,18.2	2	0.002	2.1045	0.00210
18,19	2	0.002	2.622	0.00262
18,20	1	0.001	2.898	0.00290
18,20.2	1	0.001	2.3805	0.00238
18,21	2	0.002	2.5875	0.00259
18,22	2	0.002	2.3805	0.00238
18,22.2	2	0.002	1.8975	0.00190
18,23	3	0.003	2.139	0.00214
18,23.2	2	0.002	2.3805	0.00238
18,24	1	0.001	2.2425	0.00224
18,25	3	0.003	2.484	0.00248
18,26	3	0.003	2.07	0.00207
18,27	2	0.002	2.0355	0.00204
18.2,18.2	1	0.001	0.93025	0.00093
18.2,19	2	0.002	2.318	0.00232
18.2,20	2	0.002	2.562	0.00256
18.2,20.2	2	0.002	2.1045	0.00210
18.2,21	2	0.002	2.2875	0.00229
18.2,22	1	0.001	2.1045	0.00210
18.2,22.2	2	0.002	1.6775	0.00168
18.2,23	1	0.001	1.891	0.00189
18.2,23.2	2	0.002	2.1045	0.00210
18.2,24	2	0.002	1.9825	0.00198
18.2,25	2	0.002	2.196	0.00220
18.2,26	1	0.001	1.83	0.00183
18.2,27	3	0.003	1.7995	0.00180
19,19	3	0.003	1.444	0.00144
19,20	4	0.004	3.192	0.00319
19,20.2	4	0.004	2.622	0.00262
19,21	5	0.005	2.85	0.00285
19,22	4	0.004	2.622	0.00262
19,22.2	1	0.001	2.09	0.00209
19,23	3	0.003	2.356	0.00236
19,23.2	2	0.002	2.622	0.00262
19,24	4	0.004	2.47	0.00247
19,25	1	0.001	2.736	0.00274
19,26	2	0.002	2.28	0.00228
19,27	1	0.001	2.242	0.00224
20,20	3	0.003	1.764	0.00176
20,20.2	4	0.004	2.898	0.00290
20,21	5	0.005	3.15	0.00315
20,22	1	0.001	2.898	0.00290
20,22.2	2	0.002	2.31	0.00231
20,23	3	0.003	2.604	0.00260
20,23.2	2	0.002	2.898	0.00290
20,24	2	0.002	2.73	0.00273

20, 25	2	0.002	3.024	0.00302
20, 26	2	0.002	2.52	0.00252
20, 27	1	0.001	2.478	0.00248
20.2, 20.2	3	0.003	1.19025	0.00119
20.2, 21	3	0.003	2.5875	0.00259
20.2, 22	2	0.002	2.3805	0.00238
20.2, 22.2	2	0.002	1.8975	0.00190
20.2, 23	2	0.002	2.139	0.00214
20.2, 23.2	1	0.001	2.3805	0.00238
20.2, 24	3	0.003	2.2425	0.00224
20.2, 25	2	0.002	2.484	0.00248
20.2, 26	3	0.003	2.07	0.00207
20.2, 27	1	0.001	2.0355	0.00204
21, 21	2	0.002	1.40625	0.00141
21, 22	1	0.001	2.5875	0.00259
21, 22.2	3	0.003	2.0625	0.00206
21, 23	3	0.003	2.325	0.00232
21, 23.2	3	0.003	2.5875	0.00259
21, 24	2	0.002	2.4375	0.00244
21, 25	4	0.004	2.7	0.00270
21, 26	3	0.003	2.25	0.00225
21, 27	2	0.002	2.2125	0.00221
22, 22	2	0.002	1.19025	0.00119
22, 22.2	1	0.001	1.8975	0.00190
22, 23	1	0.001	2.139	0.00214
22, 23.2	5	0.005	2.3805	0.00238
22, 24	1	0.001	2.2425	0.00224
22, 25	6	0.006	2.484	0.00248
22, 26	3	0.003	2.07	0.00207
22, 27	3	0.003	2.0355	0.00204
22.2, 22.2	2	0.002	0.75625	0.00076
22.2, 23	3	0.003	1.705	0.00170
22.2, 23.2	2	0.002	1.8975	0.00190
22.2, 24	1	0.001	1.7875	0.00179
22.2, 25	2	0.002	1.98	0.00198
22.2, 26	1	0.001	1.65	0.00165
22.2, 27	2	0.002	1.6225	0.00162
23, 23	2	0.002	0.961	0.00096
23, 23.2	2	0.002	2.139	0.00214
23, 24	2	0.002	2.015	0.00201
23, 25	1	0.001	2.232	0.00223
23, 26	2	0.002	1.86	0.00186
23, 27	1	0.001	1.829	0.00183
23.2, 23.2	3	0.003	1.19025	0.00119
23.2, 24	3	0.003	2.2425	0.00224
23.2, 25	2	0.002	2.484	0.00248
23.2, 26	3	0.003	2.07	0.00207
23.2, 27	2	0.002	2.0355	0.00204
24, 24	2	0.002	1.05625	0.00106
24, 25	2	0.002	2.34	0.00234
24, 26	1	0.001	1.95	0.00195
24, 27	1	0.001	1.9175	0.00192
25, 25	3	0.003	1.296	0.00130
25, 26	2	0.002	2.16	0.00216
25, 27	1	0.001	2.124	0.00212
26, 26	2	0.002	0.9	0.00090
26, 27	2	0.002	1.77	0.00177
27, 27	2	0.002	0.87025	0.00087
Total	1000	1	1000	1.00



**Table 92: Virtual D18S51 Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of D18S51 in 1000 Unrelated \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
8	66	0.033
9	73	0.036
10	77	0.038
10.2	75	0.037
11	73	0.036
12	72	0.036
13	69	0.035
13.2	63	0.032
14	75	0.037
14.2	75	0.037
15	62	0.031
15.2	67	0.034
16	73	0.036
17	68	0.034
17.2	67	0.034
18	69	0.035
18.2	61	0.030
19	76	0.038
20	84	0.042
20.2	69	0.035
21	75	0.037
22	69	0.035
22.2	55	0.028
23	62	0.031
23.2	69	0.035
24	65	0.033

25	72	0.036
26	60	0.030
27	59	0.029
Total	2000	1

**Table 93 : Virtual D18S51 Forensic Parameters**

Results	
Expected homozygosity	0.03477
Expected hetrozygosity	0.96523
Observed Homozygosity	0.06600
Observed Hetrozygosity	0.93400
Power of Identity	0.00278
Power of Discrimination	0.99722
PIC	0.99721
Impossible Genotype	0.00000
Allelic Representation	1.00000
Genotype Representation	1.00000

## 9. The D21S11 STR Genetic Locus

**Table 94: Virtual Observed and Expected Genotypic Frequency Distributions for the D21S11 STR Genetic Locus**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at D21S11 in 1000 Unrelated \*\*  
 \*\*\*\*\*

D21S11 Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
24, 24	2	0.002	1.12225	0.00112
24, 24.2	2	0.002	2.2445	0.00224
24, 24.3	3	0.003	2.613	0.00261
24, 25	3	0.003	2.2445	0.00224
24, 25.2	4	0.004	2.613	0.00261
24, 26	1	0.001	2.3115	0.00231
24, 27	1	0.001	2.5795	0.00258
24, 28	2	0.002	2.479	0.00248
24, 28.2	3	0.003	2.3785	0.00238
24, 29	3	0.003	2.345	0.00235
24, 29.2	1	0.001	2.211	0.00221
24, 30	3	0.003	2.077	0.00208
24, 30.2	4	0.004	2.3785	0.00238
24, 31	2	0.002	2.278	0.00228
24, 31.2	3	0.003	2.5125	0.00251
24, 32	2	0.002	2.814	0.00281
24, 32.1	2	0.002	2.2445	0.00224
24, 32.2	2	0.002	1.7755	0.00178
24, 33	2	0.002	2.4455	0.00245

24, 33.1	3	0.003	2.1105	0.00211
24, 33.2	2	0.002	2.1775	0.00218
24, 34	2	0.002	2.546	0.00255
24, 34.1	1	0.001	2.01	0.00201
24, 34.2	2	0.002	2.2445	0.00224
24, 35	1	0.001	2.3115	0.00231
24, 35.2	2	0.002	2.479	0.00248
24, 36	1	0.001	2.1775	0.00218
24, 37	2	0.002	2.01	0.00201
24, 38	4	0.004	2.144	0.00214
24.2, 24.2	2	0.002	1.12225	0.00112
24.2, 24.3	1	0.001	2.613	0.00261
24.2, 25	4	0.004	2.2445	0.00224
24.2, 25.2	3	0.003	2.613	0.00261
24.2, 26	2	0.002	2.3115	0.00231
24.2, 27	3	0.003	2.5795	0.00258
24.2, 28	4	0.004	2.479	0.00248
24.2, 28.2	2	0.002	2.3785	0.00238
24.2, 29	2	0.002	2.345	0.00235
24.2, 29.2	3	0.003	2.211	0.00221
24.2, 30	1	0.001	2.077	0.00208
24.2, 30.2	3	0.003	2.3785	0.00238
24.2, 31	3	0.003	2.278	0.00228
24.2, 31.2	3	0.003	2.5125	0.00251
24.2, 32	1	0.001	2.814	0.00281
24.2, 32.1	1	0.001	2.2445	0.00224
24.2, 32.2	1	0.001	1.7755	0.00178
24.2, 33	3	0.003	2.4455	0.00245
24.2, 33.1	1	0.001	2.1105	0.00211
24.2, 33.2	3	0.003	2.1775	0.00218
24.2, 34	2	0.002	2.546	0.00255
24.2, 34.1	1	0.001	2.01	0.00201
24.2, 34.2	1	0.001	2.2445	0.00224
24.2, 35	2	0.002	2.3115	0.00231
24.2, 35.2	4	0.004	2.479	0.00248
24.2, 36	1	0.001	2.1775	0.00218
24.2, 37	4	0.004	2.01	0.00201
24.2, 38	2	0.002	2.144	0.00214
24.3, 24.3	2	0.002	1.521	0.00152
24.3, 25	2	0.002	2.613	0.00261
24.3, 25.2	4	0.004	3.042	0.00304
24.3, 26	2	0.002	2.691	0.00269
24.3, 27	2	0.002	3.003	0.00300
24.3, 28	2	0.002	2.886	0.00289
24.3, 28.2	4	0.004	2.769	0.00277
24.3, 29	4	0.004	2.73	0.00273
24.3, 29.2	1	0.001	2.574	0.00257
24.3, 30	1	0.001	2.418	0.00242
24.3, 30.2	1	0.001	2.769	0.00277
24.3, 31	4	0.004	2.652	0.00265
24.3, 31.2	3	0.003	2.925	0.00293
24.3, 32	5	0.005	3.276	0.00328
24.3, 32.1	2	0.002	2.613	0.00261
24.3, 32.2	3	0.003	2.067	0.00207
24.3, 33	4	0.004	2.847	0.00285
24.3, 33.1	3	0.003	2.457	0.00246
24.3, 33.2	2	0.002	2.535	0.00253
24.3, 34	3	0.003	2.964	0.00296
24.3, 34.1	2	0.002	2.34	0.00234
24.3, 34.2	2	0.002	2.613	0.00261
24.3, 35	3	0.003	2.691	0.00269

24.3,35.2	4	0.004	2.886	0.00289
24.3,36	2	0.002	2.535	0.00253
24.3,37	2	0.002	2.34	0.00234
24.3,38	3	0.003	2.496	0.00250
25,25	1	0.001	1.12225	0.00112
25,25.2	2	0.002	2.613	0.00261
25,26	2	0.002	2.3115	0.00231
25,27	2	0.002	2.5795	0.00258
25,28	5	0.005	2.479	0.00248
25,28.2	1	0.001	2.3785	0.00238
25,29	2	0.002	2.345	0.00235
25,29.2	2	0.002	2.211	0.00221
25,30	2	0.002	2.077	0.00208
25,30.2	2	0.002	2.3785	0.00238
25,31	1	0.001	2.278	0.00228
25,31.2	2	0.002	2.5125	0.00251
25,32	3	0.003	2.814	0.00281
25,32.1	1	0.001	2.2445	0.00224
25,32.2	1	0.001	1.7755	0.00178
25,33	5	0.005	2.4455	0.00245
25,33.1	1	0.001	2.1105	0.00211
25,33.2	1	0.001	2.1775	0.00218
25,34	2	0.002	2.546	0.00255
25,34.1	3	0.003	2.01	0.00201
25,34.2	5	0.005	2.2445	0.00224
25,35	3	0.003	2.3115	0.00231
25,35.2	1	0.001	2.479	0.00248
25,36	3	0.003	2.1775	0.00218
25,37	1	0.001	2.01	0.00201
25,38	3	0.003	2.144	0.00214
25.2,25.2	2	0.002	1.521	0.00152
25.2,26	2	0.002	2.691	0.00269
25.2,27	3	0.003	3.003	0.00300
25.2,28	2	0.002	2.886	0.00289
25.2,28.2	5	0.005	2.769	0.00277
25.2,29	3	0.003	2.73	0.00273
25.2,29.2	2	0.002	2.574	0.00257
25.2,30	1	0.001	2.418	0.00242
25.2,30.2	4	0.004	2.769	0.00277
25.2,31	1	0.001	2.652	0.00265
25.2,31.2	3	0.003	2.925	0.00293
25.2,32	3	0.003	3.276	0.00328
25.2,32.1	2	0.002	2.613	0.00261
25.2,32.2	2	0.002	2.067	0.00207
25.2,33	2	0.002	2.847	0.00285
25.2,33.1	4	0.004	2.457	0.00246
25.2,33.2	2	0.002	2.535	0.00253
25.2,34	4	0.004	2.964	0.00296
25.2,34.1	1	0.001	2.34	0.00234
25.2,34.2	3	0.003	2.613	0.00261
25.2,35	2	0.002	2.691	0.00269
25.2,35.2	2	0.002	2.886	0.00289
25.2,36	3	0.003	2.535	0.00253
25.2,37	3	0.003	2.34	0.00234
25.2,38	2	0.002	2.496	0.00250
26,26	1	0.001	1.19025	0.00119
26,27	3	0.003	2.6565	0.00266
26,28	4	0.004	2.553	0.00255
26,28.2	2	0.002	2.4495	0.00245
26,29	4	0.004	2.415	0.00242
26,29.2	3	0.003	2.277	0.00228

26,30	3	0.003	2.139	0.00214
26,30.2	2	0.002	2.4495	0.00245
26,31	2	0.002	2.346	0.00235
26,31.2	3	0.003	2.5875	0.00259
26,32	3	0.003	2.898	0.00290
26,32.1	1	0.001	2.3115	0.00231
26,32.2	2	0.002	1.8285	0.00183
26,33	1	0.001	2.5185	0.00252
26,33.1	2	0.002	2.1735	0.00217
26,33.2	2	0.002	2.2425	0.00224
26,34	5	0.005	2.622	0.00262
26,34.1	3	0.003	2.07	0.00207
26,34.2	3	0.003	2.3115	0.00231
26,35	2	0.002	2.3805	0.00238
26,35.2	4	0.004	2.553	0.00255
26,36	2	0.002	2.2425	0.00224
26,37	1	0.001	2.07	0.00207
26,38	1	0.001	2.208	0.00221
27,27	2	0.002	1.48225	0.00148
27,28	1	0.001	2.849	0.00285
27,28.2	2	0.002	2.7335	0.00273
27,29	5	0.005	2.695	0.00270
27,29.2	3	0.003	2.541	0.00254
27,30	2	0.002	2.387	0.00239
27,30.2	5	0.005	2.7335	0.00273
27,31	3	0.003	2.618	0.00262
27,31.2	2	0.002	2.8875	0.00289
27,32	4	0.004	3.234	0.00323
27,32.1	3	0.003	2.5795	0.00258
27,32.2	1	0.001	2.0405	0.00204
27,33	3	0.003	2.8105	0.00281
27,33.1	1	0.001	2.4255	0.00243
27,33.2	2	0.002	2.5025	0.00250
27,34	2	0.002	2.926	0.00293
27,34.1	1	0.001	2.31	0.00231
27,34.2	4	0.004	2.5795	0.00258
27,35	3	0.003	2.6565	0.00266
27,35.2	2	0.002	2.849	0.00285
27,36	3	0.003	2.5025	0.00250
27,37	2	0.002	2.31	0.00231
27,38	5	0.005	2.464	0.00246
28,28	1	0.001	1.369	0.00137
28,28.2	2	0.002	2.627	0.00263
28,29	1	0.001	2.59	0.00259
28,29.2	3	0.003	2.442	0.00244
28,30	4	0.004	2.294	0.00229
28,30.2	3	0.003	2.627	0.00263
28,31	4	0.004	2.516	0.00252
28,31.2	1	0.001	2.775	0.00277
28,32	4	0.004	3.108	0.00311
28,32.1	1	0.001	2.479	0.00248
28,32.2	2	0.002	1.961	0.00196
28,33	4	0.004	2.701	0.00270
28,33.1	2	0.002	2.331	0.00233
28,33.2	2	0.002	2.405	0.00241
28,34	1	0.001	2.812	0.00281
28,34.1	1	0.001	2.22	0.00222
28,34.2	4	0.004	2.479	0.00248
28,35	2	0.002	2.553	0.00255
28,35.2	2	0.002	2.738	0.00274
28,36	2	0.002	2.405	0.00241

28, 37	4	0.004	2.22	0.00222
28, 38	3	0.003	2.368	0.00237
28.2, 28.2	2	0.002	1.26025	0.00126
28.2, 29	3	0.003	2.485	0.00249
28.2, 29.2	4	0.004	2.343	0.00234
28.2, 30	3	0.003	2.201	0.00220
28.2, 30.2	4	0.004	2.5205	0.00252
28.2, 31	2	0.002	2.414	0.00241
28.2, 31.2	2	0.002	2.6625	0.00266
28.2, 32	4	0.004	2.982	0.00298
28.2, 32.1	2	0.002	2.3785	0.00238
28.2, 32.2	3	0.003	1.8815	0.00188
28.2, 33	2	0.002	2.5915	0.00259
28.2, 33.1	2	0.002	2.2365	0.00224
28.2, 33.2	3	0.003	2.3075	0.00231
28.2, 34	1	0.001	2.698	0.00270
28.2, 34.1	1	0.001	2.13	0.00213
28.2, 34.2	2	0.002	2.3785	0.00238
28.2, 35	2	0.002	2.4495	0.00245
28.2, 35.2	2	0.002	2.627	0.00263
28.2, 36	2	0.002	2.3075	0.00231
28.2, 37	1	0.001	2.13	0.00213
28.2, 38	1	0.001	2.272	0.00227
29, 29	2	0.002	1.225	0.00123
29, 29.2	2	0.002	2.31	0.00231
29, 30	1	0.001	2.17	0.00217
29, 30.2	1	0.001	2.485	0.00249
29, 31	2	0.002	2.38	0.00238
29, 31.2	2	0.002	2.625	0.00263
29, 32	3	0.003	2.94	0.00294
29, 32.1	2	0.002	2.345	0.00235
29, 32.2	2	0.002	1.855	0.00186
29, 33	1	0.001	2.555	0.00255
29, 33.1	3	0.003	2.205	0.00221
29, 33.2	1	0.001	2.275	0.00228
29, 34	3	0.003	2.66	0.00266
29, 34.1	4	0.004	2.1	0.00210
29, 34.2	1	0.001	2.345	0.00235
29, 35	4	0.004	2.415	0.00242
29, 35.2	3	0.003	2.59	0.00259
29, 36	2	0.002	2.275	0.00228
29, 37	1	0.001	2.1	0.00210
29, 38	1	0.001	2.24	0.00224
29.2, 29.2	3	0.003	1.089	0.00109
29.2, 30	1	0.001	2.046	0.00205
29.2, 30.2	1	0.001	2.343	0.00234
29.2, 31	1	0.001	2.244	0.00224
29.2, 31.2	3	0.003	2.475	0.00248
29.2, 32	5	0.005	2.772	0.00277
29.2, 32.1	1	0.001	2.211	0.00221
29.2, 32.2	1	0.001	1.749	0.00175
29.2, 33	2	0.002	2.409	0.00241
29.2, 33.1	1	0.001	2.079	0.00208
29.2, 33.2	3	0.003	2.145	0.00215
29.2, 34	4	0.004	2.508	0.00251
29.2, 34.1	3	0.003	1.98	0.00198
29.2, 34.2	2	0.002	2.211	0.00221
29.2, 35	1	0.001	2.277	0.00228
29.2, 35.2	2	0.002	2.442	0.00244
29.2, 36	1	0.001	2.145	0.00215
29.2, 37	2	0.002	1.98	0.00198

29.2,38	2	0.002	2.112	0.00211
30,30	3	0.003	0.961	0.00096
30,30.2	1	0.001	2.201	0.00220
30,31	1	0.001	2.108	0.00211
30,31.2	2	0.002	2.325	0.00232
30,32	3	0.003	2.604	0.00260
30,32.1	2	0.002	2.077	0.00208
30,32.2	1	0.001	1.643	0.00164
30,33	2	0.002	2.263	0.00226
30,33.1	2	0.002	1.953	0.00195
30,33.2	2	0.002	2.015	0.00201
30,34	2	0.002	2.356	0.00236
30,34.1	1	0.001	1.86	0.00186
30,34.2	2	0.002	2.077	0.00208
30,35	4	0.004	2.139	0.00214
30,35.2	4	0.004	2.294	0.00229
30,36	3	0.003	2.015	0.00201
30,37	1	0.001	1.86	0.00186
30,38	1	0.001	1.984	0.00198
30.2,30.2	1	0.001	1.26025	0.00126
30.2,31	1	0.001	2.414	0.00241
30.2,31.2	1	0.001	2.6625	0.00266
30.2,32	4	0.004	2.982	0.00298
30.2,32.1	4	0.004	2.3785	0.00238
30.2,32.2	2	0.002	1.8815	0.00188
30.2,33	2	0.002	2.5915	0.00259
30.2,33.1	5	0.005	2.2365	0.00224
30.2,33.2	2	0.002	2.3075	0.00231
30.2,34	2	0.002	2.698	0.00270
30.2,34.1	3	0.003	2.13	0.00213
30.2,34.2	1	0.001	2.3785	0.00238
30.2,35	2	0.002	2.4495	0.00245
30.2,35.2	3	0.003	2.627	0.00263
30.2,36	2	0.002	2.3075	0.00231
30.2,37	2	0.002	2.13	0.00213
30.2,38	2	0.002	2.272	0.00227
31,31	2	0.002	1.156	0.00116
31,31.2	3	0.003	2.55	0.00255
31,32	1	0.001	2.856	0.00286
31,32.1	1	0.001	2.278	0.00228
31,32.2	1	0.001	1.802	0.00180
31,33	3	0.003	2.482	0.00248
31,33.1	1	0.001	2.142	0.00214
31,33.2	3	0.003	2.21	0.00221
31,34	4	0.004	2.584	0.00258
31,34.1	1	0.001	2.04	0.00204
31,34.2	3	0.003	2.278	0.00228
31,35	4	0.004	2.346	0.00235
31,35.2	2	0.002	2.516	0.00252
31,36	2	0.002	2.21	0.00221
31,37	5	0.005	2.04	0.00204
31,38	3	0.003	2.176	0.00218
31.2,31.2	4	0.004	1.40625	0.00141
31.2,32	5	0.005	3.15	0.00315
31.2,32.1	3	0.003	2.5125	0.00251
31.2,32.2	1	0.001	1.9875	0.00199
31.2,33	1	0.001	2.7375	0.00274
31.2,33.1	4	0.004	2.3625	0.00236
31.2,33.2	3	0.003	2.4375	0.00244
31.2,34	1	0.001	2.85	0.00285
31.2,34.1	3	0.003	2.25	0.00225

31.2,34.2	1	0.001	2.5125	0.00251
31.2,35	2	0.002	2.5875	0.00259
31.2,35.2	3	0.003	2.775	0.00277
31.2,36	3	0.003	2.4375	0.00244
31.2,37	1	0.001	2.25	0.00225
31.2,38	3	0.003	2.4	0.00240
32,32	1	0.001	1.764	0.00176
32,32.1	4	0.004	2.814	0.00281
32,32.2	1	0.001	2.226	0.00223
32,33	2	0.002	3.066	0.00307
32,33.1	1	0.001	2.646	0.00265
32,33.2	2	0.002	2.73	0.00273
32,34	3	0.003	3.192	0.00319
32,34.1	2	0.002	2.52	0.00252
32,34.2	3	0.003	2.814	0.00281
32,35	3	0.003	2.898	0.00290
32,35.2	3	0.003	3.108	0.00311
32,36	3	0.003	2.73	0.00273
32,37	2	0.002	2.52	0.00252
32,38	3	0.003	2.688	0.00269
32.1,32.1	3	0.003	1.12225	0.00112
32.1,32.2	3	0.003	1.7755	0.00178
32.1,33	3	0.003	2.4455	0.00245
32.1,33.1	2	0.002	2.1105	0.00211
32.1,33.2	2	0.002	2.1775	0.00218
32.1,34	2	0.002	2.546	0.00255
32.1,34.1	3	0.003	2.01	0.00201
32.1,34.2	2	0.002	2.2445	0.00224
32.1,35	2	0.002	2.3115	0.00231
32.1,35.2	4	0.004	2.479	0.00248
32.1,36	1	0.001	2.1775	0.00218
32.1,37	3	0.003	2.01	0.00201
32.1,38	2	0.002	2.144	0.00214
32.2,32.2	1	0.001	0.70225	0.00070
32.2,33	2	0.002	1.9345	0.00193
32.2,33.1	2	0.002	1.6695	0.00167
32.2,33.2	1	0.001	1.7225	0.00172
32.2,34	3	0.003	2.014	0.00201
32.2,34.1	3	0.003	1.59	0.00159
32.2,34.2	2	0.002	1.7755	0.00178
32.2,35	4	0.004	1.8285	0.00183
32.2,35.2	2	0.002	1.961	0.00196
32.2,36	1	0.001	1.7225	0.00172
32.2,37	1	0.001	1.59	0.00159
32.2,38	1	0.001	1.696	0.00170
33,33	1	0.001	1.33225	0.00133
33,33.1	1	0.001	2.2995	0.00230
33,33.2	3	0.003	2.3725	0.00237
33,34	2	0.002	2.774	0.00277
33,34.1	1	0.001	2.19	0.00219
33,34.2	2	0.002	2.4455	0.00245
33,35	3	0.003	2.5185	0.00252
33,35.2	4	0.004	2.701	0.00270
33,36	4	0.004	2.3725	0.00237
33,37	4	0.004	2.19	0.00219
33,38	3	0.003	2.336	0.00234
33.1,33.1	2	0.002	0.99225	0.00099
33.1,33.2	3	0.003	2.0475	0.00205
33.1,34	1	0.001	2.394	0.00239
33.1,34.1	1	0.001	1.89	0.00189
33.1,34.2	1	0.001	2.1105	0.00211



33.1, 35	3	0.003	2.1735	0.00217
33.1, 35.2	1	0.001	2.331	0.00233
33.1, 36	2	0.002	2.0475	0.00205
33.1, 37	2	0.002	1.89	0.00189
33.1, 38	4	0.004	2.016	0.00202
33.2, 33.2	3	0.003	1.05625	0.00106
33.2, 34	2	0.002	2.47	0.00247
33.2, 34.1	3	0.003	1.95	0.00195
33.2, 34.2	2	0.002	2.1775	0.00218
33.2, 35	2	0.002	2.2425	0.00224
33.2, 35.2	2	0.002	2.405	0.00241
33.2, 36	1	0.001	2.1125	0.00211
33.2, 37	1	0.001	1.95	0.00195
33.2, 38	2	0.002	2.08	0.00208
34, 34	5	0.005	1.444	0.00144
34, 34.1	3	0.003	2.28	0.00228
34, 34.2	2	0.002	2.546	0.00255
34, 35	2	0.002	2.622	0.00262
34, 35.2	4	0.004	2.812	0.00281
34, 36	1	0.001	2.47	0.00247
34, 37	1	0.001	2.28	0.00228
34, 38	2	0.002	2.432	0.00243
34.1, 34.1	2	0.002	0.9	0.00090
34.1, 34.2	1	0.001	2.01	0.00201
34.1, 35	1	0.001	2.07	0.00207
34.1, 35.2	1	0.001	2.22	0.00222
34.1, 36	5	0.005	1.95	0.00195
34.1, 37	1	0.001	1.8	0.00180
34.1, 38	2	0.002	1.92	0.00192
34.2, 34.2	3	0.003	1.12225	0.00112
34.2, 35	2	0.002	2.3115	0.00231
34.2, 35.2	3	0.003	2.479	0.00248
34.2, 36	2	0.002	2.1775	0.00218
34.2, 37	1	0.001	2.01	0.00201
34.2, 38	2	0.002	2.144	0.00214
35, 35	2	0.002	1.19025	0.00119
35, 35.2	2	0.002	2.553	0.00255
35, 36	2	0.002	2.2425	0.00224
35, 37	1	0.001	2.07	0.00207
35, 38	1	0.001	2.208	0.00221
35.2, 35.2	2	0.002	1.369	0.00137
35.2, 36	2	0.002	2.405	0.00241
35.2, 37	1	0.001	2.22	0.00222
35.2, 38	1	0.001	2.368	0.00237
36, 36	3	0.003	1.05625	0.00106
36, 37	2	0.002	1.95	0.00195
36, 38	1	0.001	2.08	0.00208
37, 37	3	0.003	0.9	0.00090
37, 38	2	0.002	1.92	0.00192
38, 38	1	0.001	1.024	0.00102
Total	1000	1	1000	1.00

**Table 95: Virtual D21S11 Allelic Frequency Distributions**

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 \*\* Alleles Frequencies of D21S11 in 1000 Unrelated \*\*  
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Allele	Number of Alleles	Allele Frequency
24	67	0.034
24.2	67	0.034
24.3	78	0.039
25	67	0.034
25.2	78	0.039
26	69	0.035
27	77	0.038
28	74	0.037
28.2	71	0.035
29	70	0.035
29.2	66	0.033
30	62	0.031
30.2	71	0.035
31	68	0.034
31.2	75	0.037
32	84	0.042
32.1	67	0.034
32.2	53	0.026
33	73	0.036
33.1	63	0.032
33.2	65	0.033
34	76	0.038
34.1	60	0.030
34.2	67	0.034
35	69	0.035
35.2	74	0.037
36	65	0.033

37	60	0.030
38	64	0.032
Total	2000	1

**Table 96: Virtual D21S11 Forensic Parameters**

Results	
Expected homozygosity	0.03478
Expected hetrozygosity	0.96522
Observed Homozygosity	0.06200
Observed Hetrozygosity	0.93800
Power of Identity	0.00281
Power of Discrimination	0.99719
PIC	0.99718
Impossible Genotype	0.00000
Allelic Representation	1.00000
Genotype Representation	1.00000

**10. The F13A1 STR Genetic Locus****Table 97: Virtual Observed and Expected Genotypic Frequency Distributions for the F13A1 STR Genetic Locus**

```

*****
**   Observed and Expected Genotypic Frequency Distribution   **
**               at F13A1 in 1000 Unrelated                   **
*****

```

F13A1 Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
3.2,3.2	6	0.006	5.40225	0.00540
3.2,4	17	0.017	12.5685	0.01257
3.2,5	11	0.011	11.172	0.01117
3.2,6	11	0.011	10.731	0.01073
3.2,7	10	0.01	11.8335	0.01183
3.2,8	13	0.013	10.9515	0.01095
3.2,9	9	0.009	10.9515	0.01095
3.2,10	8	0.008	11.2455	0.01125
3.2,11	12	0.012	12.2745	0.01227
3.2,12	12	0.012	10.731	0.01073
3.2,13	8	0.008	11.76	0.01176
3.2,16	8	0.008	10.437	0.01044
3.2,20	16	0.016	11.5395	0.01154
4,4	13	0.013	7.31025	0.00731
4,5	13	0.013	12.996	0.01300
4,6	17	0.017	12.483	0.01248
4,7	12	0.012	13.7655	0.01377
4,8	11	0.011	12.7395	0.01274
4,9	6	0.006	12.7395	0.01274
4,10	13	0.013	13.0815	0.01308

4,11	12	0.012	14.2785	0.01428
4,12	12	0.012	12.483	0.01248
4,13	11	0.011	13.68	0.01368
4,16	9	0.009	12.141	0.01214
4,20	12	0.012	13.4235	0.01342
5,5	13	0.013	5.776	0.00578
5,6	10	0.01	11.096	0.01110
5,7	13	0.013	12.236	0.01224
5,8	9	0.009	11.324	0.01132
5,9	8	0.008	11.324	0.01132
5,10	10	0.01	11.628	0.01163
5,11	8	0.008	12.692	0.01269
5,12	7	0.007	11.096	0.01110
5,13	11	0.011	12.16	0.01216
5,16	13	0.013	10.792	0.01079
5,20	13	0.013	11.932	0.01193
6,6	10	0.01	5.329	0.00533
6,7	13	0.013	11.753	0.01175
6,8	4	0.004	10.877	0.01088
6,9	18	0.018	10.877	0.01088
6,10	8	0.008	11.169	0.01117
6,11	7	0.007	12.191	0.01219
6,12	11	0.011	10.658	0.01066
6,13	11	0.011	11.68	0.01168
6,16	11	0.011	10.366	0.01037
6,20	5	0.005	11.461	0.01146
7,7	9	0.009	6.48025	0.00648
7,8	11	0.011	11.9945	0.01199
7,9	15	0.015	11.9945	0.01199
7,10	16	0.016	12.3165	0.01232
7,11	16	0.016	13.4435	0.01344
7,12	9	0.009	11.753	0.01175
7,13	12	0.012	12.88	0.01288
7,16	5	0.005	11.431	0.01143
7,20	11	0.011	12.6385	0.01264
8,8	11	0.011	5.55025	0.00555
8,9	11	0.011	11.1005	0.01110
8,10	10	0.01	11.3985	0.01140
8,11	18	0.018	12.4415	0.01244
8,12	11	0.011	10.877	0.01088
8,13	7	0.007	11.92	0.01192
8,16	12	0.012	10.579	0.01058
8,20	10	0.01	11.6965	0.01170
9,9	7	0.007	5.55025	0.00555
9,10	8	0.008	11.3985	0.01140
9,11	16	0.016	12.4415	0.01244
9,12	10	0.01	10.877	0.01088
9,13	18	0.018	11.92	0.01192
9,16	3	0.003	10.579	0.01058
9,20	13	0.013	11.6965	0.01170
10,10	8	0.008	5.85225	0.00585
10,11	13	0.013	12.7755	0.01278
10,12	9	0.009	11.169	0.01117
10,13	18	0.018	12.24	0.01224
10,16	13	0.013	10.863	0.01086
10,20	11	0.011	12.0105	0.01201
11,11	10	0.01	6.97225	0.00697
11,12	9	0.009	12.191	0.01219
11,13	17	0.017	13.36	0.01336
11,16	8	0.008	11.857	0.01186
11,20	11	0.011	13.1095	0.01311

12,12	13	0.013	5.329	0.00533
12,13	7	0.007	11.68	0.01168
12,16	10	0.01	10.366	0.01037
12,20	13	0.013	11.461	0.01146
13,13	9	0.009	6.4	0.00640
13,16	12	0.012	11.36	0.01136
13,20	10	0.01	12.56	0.01256
16,16	15	0.015	5.041	0.00504
16,20	8	0.008	11.147	0.01115
20,20	12	0.012	6.16225	0.00616
Total	1000	1	1000	1.00

**Table 98: Virtual F13A1 Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of F13A1 in 1000 Unrelated \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
3.2	147	0.073
4	171	0.086
5	152	0.076
6	146	0.073
7	161	0.081
8	149	0.074
9	149	0.074
10	153	0.076
11	167	0.084
12	146	0.073
13	160	0.080
16	142	0.071
20	157	0.079
Total	2000	1

**Table 99: Virtual F13A1 Forensic Parameters**

Results	
Expected homozygosity	0.07716
Expected hetrozygosity	0.92285
Observed Homozygosity	0.13600
Observed Hetrozygosity	0.86400
Power of Identity	0.01194
Power of Discrimination	0.98806
PIC	0.98792
Impossible Genotype	0.00000
Allelic Representation	1.00000
Genotype Representation	1.00000

## 11. The FES/FPS STR Genetic Locus

**Table 100: Virtual Observed and Expected Genotypic Frequency Distributions for the FES/FPS STR Genetic Locus**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at FES/FPS in 1000 Unrelated \*\*  
 \*\*\*\*\*

FES/FPS Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
8,8	28	0.028	23.104	0.02310
8,9	58	0.058	52.744	0.05274
8,10	48	0.048	47.424	0.04742
8,11	44	0.044	50.16	0.05016
8,12	57	0.057	54.568	0.05457
8,13	41	0.041	52.896	0.05290
9,9	48	0.048	30.10225	0.03010
9,10	29	0.029	54.132	0.05413
9,11	51	0.051	57.255	0.05726
9,12	59	0.059	62.2865	0.06229
9,13	54	0.054	60.378	0.06038
10,10	55	0.055	24.336	0.02434
10,11	29	0.029	51.48	0.05148
10,12	48	0.048	56.004	0.05600
10,13	48	0.048	54.288	0.05429
11,11	50	0.05	27.225	0.02723
11,12	52	0.052	59.235	0.05924
11,13	54	0.054	57.42	0.05742
12,12	51	0.051	32.22025	0.03222
12,13	41	0.041	62.466	0.06247
13,13	55	0.055	30.276	0.03028
Total	1000	1	1000	1.00

**Table 101: Virtual FES/FPS Allelic Frequency Distributions**

```
*****
** Alleles Frequencies of FES/FPS in 1000 Unrelated **
*****
```

Allele	Number of Alleles	Allele Frequency
8	304	0.152
9	347	0.173
10	312	0.156
11	330	0.165
12	359	0.179
13	348	0.174
Total	2000	1

**Table 102: Virtual FES/FPS Forensic Parameters**

Results	
Expected homozygosity	0.16726
Expected hetrozygosity	0.83274
Observed Homozygosity	0.28700
Observed Hetrozygosity	0.71300
Power of Identity	0.04936
Power of Discrimination	0.95064
PIC	0.94833
Impossible Genotype	0.00000
Allelic Representation	1.00000
Genotype Representation	1.00000

## 12. The FGA STR Genetic Locus

**Table 103: Virtual Observed and Expected Genotypic Frequency Distributions for the FGA STR Genetic Locus**

```
*****
** Observed and Expected Genotypic Frequency Distribution **
** at FGA in 1000 Unrelated **
*****
```

FGA Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
14,14	2	0.002	0.625	0.00063
14,16	1	0.001	1.35	0.00135
14,17	1	0.001	1.325	0.00133
14,17.2	1	0.001	1.25	0.00125
14,18	2	0.002	1.3	0.00130
14,18.2	1	0.001	1.175	0.00118
14,19	1	0.001	1.25	0.00125
14,19.2	2	0.002	1.35	0.00135

14,19.3	2	0.002	1.45	0.00145
14,20	1	0.001	1.4	0.00140
14,20.2	2	0.002	1.2	0.00120
14,21	1	0.001	1.45	0.00145
14,21.2	1	0.001	1.425	0.00143
14,22	1	0.001	1.45	0.00145
14,22.2	1	0.001	1.15	0.00115
14,23	1	0.001	1.275	0.00128
14,23.2	1	0.001	1.575	0.00158
14,24	2	0.002	1.175	0.00118
14,24.2	1	0.001	1.425	0.00143
14,25	1	0.001	1.3	0.00130
14,25.2	1	0.001	1.35	0.00135
14,26	2	0.002	1.5	0.00150
14,26.1	1	0.001	1.25	0.00125
14,27	1	0.001	1.225	0.00123
14,28	1	0.001	1.325	0.00133
14,29	1	0.001	1.375	0.00138
14,30	2	0.002	1.5	0.00150
14,30.2	2	0.002	1.475	0.00147
14,31	1	0.001	1.575	0.00158
14,31.2	2	0.002	1.325	0.00133
14,32	1	0.001	1.275	0.00128
14,34	1	0.001	1.275	0.00128
14,42.2	1	0.001	1.625	0.00163
14,43.2	1	0.001	1.3	0.00130
14,44.2	2	0.002	1.4	0.00140
14,45.2	1	0.001	1.35	0.00135
14,46.2	1	0.001	1.35	0.00135
16,16	1	0.001	0.729	0.00073
16,17	1	0.001	1.431	0.00143
16,17.2	1	0.001	1.35	0.00135
16,18	1	0.001	1.404	0.00140
16,18.2	1	0.001	1.269	0.00127
16,19	1	0.001	1.35	0.00135
16,19.2	2	0.002	1.458	0.00146
16,19.3	2	0.002	1.566	0.00157
16,20	1	0.001	1.512	0.00151
16,20.2	1	0.001	1.296	0.00130
16,21	1	0.001	1.566	0.00157
16,21.2	1	0.001	1.539	0.00154
16,22	1	0.001	1.566	0.00157
16,22.2	1	0.001	1.242	0.00124
16,23	1	0.001	1.377	0.00138
16,23.2	1	0.001	1.701	0.00170
16,24	1	0.001	1.269	0.00127
16,24.2	1	0.001	1.539	0.00154
16,25	1	0.001	1.404	0.00140
16,25.2	1	0.001	1.458	0.00146
16,26	1	0.001	1.62	0.00162
16,26.1	2	0.002	1.35	0.00135
16,27	2	0.002	1.323	0.00132
16,28	1	0.001	1.431	0.00143
16,29	2	0.002	1.485	0.00148
16,30	3	0.003	1.62	0.00162
16,30.2	1	0.001	1.593	0.00159
16,31	2	0.002	1.701	0.00170
16,31.2	1	0.001	1.431	0.00143
16,32	2	0.002	1.377	0.00138
16,34	2	0.002	1.377	0.00138
16,42.2	2	0.002	1.755	0.00176



16,43.2	1	0.001	1.404	0.00140
16,44.2	3	0.003	1.512	0.00151
16,45.2	3	0.003	1.458	0.00146
16,46.2	2	0.002	1.458	0.00146
17,17	1	0.001	0.70225	0.00070
17,17.2	1	0.001	1.325	0.00133
17,18	2	0.002	1.378	0.00138
17,18.2	1	0.001	1.2455	0.00125
17,19	3	0.003	1.325	0.00133
17,19.2	1	0.001	1.431	0.00143
17,19.3	3	0.003	1.537	0.00154
17,20	1	0.001	1.484	0.00148
17,20.2	1	0.001	1.272	0.00127
17,21	1	0.001	1.537	0.00154
17,21.2	2	0.002	1.5105	0.00151
17,22	1	0.001	1.537	0.00154
17,22.2	1	0.001	1.219	0.00122
17,23	1	0.001	1.3515	0.00135
17,23.2	1	0.001	1.6695	0.00167
17,24	2	0.002	1.2455	0.00125
17,24.2	1	0.001	1.5105	0.00151
17,25	1	0.001	1.378	0.00138
17,25.2	1	0.001	1.431	0.00143
17,26	3	0.003	1.59	0.00159
17,26.1	1	0.001	1.325	0.00133
17,27	2	0.002	1.2985	0.00130
17,28	1	0.001	1.4045	0.00140
17,29	1	0.001	1.4575	0.00146
17,30	1	0.001	1.59	0.00159
17,30.2	1	0.001	1.5635	0.00156
17,31	2	0.002	1.6695	0.00167
17,31.2	2	0.002	1.4045	0.00140
17,32	1	0.001	1.3515	0.00135
17,34	2	0.002	1.3515	0.00135
17,42.2	2	0.002	1.7225	0.00172
17,43.2	1	0.001	1.378	0.00138
17,44.2	2	0.002	1.484	0.00148
17,45.2	1	0.001	1.431	0.00143
17,46.2	1	0.001	1.431	0.00143
17.2,17.2	2	0.002	0.625	0.00063
17.2,18	1	0.001	1.3	0.00130
17.2,18.2	1	0.001	1.175	0.00118
17.2,19	1	0.001	1.25	0.00125
17.2,19.2	1	0.001	1.35	0.00135
17.2,19.3	1	0.001	1.45	0.00145
17.2,20	3	0.003	1.4	0.00140
17.2,20.2	1	0.001	1.2	0.00120
17.2,21	1	0.001	1.45	0.00145
17.2,21.2	1	0.001	1.425	0.00143
17.2,22	1	0.001	1.45	0.00145
17.2,22.2	1	0.001	1.15	0.00115
17.2,23	1	0.001	1.275	0.00128
17.2,23.2	2	0.002	1.575	0.00158
17.2,24	1	0.001	1.175	0.00118
17.2,24.2	2	0.002	1.425	0.00143
17.2,25	1	0.001	1.3	0.00130
17.2,25.2	2	0.002	1.35	0.00135
17.2,26	2	0.002	1.5	0.00150
17.2,26.1	1	0.001	1.25	0.00125
17.2,27	1	0.001	1.225	0.00123
17.2,28	1	0.001	1.325	0.00133

17.2,29	2	0.002	1.375	0.00138
17.2,30	1	0.001	1.5	0.00150
17.2,30.2	2	0.002	1.475	0.00147
17.2,31	1	0.001	1.575	0.00158
17.2,31.2	2	0.002	1.325	0.00133
17.2,32	1	0.001	1.275	0.00128
17.2,34	1	0.001	1.275	0.00128
17.2,42.2	1	0.001	1.625	0.00163
17.2,43.2	1	0.001	1.3	0.00130
17.2,44.2	1	0.001	1.4	0.00140
17.2,45.2	1	0.001	1.35	0.00135
17.2,46.2	2	0.002	1.35	0.00135
18,18	1	0.001	0.676	0.00068
18,18.2	1	0.001	1.222	0.00122
18,19	1	0.001	1.3	0.00130
18,19.2	1	0.001	1.404	0.00140
18,19.3	1	0.001	1.508	0.00151
18,20	2	0.002	1.456	0.00146
18,20.2	1	0.001	1.248	0.00125
18,21	1	0.001	1.508	0.00151
18,21.2	2	0.002	1.482	0.00148
18,22	1	0.001	1.508	0.00151
18,22.2	1	0.001	1.196	0.00120
18,23	1	0.001	1.326	0.00133
18,23.2	2	0.002	1.638	0.00164
18,24	1	0.001	1.222	0.00122
18,24.2	1	0.001	1.482	0.00148
18,25	2	0.002	1.352	0.00135
18,25.2	1	0.001	1.404	0.00140
18,26	2	0.002	1.56	0.00156
18,26.1	2	0.002	1.3	0.00130
18,27	1	0.001	1.274	0.00127
18,28	2	0.002	1.378	0.00138
18,29	2	0.002	1.43	0.00143
18,30	1	0.001	1.56	0.00156
18,30.2	1	0.001	1.534	0.00153
18,31	1	0.001	1.638	0.00164
18,31.2	1	0.001	1.378	0.00138
18,32	2	0.002	1.326	0.00133
18,34	1	0.001	1.326	0.00133
18,42.2	2	0.002	1.69	0.00169
18,43.2	2	0.002	1.352	0.00135
18,44.2	1	0.001	1.456	0.00146
18,45.2	2	0.002	1.404	0.00140
18,46.2	1	0.001	1.404	0.00140
18.2,18.2	1	0.001	0.55225	0.00055
18.2,19	1	0.001	1.175	0.00118
18.2,19.2	1	0.001	1.269	0.00127
18.2,19.3	2	0.002	1.363	0.00136
18.2,20	1	0.001	1.316	0.00132
18.2,20.2	1	0.001	1.128	0.00113
18.2,21	1	0.001	1.363	0.00136
18.2,21.2	1	0.001	1.3395	0.00134
18.2,22	1	0.001	1.363	0.00136
18.2,22.2	1	0.001	1.081	0.00108
18.2,23	1	0.001	1.1985	0.00120
18.2,23.2	1	0.001	1.4805	0.00148
18.2,24	1	0.001	1.1045	0.00110
18.2,24.2	1	0.001	1.3395	0.00134
18.2,25	2	0.002	1.222	0.00122
18.2,25.2	2	0.002	1.269	0.00127

18.2,26	3	0.003	1.41	0.00141
18.2,26.1	1	0.001	1.175	0.00118
18.2,27	2	0.002	1.1515	0.00115
18.2,28	1	0.001	1.2455	0.00125
18.2,29	2	0.002	1.2925	0.00129
18.2,30	1	0.001	1.41	0.00141
18.2,30.2	1	0.001	1.3865	0.00139
18.2,31	1	0.001	1.4805	0.00148
18.2,31.2	2	0.002	1.2455	0.00125
18.2,32	2	0.002	1.1985	0.00120
18.2,34	1	0.001	1.1985	0.00120
18.2,42.2	1	0.001	1.5275	0.00153
18.2,43.2	1	0.001	1.222	0.00122
18.2,44.2	1	0.001	1.316	0.00132
18.2,45.2	1	0.001	1.269	0.00127
18.2,46.2	1	0.001	1.269	0.00127
19,19	1	0.001	0.625	0.00063
19,19.2	1	0.001	1.35	0.00135
19,19.3	1	0.001	1.45	0.00145
19,20	2	0.002	1.4	0.00140
19,20.2	2	0.002	1.2	0.00120
19,21	2	0.002	1.45	0.00145
19,21.2	1	0.001	1.425	0.00143
19,22	1	0.001	1.45	0.00145
19,22.2	1	0.001	1.15	0.00115
19,23	1	0.001	1.275	0.00128
19,23.2	2	0.002	1.575	0.00158
19,24	1	0.001	1.175	0.00118
19,24.2	1	0.001	1.425	0.00143
19,25	1	0.001	1.3	0.00130
19,25.2	1	0.001	1.35	0.00135
19,26	1	0.001	1.5	0.00150
19,26.1	3	0.003	1.25	0.00125
19,27	1	0.001	1.225	0.00123
19,28	1	0.001	1.325	0.00133
19,29	1	0.001	1.375	0.00138
19,30	3	0.003	1.5	0.00150
19,30.2	1	0.001	1.475	0.00147
19,31	1	0.001	1.575	0.00158
19,31.2	1	0.001	1.325	0.00133
19,32	1	0.001	1.275	0.00128
19,34	1	0.001	1.275	0.00128
19,42.2	2	0.002	1.625	0.00163
19,43.2	1	0.001	1.3	0.00130
19,44.2	2	0.002	1.4	0.00140
19,45.2	1	0.001	1.35	0.00135
19,46.2	1	0.001	1.35	0.00135
19.2,19.2	1	0.001	0.729	0.00073
19.2,19.3	1	0.001	1.566	0.00157
19.2,20	1	0.001	1.512	0.00151
19.2,20.2	2	0.002	1.296	0.00130
19.2,21	1	0.001	1.566	0.00157
19.2,21.2	1	0.001	1.539	0.00154
19.2,22	1	0.001	1.566	0.00157
19.2,22.2	1	0.001	1.242	0.00124
19.2,23	2	0.002	1.377	0.00138
19.2,23.2	1	0.001	1.701	0.00170
19.2,24	1	0.001	1.269	0.00127
19.2,24.2	1	0.001	1.539	0.00154
19.2,25	1	0.001	1.404	0.00140
19.2,25.2	1	0.001	1.458	0.00146

19.2,26	3	0.003	1.62	0.00162
19.2,26.1	3	0.003	1.35	0.00135
19.2,27	2	0.002	1.323	0.00132
19.2,28	1	0.001	1.431	0.00143
19.2,29	1	0.001	1.485	0.00148
19.2,30	2	0.002	1.62	0.00162
19.2,30.2	1	0.001	1.593	0.00159
19.2,31	1	0.001	1.701	0.00170
19.2,31.2	1	0.001	1.431	0.00143
19.2,32	1	0.001	1.377	0.00138
19.2,34	1	0.001	1.377	0.00138
19.2,42.2	1	0.001	1.755	0.00176
19.2,43.2	2	0.002	1.404	0.00140
19.2,44.2	2	0.002	1.512	0.00151
19.2,45.2	4	0.004	1.458	0.00146
19.2,46.2	2	0.002	1.458	0.00146
19.3,19.3	3	0.003	0.841	0.00084
19.3,20	2	0.002	1.624	0.00162
19.3,20.2	1	0.001	1.392	0.00139
19.3,21	2	0.002	1.682	0.00168
19.3,21.2	1	0.001	1.653	0.00165
19.3,22	3	0.003	1.682	0.00168
19.3,22.2	1	0.001	1.334	0.00133
19.3,23	2	0.002	1.479	0.00148
19.3,23.2	2	0.002	1.827	0.00183
19.3,24	1	0.001	1.363	0.00136
19.3,24.2	1	0.001	1.653	0.00165
19.3,25	1	0.001	1.508	0.00151
19.3,25.2	1	0.001	1.566	0.00157
19.3,26	2	0.002	1.74	0.00174
19.3,26.1	1	0.001	1.45	0.00145
19.3,27	1	0.001	1.421	0.00142
19.3,28	1	0.001	1.537	0.00154
19.3,29	1	0.001	1.595	0.00160
19.3,30	2	0.002	1.74	0.00174
19.3,30.2	1	0.001	1.711	0.00171
19.3,31	1	0.001	1.827	0.00183
19.3,31.2	1	0.001	1.537	0.00154
19.3,32	1	0.001	1.479	0.00148
19.3,34	1	0.001	1.479	0.00148
19.3,42.2	2	0.002	1.885	0.00189
19.3,43.2	2	0.002	1.508	0.00151
19.3,44.2	1	0.001	1.624	0.00162
19.3,45.2	2	0.002	1.566	0.00157
19.3,46.2	1	0.001	1.566	0.00157
20,20	1	0.001	0.784	0.00078
20,20.2	2	0.002	1.344	0.00134
20,21	1	0.001	1.624	0.00162
20,21.2	1	0.001	1.596	0.00160
20,22	1	0.001	1.624	0.00162
20,22.2	2	0.002	1.288	0.00129
20,23	2	0.002	1.428	0.00143
20,23.2	2	0.002	1.764	0.00176
20,24	1	0.001	1.316	0.00132
20,24.2	1	0.001	1.596	0.00160
20,25	1	0.001	1.456	0.00146
20,25.2	2	0.002	1.512	0.00151
20,26	1	0.001	1.68	0.00168
20,26.1	2	0.002	1.4	0.00140
20,27	1	0.001	1.372	0.00137
20,28	2	0.002	1.484	0.00148

20,29	1	0.001	1.54	0.00154
20,30	1	0.001	1.68	0.00168
20,30.2	2	0.002	1.652	0.00165
20,31	4	0.004	1.764	0.00176
20,31.2	1	0.001	1.484	0.00148
20,32	1	0.001	1.428	0.00143
20,34	1	0.001	1.428	0.00143
20,42.2	1	0.001	1.82	0.00182
20,43.2	1	0.001	1.456	0.00146
20,44.2	2	0.002	1.568	0.00157
20,45.2	1	0.001	1.512	0.00151
20,46.2	2	0.002	1.512	0.00151
20.2,20.2	1	0.001	0.576	0.00058
20.2,21	1	0.001	1.392	0.00139
20.2,21.2	1	0.001	1.368	0.00137
20.2,22	1	0.001	1.392	0.00139
20.2,22.2	1	0.001	1.104	0.00110
20.2,23	1	0.001	1.224	0.00122
20.2,23.2	1	0.001	1.512	0.00151
20.2,24	1	0.001	1.128	0.00113
20.2,24.2	1	0.001	1.368	0.00137
20.2,25	1	0.001	1.248	0.00125
20.2,25.2	1	0.001	1.296	0.00130
20.2,26	1	0.001	1.44	0.00144
20.2,26.1	1	0.001	1.2	0.00120
20.2,27	1	0.001	1.176	0.00118
20.2,28	3	0.003	1.272	0.00127
20.2,29	1	0.001	1.32	0.00132
20.2,30	1	0.001	1.44	0.00144
20.2,30.2	2	0.002	1.416	0.00142
20.2,31	2	0.002	1.512	0.00151
20.2,31.2	1	0.001	1.272	0.00127
20.2,32	1	0.001	1.224	0.00122
20.2,34	1	0.001	1.224	0.00122
20.2,42.2	1	0.001	1.56	0.00156
20.2,43.2	2	0.002	1.248	0.00125
20.2,44.2	2	0.002	1.344	0.00134
20.2,45.2	1	0.001	1.296	0.00130
20.2,46.2	1	0.001	1.296	0.00130
21,21	1	0.001	0.841	0.00084
21,21.2	1	0.001	1.653	0.00165
21,22	1	0.001	1.682	0.00168
21,22.2	2	0.002	1.334	0.00133
21,23	1	0.001	1.479	0.00148
21,23.2	4	0.004	1.827	0.00183
21,24	1	0.001	1.363	0.00136
21,24.2	3	0.003	1.653	0.00165
21,25	2	0.002	1.508	0.00151
21,25.2	1	0.001	1.566	0.00157
21,26	2	0.002	1.74	0.00174
21,26.1	1	0.001	1.45	0.00145
21,27	1	0.001	1.421	0.00142
21,28	2	0.002	1.537	0.00154
21,29	1	0.001	1.595	0.00160
21,30	1	0.001	1.74	0.00174
21,30.2	2	0.002	1.711	0.00171
21,31	1	0.001	1.827	0.00183
21,31.2	3	0.003	1.537	0.00154
21,32	2	0.002	1.479	0.00148
21,34	3	0.003	1.479	0.00148
21,42.2	2	0.002	1.885	0.00189

21,43.2	2	0.002	1.508	0.00151
21,44.2	2	0.002	1.624	0.00162
21,45.2	1	0.001	1.566	0.00157
21,46.2	1	0.001	1.566	0.00157
21.2,21.2	1	0.001	0.81225	0.00081
21.2,22	2	0.002	1.653	0.00165
21.2,22.2	1	0.001	1.311	0.00131
21.2,23	2	0.002	1.4535	0.00145
21.2,23.2	3	0.003	1.7955	0.00180
21.2,24	2	0.002	1.3395	0.00134
21.2,24.2	1	0.001	1.6245	0.00162
21.2,25	2	0.002	1.482	0.00148
21.2,25.2	2	0.002	1.539	0.00154
21.2,26	1	0.001	1.71	0.00171
21.2,26.1	1	0.001	1.425	0.00143
21.2,27	1	0.001	1.3965	0.00140
21.2,28	1	0.001	1.5105	0.00151
21.2,29	2	0.002	1.5675	0.00157
21.2,30	2	0.002	1.71	0.00171
21.2,30.2	1	0.001	1.6815	0.00168
21.2,31	2	0.002	1.7955	0.00180
21.2,31.2	1	0.001	1.5105	0.00151
21.2,32	2	0.002	1.4535	0.00145
21.2,34	3	0.003	1.4535	0.00145
21.2,42.2	4	0.004	1.8525	0.00185
21.2,43.2	1	0.001	1.482	0.00148
21.2,44.2	2	0.002	1.596	0.00160
21.2,45.2	1	0.001	1.539	0.00154
21.2,46.2	1	0.001	1.539	0.00154
22,22	3	0.003	0.841	0.00084
22,22.2	1	0.001	1.334	0.00133
22,23	1	0.001	1.479	0.00148
22,23.2	1	0.001	1.827	0.00183
22,24	2	0.002	1.363	0.00136
22,24.2	1	0.001	1.653	0.00165
22,25	1	0.001	1.508	0.00151
22,25.2	1	0.001	1.566	0.00157
22,26	2	0.002	1.74	0.00174
22,26.1	1	0.001	1.45	0.00145
22,27	1	0.001	1.421	0.00142
22,28	2	0.002	1.537	0.00154
22,29	3	0.003	1.595	0.00160
22,30	3	0.003	1.74	0.00174
22,30.2	2	0.002	1.711	0.00171
22,31	2	0.002	1.827	0.00183
22,31.2	1	0.001	1.537	0.00154
22,32	1	0.001	1.479	0.00148
22,34	2	0.002	1.479	0.00148
22,42.2	3	0.003	1.885	0.00189
22,43.2	2	0.002	1.508	0.00151
22,44.2	1	0.001	1.624	0.00162
22,45.2	1	0.001	1.566	0.00157
22,46.2	1	0.001	1.566	0.00157
22.2,22.2	1	0.001	0.529	0.00053
22.2,23	2	0.002	1.173	0.00117
22.2,23.2	1	0.001	1.449	0.00145
22.2,24	1	0.001	1.081	0.00108
22.2,24.2	1	0.001	1.311	0.00131
22.2,25	1	0.001	1.196	0.00120
22.2,25.2	2	0.002	1.242	0.00124
22.2,26	1	0.001	1.38	0.00138

22.2,26.1	2	0.002	1.15	0.00115
22.2,27	1	0.001	1.127	0.00113
22.2,28	1	0.001	1.219	0.00122
22.2,29	1	0.001	1.265	0.00127
22.2,30	1	0.001	1.38	0.00138
22.2,30.2	2	0.002	1.357	0.00136
22.2,31	1	0.001	1.449	0.00145
22.2,31.2	1	0.001	1.219	0.00122
22.2,32	1	0.001	1.173	0.00117
22.2,34	1	0.001	1.173	0.00117
22.2,42.2	2	0.002	1.495	0.00150
22.2,43.2	1	0.001	1.196	0.00120
22.2,44.2	2	0.002	1.288	0.00129
22.2,45.2	1	0.001	1.242	0.00124
22.2,46.2	1	0.001	1.242	0.00124
23,23	1	0.001	0.65025	0.00065
23,23.2	1	0.001	1.6065	0.00161
23,24	1	0.001	1.1985	0.00120
23,24.2	3	0.003	1.4535	0.00145
23,25	2	0.002	1.326	0.00133
23,25.2	1	0.001	1.377	0.00138
23,26	2	0.002	1.53	0.00153
23,26.1	1	0.001	1.275	0.00128
23,27	2	0.002	1.2495	0.00125
23,28	1	0.001	1.3515	0.00135
23,29	1	0.001	1.4025	0.00140
23,30	1	0.001	1.53	0.00153
23,30.2	2	0.002	1.5045	0.00150
23,31	1	0.001	1.6065	0.00161
23,31.2	1	0.001	1.3515	0.00135
23,32	1	0.001	1.3005	0.00130
23,34	1	0.001	1.3005	0.00130
23,42.2	1	0.001	1.6575	0.00166
23,43.2	1	0.001	1.326	0.00133
23,44.2	1	0.001	1.428	0.00143
23,45.2	2	0.002	1.377	0.00138
23,46.2	2	0.002	1.377	0.00138
23.2,23.2	3	0.003	0.99225	0.00099
23.2,24	2	0.002	1.4805	0.00148
23.2,24.2	2	0.002	1.7955	0.00180
23.2,25	1	0.001	1.638	0.00164
23.2,25.2	3	0.003	1.701	0.00170
23.2,26	1	0.001	1.89	0.00189
23.2,26.1	1	0.001	1.575	0.00158
23.2,27	1	0.001	1.5435	0.00154
23.2,28	2	0.002	1.6695	0.00167
23.2,29	1	0.001	1.7325	0.00173
23.2,30	1	0.001	1.89	0.00189
23.2,30.2	2	0.002	1.8585	0.00186
23.2,31	1	0.001	1.9845	0.00198
23.2,31.2	2	0.002	1.6695	0.00167
23.2,32	1	0.001	1.6065	0.00161
23.2,34	1	0.001	1.6065	0.00161
23.2,42.2	2	0.002	2.0475	0.00205
23.2,43.2	2	0.002	1.638	0.00164
23.2,44.2	1	0.001	1.764	0.00176
23.2,45.2	2	0.002	1.701	0.00170
23.2,46.2	2	0.002	1.701	0.00170
24,24	2	0.002	0.55225	0.00055
24,24.2	1	0.001	1.3395	0.00134
24,25	1	0.001	1.222	0.00122

24,25.2	1	0.001	1.269	0.00127
24,26	1	0.001	1.41	0.00141
24,26.1	1	0.001	1.175	0.00118
24,27	1	0.001	1.1515	0.00115
24,28	2	0.002	1.2455	0.00125
24,29	1	0.001	1.2925	0.00129
24,30	1	0.001	1.41	0.00141
24,30.2	1	0.001	1.3865	0.00139
24,31	2	0.002	1.4805	0.00148
24,31.2	1	0.001	1.2455	0.00125
24,32	1	0.001	1.1985	0.00120
24,34	1	0.001	1.1985	0.00120
24,42.2	1	0.001	1.5275	0.00153
24,43.2	1	0.001	1.222	0.00122
24,44.2	1	0.001	1.316	0.00132
24,45.2	1	0.001	1.269	0.00127
24,46.2	1	0.001	1.269	0.00127
24.2,24.2	2	0.002	0.81225	0.00081
24.2,25	1	0.001	1.482	0.00148
24.2,25.2	1	0.001	1.539	0.00154
24.2,26	2	0.002	1.71	0.00171
24.2,26.1	1	0.001	1.425	0.00143
24.2,27	1	0.001	1.3965	0.00140
24.2,28	2	0.002	1.5105	0.00151
24.2,29	2	0.002	1.5675	0.00157
24.2,30	3	0.003	1.71	0.00171
24.2,30.2	2	0.002	1.6815	0.00168
24.2,31	1	0.001	1.7955	0.00180
24.2,31.2	2	0.002	1.5105	0.00151
24.2,32	1	0.001	1.4535	0.00145
24.2,34	1	0.001	1.4535	0.00145
24.2,42.2	2	0.002	1.8525	0.00185
24.2,43.2	2	0.002	1.482	0.00148
24.2,44.2	1	0.001	1.596	0.00160
24.2,45.2	1	0.001	1.539	0.00154
24.2,46.2	3	0.003	1.539	0.00154
25,25	2	0.002	0.676	0.00068
25,25.2	2	0.002	1.404	0.00140
25,26	3	0.003	1.56	0.00156
25,26.1	1	0.001	1.3	0.00130
25,27	1	0.001	1.274	0.00127
25,28	1	0.001	1.378	0.00138
25,29	3	0.003	1.43	0.00143
25,30	1	0.001	1.56	0.00156
25,30.2	1	0.001	1.534	0.00153
25,31	1	0.001	1.638	0.00164
25,31.2	1	0.001	1.378	0.00138
25,32	1	0.001	1.326	0.00133
25,34	2	0.002	1.326	0.00133
25,42.2	2	0.002	1.69	0.00169
25,43.2	1	0.001	1.352	0.00135
25,44.2	1	0.001	1.456	0.00146
25,45.2	1	0.001	1.404	0.00140
25,46.2	1	0.001	1.404	0.00140
25.2,25.2	2	0.002	0.729	0.00073
25.2,26	1	0.001	1.62	0.00162
25.2,26.1	1	0.001	1.35	0.00135
25.2,27	1	0.001	1.323	0.00132
25.2,28	2	0.002	1.431	0.00143
25.2,29	2	0.002	1.485	0.00148
25.2,30	1	0.001	1.62	0.00162



25.2,30.2	2	0.002	1.593	0.00159
25.2,31	1	0.001	1.701	0.00170
25.2,31.2	2	0.002	1.431	0.00143
25.2,32	1	0.001	1.377	0.00138
25.2,34	1	0.001	1.377	0.00138
25.2,42.2	1	0.001	1.755	0.00176
25.2,43.2	1	0.001	1.404	0.00140
25.2,44.2	1	0.001	1.512	0.00151
25.2,45.2	1	0.001	1.458	0.00146
25.2,46.2	3	0.003	1.458	0.00146
26,26	1	0.001	0.9	0.00090
26,26.1	1	0.001	1.5	0.00150
26,27	1	0.001	1.47	0.00147
26,28	1	0.001	1.59	0.00159
26,29	1	0.001	1.65	0.00165
26,30	1	0.001	1.8	0.00180
26,30.2	1	0.001	1.77	0.00177
26,31	2	0.002	1.89	0.00189
26,31.2	1	0.001	1.59	0.00159
26,32	1	0.001	1.53	0.00153
26,34	2	0.002	1.53	0.00153
26,42.2	2	0.002	1.95	0.00195
26,43.2	1	0.001	1.56	0.00156
26,44.2	3	0.003	1.68	0.00168
26,45.2	1	0.001	1.62	0.00162
26,46.2	2	0.002	1.62	0.00162
26.1,26.1	1	0.001	0.625	0.00063
26.1,27	1	0.001	1.225	0.00123
26.1,28	1	0.001	1.325	0.00133
26.1,29	1	0.001	1.375	0.00138
26.1,30	1	0.001	1.5	0.00150
26.1,30.2	2	0.002	1.475	0.00147
26.1,31	2	0.002	1.575	0.00158
26.1,31.2	1	0.001	1.325	0.00133
26.1,32	1	0.001	1.275	0.00128
26.1,34	1	0.001	1.275	0.00128
26.1,42.2	1	0.001	1.625	0.00163
26.1,43.2	2	0.002	1.3	0.00130
26.1,44.2	2	0.002	1.4	0.00140
26.1,45.2	1	0.001	1.35	0.00135
26.1,46.2	1	0.001	1.35	0.00135
27,27	1	0.001	0.60025	0.00060
27,28	1	0.001	1.2985	0.00130
27,29	1	0.001	1.3475	0.00135
27,30	1	0.001	1.47	0.00147
27,30.2	1	0.001	1.4455	0.00145
27,31	2	0.002	1.5435	0.00154
27,31.2	3	0.003	1.2985	0.00130
27,32	1	0.001	1.2495	0.00125
27,34	1	0.001	1.2495	0.00125
27,42.2	2	0.002	1.5925	0.00159
27,43.2	1	0.001	1.274	0.00127
27,44.2	1	0.001	1.372	0.00137
27,45.2	2	0.002	1.323	0.00132
27,46.2	2	0.002	1.323	0.00132
28,28	1	0.001	0.70225	0.00070
28,29	1	0.001	1.4575	0.00146
28,30	2	0.002	1.59	0.00159
28,30.2	2	0.002	1.5635	0.00156
28,31	1	0.001	1.6695	0.00167
28,31.2	1	0.001	1.4045	0.00140

28,32	1	0.001	1.3515	0.00135
28,34	1	0.001	1.3515	0.00135
28,42.2	1	0.001	1.7225	0.00172
28,43.2	1	0.001	1.378	0.00138
28,44.2	2	0.002	1.484	0.00148
28,45.2	2	0.002	1.431	0.00143
28,46.2	2	0.002	1.431	0.00143
29,29	1	0.001	0.75625	0.00076
29,30	1	0.001	1.65	0.00165
29,30.2	3	0.003	1.6225	0.00162
29,31	2	0.002	1.7325	0.00173
29,31.2	1	0.001	1.4575	0.00146
29,32	1	0.001	1.4025	0.00140
29,34	1	0.001	1.4025	0.00140
29,42.2	2	0.002	1.7875	0.00179
29,43.2	1	0.001	1.43	0.00143
29,44.2	1	0.001	1.54	0.00154
29,45.2	2	0.002	1.485	0.00148
29,46.2	2	0.002	1.485	0.00148
30,30	2	0.002	0.9	0.00090
30,30.2	1	0.001	1.77	0.00177
30,31	3	0.003	1.89	0.00189
30,31.2	2	0.002	1.59	0.00159
30,32	1	0.001	1.53	0.00153
30,34	2	0.002	1.53	0.00153
30,42.2	3	0.003	1.95	0.00195
30,43.2	1	0.001	1.56	0.00156
30,44.2	1	0.001	1.68	0.00168
30,45.2	2	0.002	1.62	0.00162
30,46.2	1	0.001	1.62	0.00162
30.2,30.2	1	0.001	0.87025	0.00087
30.2,31	4	0.004	1.8585	0.00186
30.2,31.2	2	0.002	1.5635	0.00156
30.2,32	1	0.001	1.5045	0.00150
30.2,34	2	0.002	1.5045	0.00150
30.2,42.2	1	0.001	1.9175	0.00192
30.2,43.2	1	0.001	1.534	0.00153
30.2,44.2	2	0.002	1.652	0.00165
30.2,45.2	1	0.001	1.593	0.00159
30.2,46.2	1	0.001	1.593	0.00159
31,31	1	0.001	0.99225	0.00099
31,31.2	1	0.001	1.6695	0.00167
31,32	4	0.004	1.6065	0.00161
31,34	1	0.001	1.6065	0.00161
31,42.2	3	0.003	2.0475	0.00205
31,43.2	2	0.002	1.638	0.00164
31,44.2	1	0.001	1.764	0.00176
31,45.2	2	0.002	1.701	0.00170
31,46.2	1	0.001	1.701	0.00170
31.2,31.2	1	0.001	0.70225	0.00070
31.2,32	2	0.002	1.3515	0.00135
31.2,34	2	0.002	1.3515	0.00135
31.2,42.2	1	0.001	1.7225	0.00172
31.2,43.2	1	0.001	1.378	0.00138
31.2,44.2	1	0.001	1.484	0.00148
31.2,45.2	1	0.001	1.431	0.00143
31.2,46.2	1	0.001	1.431	0.00143
32,32	2	0.002	0.65025	0.00065
32,34	1	0.001	1.3005	0.00130
32,42.2	3	0.003	1.6575	0.00166
32,43.2	1	0.001	1.326	0.00133

32,44.2	1	0.001	1.428	0.00143
32,45.2	1	0.001	1.377	0.00138
32,46.2	1	0.001	1.377	0.00138
34,34	1	0.001	0.65025	0.00065
34,42.2	2	0.002	1.6575	0.00166
34,43.2	1	0.001	1.326	0.00133
34,44.2	1	0.001	1.428	0.00143
34,45.2	1	0.001	1.377	0.00138
34,46.2	1	0.001	1.377	0.00138
42.2,42.2	1	0.001	1.05625	0.00106
42.2,43.2	2	0.002	1.69	0.00169
42.2,44.2	2	0.002	1.82	0.00182
42.2,45.2	1	0.001	1.755	0.00176
42.2,46.2	1	0.001	1.755	0.00176
43.2,43.2	1	0.001	0.676	0.00068
43.2,44.2	1	0.001	1.456	0.00146
43.2,45.2	3	0.003	1.404	0.00140
43.2,46.2	2	0.002	1.404	0.00140
44.2,44.2	1	0.001	0.784	0.00078
44.2,45.2	1	0.001	1.512	0.00151
44.2,46.2	2	0.002	1.512	0.00151
45.2,45.2	1	0.001	0.729	0.00073
45.2,46.2	1	0.001	1.458	0.00146
46.2,46.2	1	0.001	0.729	0.00073
Total	1000	1	1000	1.00

**Table 104: Virtual FGA Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of FGA in 1000 Unrelated \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
14	50	0.025
16	54	0.027
17	53	0.026
17.2	50	0.025
18	52	0.026
18.2	47	0.024
19	50	0.025
19.2	54	0.027
19.3	58	0.029
20	56	0.028
20.2	48	0.024
21	58	0.029
21.2	57	0.029

22	58	0.029
22.2	46	0.023
23	51	0.025
23.2	63	0.032
24	47	0.024
24.2	57	0.029
25	52	0.026
25.2	54	0.027
26	60	0.030
26.1	50	0.025
27	49	0.025
28	53	0.026
29	55	0.028
30	60	0.030
30.2	59	0.029
31	63	0.032
31.2	53	0.026
32	51	0.025
34	51	0.025
42.2	65	0.033
43.2	52	0.026
44.2	56	0.028
45.2	54	0.027
46.2	54	0.027
Total	2000	1

**Table 105: Virtual FGA Forensic Parameters**

Results	
Expected homozygosity	0.02722
Expected hetrozygosity	0.97278
Observed Homozygosity	0.05100
Observed Hetrozygosity	0.94900
Power of Identity	0.00171
Power of Discrimination	0.99829
PIC	0.99829
Impossible Genotype	0.00000
Allelic Representation	1.00000
Genotype Representation	1.00000

**13. The Penta D STR Genetic Locus****Table 106: Virtual Observed and Expected Genotypic Frequency Distributions for the Penta D STR Genetic Locus**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at Penta D in 1000 Unrelated \*\*  
 \*\*\*\*\*

Penta D Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
2.2,2.2	7	0.007	3.54025	0.00354
2.2,3.2	5	0.005	5.8905	0.00589
2.2,5	5	0.005	6.069	0.00607
2.2,6	3	0.003	7.021	0.00702
2.2,7	7	0.007	6.783	0.00678
2.2,8	6	0.006	7.973	0.00797
2.2,9	4	0.004	6.664	0.00666
2.2,9.3	2	0.002	5.6525	0.00565
2.2,10	11	0.011	6.664	0.00666
2.2,11	6	0.006	6.4855	0.00649
2.2,11.2	5	0.005	7.0805	0.00708
2.2,12	3	0.003	6.545	0.00654
2.2,13	5	0.005	6.6045	0.00660
2.2,13.2	8	0.008	6.3665	0.00637
2.2,14	11	0.011	6.7235	0.00672
2.2,15	10	0.01	6.545	0.00654
2.2,16	8	0.008	6.664	0.00666
2.2,17	6	0.006	6.188	0.00619
3.2,3.2	4	0.004	2.45025	0.00245
3.2,5	3	0.003	5.049	0.00505
3.2,6	5	0.005	5.841	0.00584
3.2,7	8	0.008	5.643	0.00564
3.2,8	3	0.003	6.633	0.00663
3.2,9	8	0.008	5.544	0.00554
3.2,9.3	5	0.005	4.7025	0.00470
3.2,10	7	0.007	5.544	0.00554
3.2,11	7	0.007	5.3955	0.00540
3.2,11.2	3	0.003	5.8905	0.00589
3.2,12	7	0.007	5.445	0.00545

3.2,13	2	0.002	5.4945	0.00549
3.2,13.2	5	0.005	5.2965	0.00530
3.2,14	7	0.007	5.5935	0.00559
3.2,15	4	0.004	5.445	0.00545
3.2,16	4	0.004	5.544	0.00554
3.2,17	8	0.008	5.148	0.00515
5,5	6	0.006	2.601	0.00260
5,6	5	0.005	6.018	0.00602
5,7	3	0.003	5.814	0.00581
5,8	7	0.007	6.834	0.00683
5,9	3	0.003	5.712	0.00571
5,9.3	5	0.005	4.845	0.00484
5,10	6	0.006	5.712	0.00571
5,11	3	0.003	5.559	0.00556
5,11.2	6	0.006	6.069	0.00607
5,12	3	0.003	5.61	0.00561
5,13	9	0.009	5.661	0.00566
5,13.2	5	0.005	5.457	0.00546
5,14	6	0.006	5.763	0.00576
5,15	4	0.004	5.61	0.00561
5,16	10	0.01	5.712	0.00571
5,17	7	0.007	5.304	0.00530
6,6	11	0.011	3.481	0.00348
6,7	7	0.007	6.726	0.00673
6,8	12	0.012	7.906	0.00791
6,9	9	0.009	6.608	0.00661
6,9.3	6	0.006	5.605	0.00560
6,10	5	0.005	6.608	0.00661
6,11	4	0.004	6.431	0.00643
6,11.2	6	0.006	7.021	0.00702
6,12	6	0.006	6.49	0.00649
6,13	4	0.004	6.549	0.00655
6,13.2	6	0.006	6.313	0.00631
6,14	6	0.006	6.667	0.00667
6,15	5	0.005	6.49	0.00649
6,16	2	0.002	6.608	0.00661
6,17	5	0.005	6.136	0.00614
7,7	4	0.004	3.249	0.00325
7,8	9	0.009	7.638	0.00764
7,9	7	0.007	6.384	0.00638
7,9.3	8	0.008	5.415	0.00542
7,10	3	0.003	6.384	0.00638
7,11	2	0.002	6.213	0.00621
7,11.2	8	0.008	6.783	0.00678
7,12	7	0.007	6.27	0.00627
7,13	6	0.006	6.327	0.00633
7,13.2	1	0.001	6.099	0.00610
7,14	6	0.006	6.441	0.00644
7,15	8	0.008	6.27	0.00627
7,16	8	0.008	6.384	0.00638
7,17	8	0.008	5.928	0.00593
8,8	5	0.005	4.489	0.00449
8,9	8	0.008	7.504	0.00750
8,9.3	8	0.008	6.365	0.00637
8,10	6	0.006	7.504	0.00750
8,11	8	0.008	7.303	0.00730
8,11.2	11	0.011	7.973	0.00797
8,12	6	0.006	7.37	0.00737
8,13	9	0.009	7.437	0.00744
8,13.2	6	0.006	7.169	0.00717
8,14	7	0.007	7.571	0.00757

8,15	6	0.006	7.37	0.00737
8,16	3	0.003	7.504	0.00750
8,17	9	0.009	6.968	0.00697
9,9	3	0.003	3.136	0.00314
9,9.3	3	0.003	5.32	0.00532
9,10	6	0.006	6.272	0.00627
9,11	7	0.007	6.104	0.00610
9,11.2	8	0.008	6.664	0.00666
9,12	8	0.008	6.16	0.00616
9,13	5	0.005	6.216	0.00622
9,13.2	6	0.006	5.992	0.00599
9,14	7	0.007	6.328	0.00633
9,15	5	0.005	6.16	0.00616
9,16	8	0.008	6.272	0.00627
9,17	4	0.004	5.824	0.00582
9.3,9.3	5	0.005	2.25625	0.00226
9.3,10	3	0.003	5.32	0.00532
9.3,11	6	0.006	5.1775	0.00518
9.3,11.2	7	0.007	5.6525	0.00565
9.3,12	6	0.006	5.225	0.00523
9.3,13	2	0.002	5.2725	0.00527
9.3,13.2	6	0.006	5.0825	0.00508
9.3,14	5	0.005	5.3675	0.00537
9.3,15	5	0.005	5.225	0.00523
9.3,16	4	0.004	5.32	0.00532
9.3,17	4	0.004	4.94	0.00494
10,10	10	0.01	3.136	0.00314
10,11	8	0.008	6.104	0.00610
10,11.2	2	0.002	6.664	0.00666
10,12	8	0.008	6.16	0.00616
10,13	6	0.006	6.216	0.00622
10,13.2	3	0.003	5.992	0.00599
10,14	3	0.003	6.328	0.00633
10,15	7	0.007	6.16	0.00616
10,16	5	0.005	6.272	0.00627
10,17	3	0.003	5.824	0.00582
11,11	7	0.007	2.97025	0.00297
11,11.2	8	0.008	6.4855	0.00649
11,12	4	0.004	5.995	0.00600
11,13	5	0.005	6.0495	0.00605
11,13.2	5	0.005	5.8315	0.00583
11,14	4	0.004	6.1585	0.00616
11,15	6	0.006	5.995	0.00600
11,16	7	0.007	6.104	0.00610
11,17	5	0.005	5.668	0.00567
11.2,11.2	7	0.007	3.54025	0.00354
11.2,12	5	0.005	6.545	0.00654
11.2,13	11	0.011	6.6045	0.00660
11.2,13.2	5	0.005	6.3665	0.00637
11.2,14	6	0.006	6.7235	0.00672
11.2,15	6	0.006	6.545	0.00654
11.2,16	6	0.006	6.664	0.00666
11.2,17	2	0.002	6.188	0.00619
12,12	7	0.007	3.025	0.00302
12,13	2	0.002	6.105	0.00611
12,13.2	5	0.005	5.885	0.00588
12,14	6	0.006	6.215	0.00622
12,15	4	0.004	6.05	0.00605
12,16	9	0.009	6.16	0.00616
12,17	7	0.007	5.72	0.00572
13,13	6	0.006	3.08025	0.00308

13,13.2	8	0.008	5.9385	0.00594
13,14	7	0.007	6.2715	0.00627
13,15	5	0.005	6.105	0.00611
13,16	8	0.008	6.216	0.00622
13,17	5	0.005	5.772	0.00577
13.2,13.2	9	0.009	2.86225	0.00286
13.2,14	2	0.002	6.0455	0.00605
13.2,15	5	0.005	5.885	0.00588
13.2,16	4	0.004	5.992	0.00599
13.2,17	9	0.009	5.564	0.00556
14,14	9	0.009	3.19225	0.00319
14,15	6	0.006	6.215	0.00622
14,16	4	0.004	6.328	0.00633
14,17	2	0.002	5.876	0.00588
15,15	6	0.006	3.025	0.00302
15,16	7	0.007	6.16	0.00616
15,17	5	0.005	5.72	0.00572
16,16	4	0.004	3.136	0.00314
16,17	7	0.007	5.824	0.00582
17,17	4	0.004	2.704	0.00270
Total	1000	1	1000	1.00

**Table 107: Virtual Penta D Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of Penta D in 1000 Unrelated \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
2.2	119	0.059
3.2	99	0.050
5	102	0.051
6	118	0.059
7	114	0.057
8	134	0.067
9	112	0.056
9.3	95	0.048
10	112	0.056
11	109	0.054
11.2	119	0.059
12	110	0.055
13	111	0.056
13.2	107	0.053
14	113	0.057



15	110	0.055
16	112	0.056
17	104	0.052
Total	2000	1

**Table 108: Virtual Penta D Forensic Parameters**

Results	
Expected homozygosity	0.05587
Expected hetrozygosity	0.94413
Observed Homozygosity	0.11400
Observed Hetrozygosity	0.88600
Power of Identity	0.00668
Power of Discrimination	0.99332
PIC	0.99327
Impossible Genotype	0.00000
Allelic Representation	1.00000
Genotype Representation	1.00000

#### 14. The Penta E STR Genetic Locus

**Table 109: Virtual Observed and Expected Genotypic Frequency Distributions for the Penta E STR Genetic Locus**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at Penta E in 1000 Unrelated \*\*  
 \*\*\*\*\*

Penta E Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
5,5	8	0.008	1.764	0.00176
5,6	3	0.003	3.948	0.00395
5,7	4	0.004	3.78	0.00378
5,8	2	0.002	3.57	0.00357
5,9	3	0.003	3.864	0.00386
5,10	2	0.002	3.99	0.00399
5,11	4	0.004	3.654	0.00365
5,12	4	0.004	3.612	0.00361
5,13	1	0.001	2.898	0.00290
5,13.2	3	0.003	3.528	0.00353
5,14	1	0.001	2.982	0.00298
5,15	6	0.006	4.494	0.00449
5,16	1	0.001	4.116	0.00412
5,17	4	0.004	3.948	0.00395
5,18	2	0.002	3.57	0.00357
5,19	2	0.002	3.906	0.00391
5,20	3	0.003	3.402	0.00340
5,20.3	4	0.004	3.15	0.00315
5,21	4	0.004	3.822	0.00382

5,22	4	0.004	3.696	0.00370
5,23	3	0.003	3.654	0.00365
5,24	4	0.004	3.57	0.00357
5,25	4	0.004	3.318	0.00332
6,6	3	0.003	2.209	0.00221
6,7	5	0.005	4.23	0.00423
6,8	5	0.005	3.995	0.00400
6,9	4	0.004	4.324	0.00432
6,10	4	0.004	4.465	0.00447
6,11	3	0.003	4.089	0.00409
6,12	3	0.003	4.042	0.00404
6,13	4	0.004	3.243	0.00324
6,13.2	3	0.003	3.948	0.00395
6,14	2	0.002	3.337	0.00334
6,15	2	0.002	5.029	0.00503
6,16	4	0.004	4.606	0.00461
6,17	5	0.005	4.418	0.00442
6,18	2	0.002	3.995	0.00400
6,19	5	0.005	4.371	0.00437
6,20	4	0.004	3.807	0.00381
6,20.3	5	0.005	3.525	0.00352
6,21	5	0.005	4.277	0.00428
6,22	5	0.005	4.136	0.00414
6,23	4	0.004	4.089	0.00409
6,24	5	0.005	3.995	0.00400
6,25	6	0.006	3.713	0.00371
7,7	2	0.002	2.025	0.00202
7,8	3	0.003	3.825	0.00383
7,9	5	0.005	4.14	0.00414
7,10	5	0.005	4.275	0.00428
7,11	2	0.002	3.915	0.00391
7,12	5	0.005	3.87	0.00387
7,13	3	0.003	3.105	0.00311
7,13.2	4	0.004	3.78	0.00378
7,14	2	0.002	3.195	0.00319
7,15	1	0.001	4.815	0.00481
7,16	3	0.003	4.41	0.00441
7,17	8	0.008	4.23	0.00423
7,18	6	0.006	3.825	0.00383
7,19	5	0.005	4.185	0.00418
7,20	3	0.003	3.645	0.00364
7,20.3	4	0.004	3.375	0.00337
7,21	4	0.004	4.095	0.00409
7,22	5	0.005	3.96	0.00396
7,23	2	0.002	3.915	0.00391
7,24	3	0.003	3.825	0.00383
7,25	4	0.004	3.555	0.00356
8,8	5	0.005	1.80625	0.00181
8,9	2	0.002	3.91	0.00391
8,10	5	0.005	4.0375	0.00404
8,11	3	0.003	3.6975	0.00370
8,12	2	0.002	3.655	0.00365
8,13	2	0.002	2.9325	0.00293
8,13.2	5	0.005	3.57	0.00357
8,14	4	0.004	3.0175	0.00302
8,15	4	0.004	4.5475	0.00455
8,16	6	0.006	4.165	0.00417
8,17	6	0.006	3.995	0.00400
8,18	3	0.003	3.6125	0.00361
8,19	5	0.005	3.9525	0.00395
8,20	4	0.004	3.4425	0.00344

8,20.3	4	0.004	3.1875	0.00319
8,21	2	0.002	3.8675	0.00387
8,22	1	0.001	3.74	0.00374
8,23	1	0.001	3.6975	0.00370
8,24	1	0.001	3.6125	0.00361
8,25	5	0.005	3.3575	0.00336
9,9	3	0.003	2.116	0.00212
9,10	5	0.005	4.37	0.00437
9,11	5	0.005	4.002	0.00400
9,12	1	0.001	3.956	0.00396
9,13	2	0.002	3.174	0.00317
9,13.2	2	0.002	3.864	0.00386
9,14	2	0.002	3.266	0.00327
9,15	10	0.01	4.922	0.00492
9,16	4	0.004	4.508	0.00451
9,17	4	0.004	4.324	0.00432
9,18	4	0.004	3.91	0.00391
9,19	6	0.006	4.278	0.00428
9,20	3	0.003	3.726	0.00373
9,20.3	2	0.002	3.45	0.00345
9,21	3	0.003	4.186	0.00419
9,22	4	0.004	4.048	0.00405
9,23	5	0.005	4.002	0.00400
9,24	4	0.004	3.91	0.00391
9,25	6	0.006	3.634	0.00363
10,10	3	0.003	2.25625	0.00226
10,11	2	0.002	4.1325	0.00413
10,12	5	0.005	4.085	0.00409
10,13	2	0.002	3.2775	0.00328
10,13.2	4	0.004	3.99	0.00399
10,14	5	0.005	3.3725	0.00337
10,15	4	0.004	5.0825	0.00508
10,16	5	0.005	4.655	0.00466
10,17	4	0.004	4.465	0.00447
10,18	5	0.005	4.0375	0.00404
10,19	5	0.005	4.4175	0.00442
10,20	3	0.003	3.8475	0.00385
10,20.3	4	0.004	3.5625	0.00356
10,21	5	0.005	4.3225	0.00432
10,22	6	0.006	4.18	0.00418
10,23	2	0.002	4.1325	0.00413
10,24	4	0.004	4.0375	0.00404
10,25	3	0.003	3.7525	0.00375
11,11	3	0.003	1.89225	0.00189
11,12	4	0.004	3.741	0.00374
11,13	2	0.002	3.0015	0.00300
11,13.2	3	0.003	3.654	0.00365
11,14	4	0.004	3.0885	0.00309
11,15	7	0.007	4.6545	0.00465
11,16	4	0.004	4.263	0.00426
11,17	2	0.002	4.089	0.00409
11,18	6	0.006	3.6975	0.00370
11,19	4	0.004	4.0455	0.00405
11,20	4	0.004	3.5235	0.00352
11,20.3	6	0.006	3.2625	0.00326
11,21	3	0.003	3.9585	0.00396
11,22	4	0.004	3.828	0.00383
11,23	4	0.004	3.7845	0.00378
11,24	3	0.003	3.6975	0.00370
11,25	2	0.002	3.4365	0.00344
12,12	3	0.003	1.849	0.00185

12,13	3	0.003	2.967	0.00297
12,13.2	4	0.004	3.612	0.00361
12,14	3	0.003	3.053	0.00305
12,15	2	0.002	4.601	0.00460
12,16	5	0.005	4.214	0.00421
12,17	3	0.003	4.042	0.00404
12,18	4	0.004	3.655	0.00365
12,19	2	0.002	3.999	0.00400
12,20	5	0.005	3.483	0.00348
12,20.3	2	0.002	3.225	0.00322
12,21	5	0.005	3.913	0.00391
12,22	5	0.005	3.784	0.00378
12,23	5	0.005	3.741	0.00374
12,24	2	0.002	3.655	0.00365
12,25	6	0.006	3.397	0.00340
13,13	3	0.003	1.19025	0.00119
13,13.2	4	0.004	2.898	0.00290
13,14	2	0.002	2.4495	0.00245
13,15	4	0.004	3.6915	0.00369
13,16	4	0.004	3.381	0.00338
13,17	2	0.002	3.243	0.00324
13,18	3	0.003	2.9325	0.00293
13,19	3	0.003	3.2085	0.00321
13,20	4	0.004	2.7945	0.00279
13,20.3	1	0.001	2.5875	0.00259
13,21	4	0.004	3.1395	0.00314
13,22	2	0.002	3.036	0.00304
13,23	4	0.004	3.0015	0.00300
13,24	5	0.005	2.9325	0.00293
13,25	2	0.002	2.7255	0.00273
13.2,13.2	1	0.001	1.764	0.00176
13.2,14	4	0.004	2.982	0.00298
13.2,15	6	0.006	4.494	0.00449
13.2,16	5	0.005	4.116	0.00412
13.2,17	3	0.003	3.948	0.00395
13.2,18	6	0.006	3.57	0.00357
13.2,19	3	0.003	3.906	0.00391
13.2,20	3	0.003	3.402	0.00340
13.2,20.3	5	0.005	3.15	0.00315
13.2,21	5	0.005	3.822	0.00382
13.2,22	3	0.003	3.696	0.00370
13.2,23	3	0.003	3.654	0.00365
13.2,24	1	0.001	3.57	0.00357
13.2,25	3	0.003	3.318	0.00332
14,14	1	0.001	1.26025	0.00126
14,15	4	0.004	3.7985	0.00380
14,16	4	0.004	3.479	0.00348
14,17	5	0.005	3.337	0.00334
14,18	3	0.003	3.0175	0.00302
14,19	3	0.003	3.3015	0.00330
14,20	1	0.001	2.8755	0.00288
14,20.3	3	0.003	2.6625	0.00266
14,21	4	0.004	3.2305	0.00323
14,22	3	0.003	3.124	0.00312
14,23	2	0.002	3.0885	0.00309
14,24	5	0.005	3.0175	0.00302
14,25	3	0.003	2.8045	0.00280
15,15	4	0.004	2.86225	0.00286
15,16	7	0.007	5.243	0.00524
15,17	4	0.004	5.029	0.00503
15,18	2	0.002	4.5475	0.00455

15,19	4	0.004	4.9755	0.00498
15,20	3	0.003	4.3335	0.00433
15,20.3	4	0.004	4.0125	0.00401
15,21	4	0.004	4.8685	0.00487
15,22	6	0.006	4.708	0.00471
15,23	4	0.004	4.6545	0.00465
15,24	8	0.008	4.5475	0.00455
15,25	3	0.003	4.2265	0.00423
16,16	2	0.002	2.401	0.00240
16,17	5	0.005	4.606	0.00461
16,18	7	0.007	4.165	0.00417
16,19	4	0.004	4.557	0.00456
16,20	6	0.006	3.969	0.00397
16,20.3	3	0.003	3.675	0.00367
16,21	3	0.003	4.459	0.00446
16,22	3	0.003	4.312	0.00431
16,23	6	0.006	4.263	0.00426
16,24	2	0.002	4.165	0.00417
16,25	3	0.003	3.871	0.00387
17,17	4	0.004	2.209	0.00221
17,18	3	0.003	3.995	0.00400
17,19	3	0.003	4.371	0.00437
17,20	4	0.004	3.807	0.00381
17,20.3	4	0.004	3.525	0.00352
17,21	4	0.004	4.277	0.00428
17,22	3	0.003	4.136	0.00414
17,23	5	0.005	4.089	0.00409
17,24	4	0.004	3.995	0.00400
17,25	1	0.001	3.713	0.00371
18,18	1	0.001	1.80625	0.00181
18,19	3	0.003	3.9525	0.00395
18,20	3	0.003	3.4425	0.00344
18,20.3	3	0.003	3.1875	0.00319
18,21	3	0.003	3.8675	0.00387
18,22	3	0.003	3.74	0.00374
18,23	7	0.007	3.6975	0.00370
18,24	2	0.002	3.6125	0.00361
18,25	3	0.003	3.3575	0.00336
19,19	6	0.006	2.16225	0.00216
19,20	4	0.004	3.7665	0.00377
19,20.3	4	0.004	3.4875	0.00349
19,21	4	0.004	4.2315	0.00423
19,22	3	0.003	4.092	0.00409
19,23	3	0.003	4.0455	0.00405
19,24	3	0.003	3.9525	0.00395
19,25	3	0.003	3.6735	0.00367
20,20	2	0.002	1.64025	0.00164
20,20.3	1	0.001	3.0375	0.00304
20,21	2	0.002	3.6855	0.00369
20,22	5	0.005	3.564	0.00356
20,23	4	0.004	3.5235	0.00352
20,24	2	0.002	3.4425	0.00344
20,25	6	0.006	3.1995	0.00320
20.3,20.3	2	0.002	1.40625	0.00141
20.3,21	1	0.001	3.4125	0.00341
20.3,22	3	0.003	3.3	0.00330
20.3,23	3	0.003	3.2625	0.00326
20.3,24	3	0.003	3.1875	0.00319
20.3,25	2	0.002	2.9625	0.00296
21,21	4	0.004	2.07025	0.00207
21,22	5	0.005	4.004	0.00400

21,23	3	0.003	3.9585	0.00396
21,24	7	0.007	3.8675	0.00387
21,25	3	0.003	3.5945	0.00359
22,22	3	0.003	1.936	0.00194
22,23	4	0.004	3.828	0.00383
22,24	2	0.002	3.74	0.00374
22,25	3	0.003	3.476	0.00348
23,23	3	0.003	1.89225	0.00189
23,24	3	0.003	3.6975	0.00370
23,25	4	0.004	3.4365	0.00344
24,24	5	0.005	1.80625	0.00181
24,25	2	0.002	3.3575	0.00336
25,25	1	0.001	1.56025	0.00156
Total	1000	1	999.99999999	1.00

**Table 110: Virtual Penta E Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of Penta E in 1000 Unrelated \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
5	84	0.042
6	94	0.047
7	90	0.045
8	85	0.043
9	92	0.046
10	95	0.048
11	87	0.043
12	86	0.043
13	69	0.035
13.2	84	0.042
14	71	0.035
15	107	0.053
16	98	0.049
17	94	0.047
18	85	0.043
19	93	0.046
20	81	0.041
20.3	75	0.037

21	91	0.045
22	88	0.044
23	87	0.043
24	85	0.043
25	79	0.040
Total	2000	1

**Table 111: Virtual Penta E Forensic Parameters**

Results	
Expected homozygosity	0.04388
Expected hetrozygosity	0.95612
Observed Homozygosity	0.07200
Observed Hetrozygosity	0.92800
Power of Identity	0.00424
Power of Discrimination	0.99576
PIC	0.99574
Impossible Genotype	0.00000
Allelic Representation	1.00000
Genotype Representation	1.00000

## 15. The TH01 STR Genetic Locus

**Table 112: Virtual Observed and Expected Genotypic Frequency Distributions for the TH01 STR Genetic Locus**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at TH01 in 1000 Unrelated \*\*  
 \*\*\*\*\*

TH01 Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
4,4	11	0.011	6.80625	0.00681
4,5	15	0.015	15.5925	0.01559
4,6	9	0.009	14.7675	0.01477
4,7	14	0.014	16.665	0.01667
4,8	12	0.012	15.84	0.01584
4,8.3	16	0.016	15.5925	0.01559
4,9	17	0.017	14.355	0.01435
4,9.3	16	0.016	15.015	0.01502
4,10	16	0.016	15.015	0.01502
4,11	17	0.017	15.2625	0.01526
4,13.3	11	0.011	13.2825	0.01328
5,5	14	0.014	8.93025	0.00893
5,6	15	0.015	16.9155	0.01692
5,7	16	0.016	19.089	0.01909
5,8	20	0.02	18.144	0.01814
5,8.3	18	0.018	17.8605	0.01786

5,9	14	0.014	16.443	0.01644
5,9.3	14	0.014	17.199	0.01720
5,10	18	0.018	17.199	0.01720
5,11	18	0.018	17.4825	0.01748
5,13.3	13	0.013	15.2145	0.01521
6,6	19	0.019	8.01025	0.00801
6,7	18	0.018	18.079	0.01808
6,8	10	0.01	17.184	0.01718
6,8.3	12	0.012	16.9155	0.01692
6,9	8	0.008	15.573	0.01557
6,9.3	22	0.022	16.289	0.01629
6,10	15	0.015	16.289	0.01629
6,11	19	0.019	16.5575	0.01656
6,13.3	13	0.013	14.4095	0.01441
7,7	18	0.018	10.201	0.01020
7,8	17	0.017	19.392	0.01939
7,8.3	15	0.015	19.089	0.01909
7,9	22	0.022	17.574	0.01757
7,9.3	11	0.011	18.382	0.01838
7,10	22	0.022	18.382	0.01838
7,11	18	0.018	18.685	0.01869
7,13.3	13	0.013	16.261	0.01626
8,8	19	0.019	9.216	0.00922
8,8.3	18	0.018	18.144	0.01814
8,9	14	0.014	16.704	0.01670
8,9.3	14	0.014	17.472	0.01747
8,10	17	0.017	17.472	0.01747
8,11	19	0.019	17.76	0.01776
8,13.3	13	0.013	15.456	0.01546
8.3,8.3	15	0.015	8.93025	0.00893
8.3,9	19	0.019	16.443	0.01644
8.3,9.3	16	0.016	17.199	0.01720
8.3,10	10	0.01	17.199	0.01720
8.3,11	18	0.018	17.4825	0.01748
8.3,13.3	17	0.017	15.2145	0.01521
9,9	13	0.013	7.569	0.00757
9,9.3	19	0.019	15.834	0.01583
9,10	13	0.013	15.834	0.01583
9,11	10	0.01	16.095	0.01609
9,13.3	12	0.012	14.007	0.01401
9.3,9.3	14	0.014	8.281	0.00828
9.3,10	18	0.018	16.562	0.01656
9.3,11	11	0.011	16.835	0.01683
9.3,13.3	13	0.013	14.651	0.01465
10,10	11	0.011	8.281	0.00828
10,11	14	0.014	16.835	0.01683
10,13.3	17	0.017	14.651	0.01465
11,11	17	0.017	8.55625	0.00856
11,13.3	7	0.007	14.8925	0.01489
13.3,13.3	16	0.016	6.48025	0.00648
Total	1000	1	999.99999999	1.00



**Table 113: Virtual TH01 Allelic Frequency Distributions**

```

*****
** Alleles Frequencies of TH01 in 1000 Unrelated **
*****

```

Allele	Number of Alleles	Allele Frequency
4	165	0.083
5	189	0.095
6	179	0.089
7	202	0.101
8	192	0.096
8.3	189	0.095
9	174	0.087
9.3	182	0.091
10	182	0.091
11	185	0.092
13.3	161	0.081
Total	2000	1

**Table 114: Virtual TH01 Forensic Parameters**

Results	
Expected homozygosity	0.09126
Expected hetrozygosity	0.90874
Observed Homozygosity	0.16700
Observed Hetrozygosity	0.83300
Power of Identity	0.01590
Power of Discrimination	0.98410
PIC	0.98385
Impossible Genotype	0.00000
Allelic Representation	1.00000
Genotype Representation	1.00000

## 16. The TPOX STR Genetic Locus

**Table 115: Virtual Observed and Expected Genotypic Frequency Distributions for the TPOX STR Genetic Locus**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at TPOX in 1000 Unrelated \*\*  
 \*\*\*\*\*

TPOX Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
6,6	13	0.013	8.464	0.00846
6,7	25	0.025	18.308	0.01831
6,8	15	0.015	19.412	0.01941
6,9	14	0.014	18.216	0.01822
6,10	21	0.021	20.24	0.02024
6,11	12	0.012	18.492	0.01849
6,12	17	0.017	17.112	0.01711
6,13	19	0.019	17.388	0.01739
6,14	16	0.016	19.412	0.01941
6,15	19	0.019	18.492	0.01849
7,7	19	0.019	9.90025	0.00990
7,8	18	0.018	20.9945	0.02099
7,9	17	0.017	19.701	0.01970
7,10	16	0.016	21.89	0.02189
7,11	13	0.013	19.9995	0.02000
7,12	12	0.012	18.507	0.01851
7,13	19	0.019	18.8055	0.01881
7,14	17	0.017	20.9945	0.02099
7,15	24	0.024	19.9995	0.02000
8,8	24	0.024	11.13025	0.01113
8,9	19	0.019	20.889	0.02089
8,10	18	0.018	23.21	0.02321
8,11	28	0.028	21.2055	0.02121
8,12	14	0.014	19.623	0.01962
8,13	16	0.016	19.9395	0.01994
8,14	24	0.024	22.2605	0.02226
8,15	11	0.011	21.2055	0.02121
9,9	22	0.022	9.801	0.00980
9,10	24	0.024	21.78	0.02178
9,11	17	0.017	19.899	0.01990
9,12	14	0.014	18.414	0.01841
9,13	12	0.012	18.711	0.01871
9,14	17	0.017	20.889	0.02089
9,15	20	0.02	19.899	0.01990
10,10	19	0.019	12.1	0.01210
10,11	23	0.023	22.11	0.02211
10,12	16	0.016	20.46	0.02046
10,13	19	0.019	20.79	0.02079
10,14	26	0.026	23.21	0.02321
10,15	19	0.019	22.11	0.02211
11,11	19	0.019	10.10025	0.01010
11,12	19	0.019	18.693	0.01869
11,13	17	0.017	18.9945	0.01899
11,14	17	0.017	21.2055	0.02121
11,15	17	0.017	20.2005	0.02020
12,12	18	0.018	8.649	0.00865
12,13	25	0.025	17.577	0.01758
12,14	16	0.016	19.623	0.01962

12,15	17	0.017	18.693	0.01869
13,13	15	0.015	8.93025	0.00893
13,14	15	0.015	19.9395	0.01994
13,15	17	0.017	18.9945	0.01899
14,14	22	0.022	11.13025	0.01113
14,15	19	0.019	21.2055	0.02121
15,15	19	0.019	10.10025	0.01010
Total	1000	1	1000	1.00

**Table 116: Virtual TPOX Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of TPOX in 1000 Unrelated \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
6	184	0.092
7	199	0.100
8	211	0.105
9	198	0.099
10	220	0.110
11	201	0.101
12	186	0.093
13	189	0.095
14	211	0.105
15	201	0.101
Total	2000	1

**Table 117: Virtual TPOX Forensic Parameters**

Results	
Expected homozygosity	0.10031
Expected hetrozygosity	0.89969
Observed Homozygosity	0.19000
Observed Hetrozygosity	0.81000
Power of Identity	0.01898
Power of Discrimination	0.98102
PIC	0.98067
Impossible Genotype	0.00000
Allelic Representation	1.00000
Genotype Representation	1.00000

## 17. The vWA STR Genetic STR Locus

**Table 118: Virtual Observed and Expected Genotypic Frequency Distributions for the vWA STR Genetic Locus**

\*\*\*\*\*  
 \*\* Observed and Expected Genotypic Frequency Distribution \*\*  
 \*\* at VWA in 1000 Unrelated \*\*  
 \*\*\*\*\*

VWA Genotype	Observed Number	Observed Frequency	Expected Number	Expected Frequency
10,10	10	0.01	5.25625	0.00526
10,11	8	0.008	9.86	0.00986
10,12	12	0.012	11.0925	0.01109
10,13	14	0.014	12.47	0.01247
10,14	9	0.009	12.18	0.01218
10,15	4	0.004	9.9325	0.00993
10,16	6	0.006	11.745	0.01175
10,17	11	0.011	12.5425	0.01254
10,18	9	0.009	10.15	0.01015
10,19	11	0.011	10.44	0.01044
10,20	15	0.015	12.47	0.01247
10,21	10	0.01	10.73	0.01073
10,22	16	0.016	10.875	0.01087
11,11	11	0.011	4.624	0.00462
11,12	14	0.014	10.404	0.01040
11,13	11	0.011	11.696	0.01170
11,14	5	0.005	11.424	0.01142
11,15	7	0.007	9.316	0.00932
11,16	6	0.006	11.016	0.01102
11,17	8	0.008	11.764	0.01176
11,18	13	0.013	9.52	0.00952
11,19	11	0.011	9.792	0.00979
11,20	16	0.016	11.696	0.01170
11,21	9	0.009	10.064	0.01006
11,22	6	0.006	10.2	0.01020
12,12	9	0.009	5.85225	0.00585
12,13	12	0.012	13.158	0.01316
12,14	8	0.008	12.852	0.01285
12,15	10	0.01	10.4805	0.01048
12,16	11	0.011	12.393	0.01239
12,17	17	0.017	13.2345	0.01323
12,18	7	0.007	10.71	0.01071
12,19	13	0.013	11.016	0.01102
12,20	8	0.008	13.158	0.01316
12,21	10	0.01	11.322	0.01132
12,22	13	0.013	11.475	0.01147
13,13	15	0.015	7.396	0.00740
13,14	19	0.019	14.448	0.01445
13,15	9	0.009	11.782	0.01178
13,16	14	0.014	13.932	0.01393
13,17	11	0.011	14.878	0.01488
13,18	13	0.013	12.04	0.01204
13,19	9	0.009	12.384	0.01238
13,20	10	0.01	14.792	0.01479
13,21	9	0.009	12.728	0.01273
13,22	11	0.011	12.9	0.01290
14,14	14	0.014	7.056	0.00706
14,15	13	0.013	11.508	0.01151

14,16	23	0.023	13.608	0.01361
14,17	16	0.016	14.532	0.01453
14,18	3	0.003	11.76	0.01176
14,19	14	0.014	12.096	0.01210
14,20	14	0.014	14.448	0.01445
14,21	8	0.008	12.432	0.01243
14,22	8	0.008	12.6	0.01260
15,15	8	0.008	4.69225	0.00469
15,16	12	0.012	11.097	0.01110
15,17	19	0.019	11.8505	0.01185
15,18	11	0.011	9.59	0.00959
15,19	7	0.007	9.864	0.00986
15,20	14	0.014	11.782	0.01178
15,21	9	0.009	10.138	0.01014
15,22	6	0.006	10.275	0.01028
16,16	9	0.009	6.561	0.00656
16,17	9	0.009	14.013	0.01401
16,18	10	0.01	11.34	0.01134
16,19	17	0.017	11.664	0.01166
16,20	13	0.013	13.932	0.01393
16,21	11	0.011	11.988	0.01199
16,22	12	0.012	12.15	0.01215
17,17	12	0.012	7.48225	0.00748
17,18	8	0.008	12.11	0.01211
17,19	7	0.007	12.456	0.01246
17,20	13	0.013	14.878	0.01488
17,21	15	0.015	12.802	0.01280
17,22	15	0.015	12.975	0.01297
18,18	13	0.013	4.9	0.00490
18,19	11	0.011	10.08	0.01008
18,20	10	0.01	12.04	0.01204
18,21	8	0.008	10.36	0.01036
18,22	11	0.011	10.5	0.01050
19,19	9	0.009	5.184	0.00518
19,20	8	0.008	12.384	0.01238
19,21	8	0.008	10.656	0.01066
19,22	10	0.01	10.8	0.01080
20,20	11	0.011	7.396	0.00740
20,21	18	0.018	12.728	0.01273
20,22	11	0.011	12.9	0.01290
21,21	12	0.012	5.476	0.00548
21,22	9	0.009	11.1	0.01110
22,22	11	0.011	5.625	0.00562
Total	1000	1	1000	1.00

**Table 119: Virtual vWA Allelic Frequency Distributions**

\*\*\*\*\*  
 \*\* Alleles Frequencies of VWA in 1000 Unrelated \*\*  
 \*\*\*\*\*

Allele	Number of Alleles	Allele Frequency
10	145	0.072
11	136	0.068
12	153	0.076

13	172	0.086
14	168	0.084
15	137	0.069
16	162	0.081
17	173	0.086
18	140	0.070
19	144	0.072
20	172	0.086
21	148	0.074
22	150	0.075
Total	2000	1

**Table 120: Virtual vWA Forensic Parameters**

Results	
Expected homozygosity	0.07750
Expected hetrozygosity	0.92250
Observed Homozygosity	0.14400
Observed Hetrozygosity	0.85600
Power of Identity	0.01209
Power of Discrimination	0.98791
PIC	0.98777
Impossible Genotype	0.00000
Allelic Representation	1.00000
Genotype Representation	1.00000

Table 121 shows a summary of results that are obtained previously and appeared within this chapter. the bolded  $p$  values perform a significant differences in the obtained results.

**Table 121: Summary of Results**

Parameter Locus	Real $P_D$	Virtual $P_D$			$p$ Value	Real $H_{obs}$	Virtual $H_{obs}$	$p$ Value	$I_G$	AR%	GR %
		Min.	Avg.	Max.							
TH01	0.94360	0.98337	0.98393	0.98437	0.151	0.75	0.833	0.0751	38	63.636	42.424
TPOX	0.8284	0.98004	0.98090	0.98138	<b>0.0003</b>	0.45	0.81	<b>0.0000</b>	34	60	38.182
$vWA$	0.90800	0.98758	0.98811	0.98845	<b>0.0139</b>	0.84	0.856	0.3765	55	61.538	39.56
Penta D	0.95700	0.99303	0.99333	0.99360	0.097	0.87	0.886	0.3650	80	72.222	53.216
Penta E	0.97640	0.99542	0.99566	0.99583	0.2417	0.73	0.928	<b>0.0001</b>	156	65.217	43.478
CSF1PO	0.85320	0.98577	0.98627	0.98670	<b>0.0006</b>	0.67	0.847	<b>0.0019</b>	42	66.667	46.154
FGA	0.95300	0.99823	0.99828	0.99833	<b>0.039</b>	0.84	0.949	<b>0.0065</b>	637	29.73	9.388
FES/FPS	0.87640	0.95033	0.95144	0.95213	0.0572	0.74	0.713	0.3344	0	100	100
F13A1	0.91660	0.98768	0.98811	0.98848	<b>0.0178</b>	0.78	0.864	0.0610	0	100	100
D3S1358	0.89240	0.98570	0.98627	0.98664	<b>0.0057</b>	0.84	0.851	0.4149	42	66.667	46.154
D5S818	0.89860	0.98018	0.98089	0.98135	<b>0.0146</b>	0.72	0.815	0.0567	34	60	38.182
D7S820	0.92120	0.98339	0.98393	0.98437	<b>0.0365</b>	0.80	0.852	0.1666	38	63.636	42.424
D8S1179	0.93480	0.99367	0.99393	0.99416	<b>0.0244</b>	0.76	0.898	<b>0.0051</b>	135	52.632	28.947
D13S317	0.89200	0.98026	0.98090	0.98131	<b>0.0102</b>	0.79	0.822	0.2839	27	70	50.909
D16S539	0.88260	0.98023	0.98089	0.98137	<b>0.0061</b>	0.82	0.824	0.4706	27	70	50.909
D18S51	0.96180	0.99702	0.99714	0.99727	0.078	0.88	0.934	0.0951	344	44.828	20.920
D21S11	0.95040	0.99703	0.99714	0.99726	0.0392	0.80	0.938	<b>0.0021</b>	330	48.276	24.138

A list of all experiments that related to the selected population will come out, each experiment has the ordered Genetic Loci for six forensic parameters (P<sub>D</sub>, Homozygosity, Hetrozigosity, PI, PIC, I). the user could also see the Genetic Loci for each six forensic parameters as a graph by click on Show Graph link. this is described in figure 19.

Exp.ID	Forensic Parameter	Better Genetic Loci	Graph
Exp. 1	PD	D21S11, Penta D, D13S317, TPOX, D8S1179, FGA	Show Graph
	Homo	TPOX, D8S1179, D21S11, D13S317, FGA, Penta D	Show Graph
	Hetro	Penta D, D13S317, FGA, D21S11, D8S1179, TPOX	Show Graph
	PI	FGA, D8S1179, TPOX, D13S317, Penta D, D21S11	Show Graph
	PIC	D21S11, Penta D, D13S317, TPOX, D8S1179, FGA	Show Graph
	I	TPOX, D13S317, D21S11, D8S1179, FGA, Penta D	Show Graph
Exp. 8	PD	Penta E, D18S51, FGA, Penta D, D21S11, TH01, D8S1179, D7S820, F13A1, VWA, D5S818, D3S1358, D13S317, D16S539, FES/FPS, CSF1PO, TPOX	Show Graph
	Homo	TPOX, CSF1PO, D5S818, Penta E, FES/FPS, TH01, D8S1179, F13A1, D13S317, D7S820, D21S11, D16S539, VWA, FGA, D3S1358, Penta D, D18S51	Show Graph
	Hetro	D18S51, Penta D, VWA, FGA, D3S1358, D16S539, D21S11, D7S820, D13S317, F13A1, D8S1179, TH01, FES/FPS, Penta E, D5S818, CSF1PO, TPOX	Show Graph
	PI	TPOX, CSF1PO, FES/FPS, D16S539, D13S317, D3S1358, D5S818, VWA, F13A1, D7S820, D8S1179, TH01, D21S11, Penta D, FGA, D18S51, Penta E	Show Graph
	PIC	Penta E, D18S51, FGA, Penta D, D21S11, TH01, D8S1179, D7S820, F13A1, VWA, D5S818, D13S317, D3S1358, D16S539, FES/FPS, CSF1PO, TPOX	Show Graph
	I	FGA, D18S51, D21S11, Penta E, D8S1179, Penta D, VWA, CSF1PO, D3S1358, TH01, D7S820, D5S818, TPOX, D13S317, D16S539, FES/FPS, F13A1	Show Graph
	PD	D21S11	Show Graph
	Homo	D21S11	Show Graph

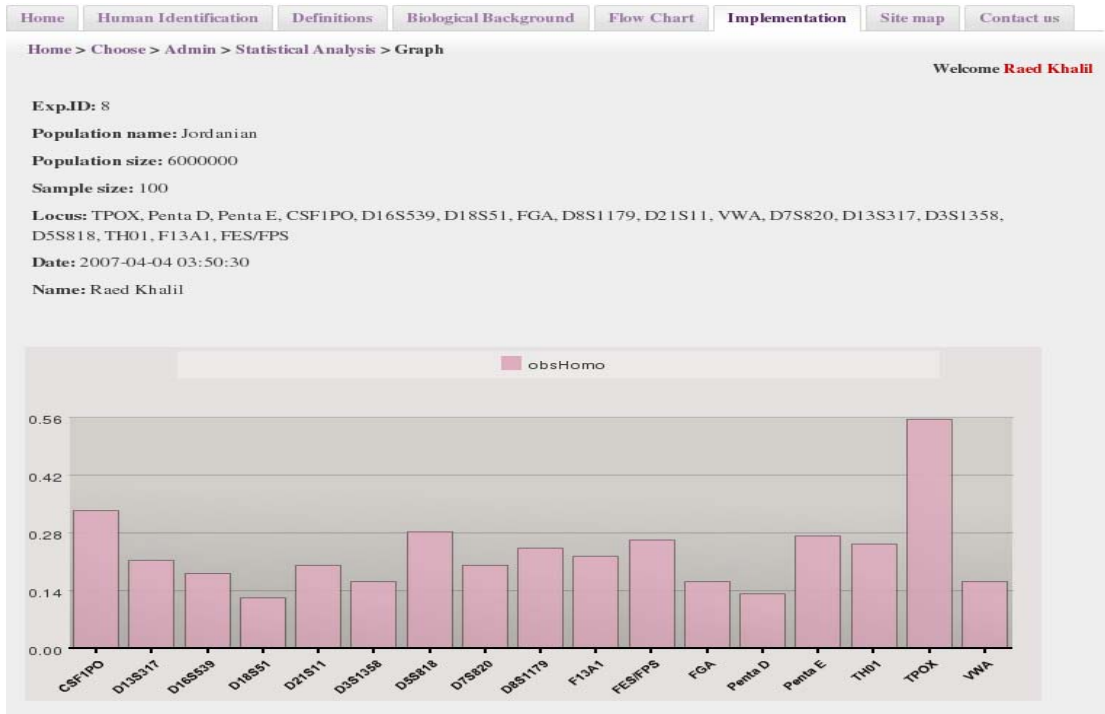
Figure 19: Statistical Analysis Data for Population



Figures 20 to 25 show the Genetic Loci for each forensic parameter in order to assist to determine the choice of better genetic loci.



Figure 20: Statistical Analysis Graph / P<sub>D</sub>



**Figure 21: Statistical Analysis Graph / HomoObs**



**Figure 22: Statistical Analysis Graph / HeteroObs**

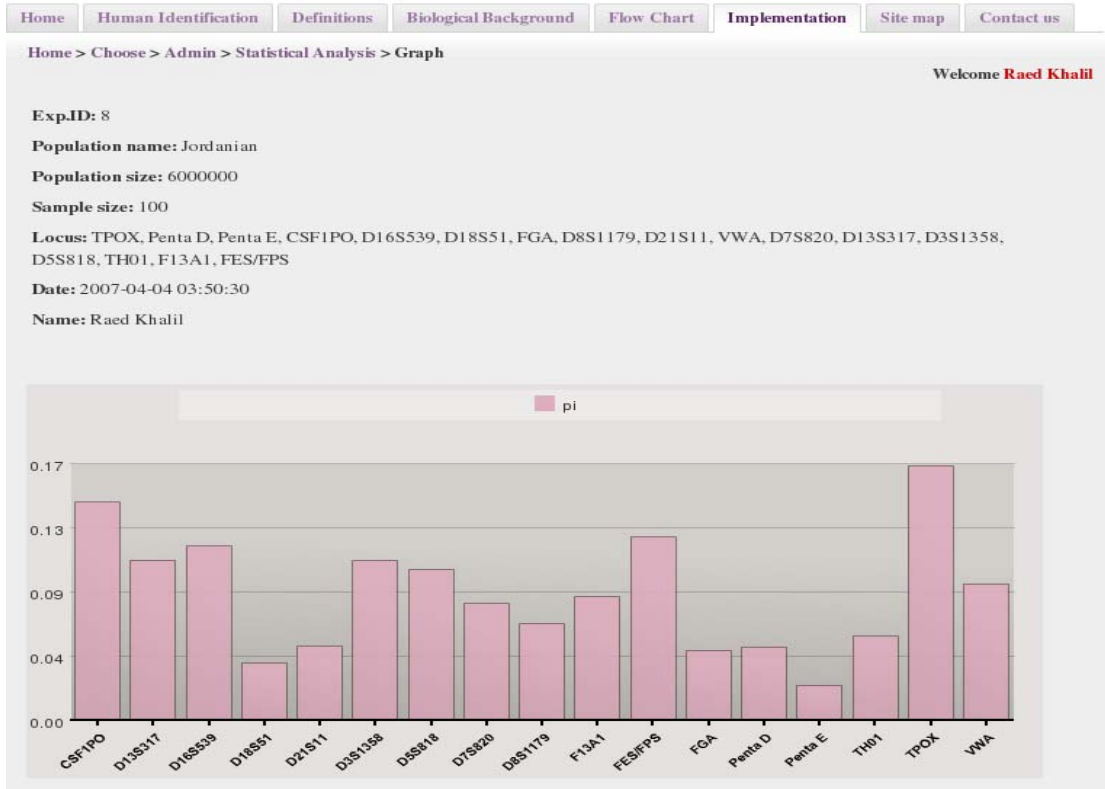


Figure 23: Statistical Analysis Graph / P<sub>1</sub>



Figure 24: Statistical Analysis Graph / PIC

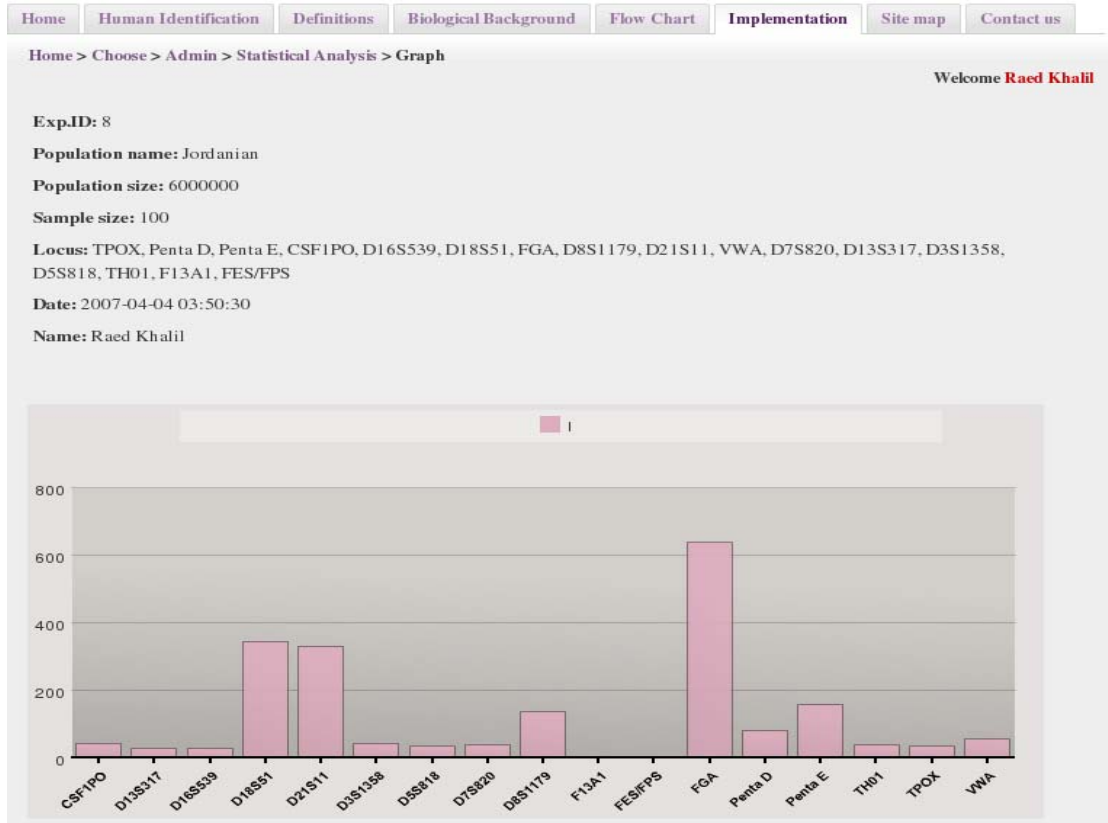


Figure 25: Statistical Analysis Graph / I<sub>G</sub>

## (5) DISCUSSION

The advent of STRs into forensic arenas has revolutionized criminal and legal investigations. STRs are repetitive sequences scattered in large numbers through the human genome (Hudson et al., 1995; Weber and May, 1989). For the past years, the criminal and justice authorities worldwide have utilized the ability of such sequences to solve questionable settings including paternity disputes and human individualization and identification (Budowle and Baechrel, 1990; Gamero et al. 2000).

Several genetic and characteristic parameters were established and adopted for the selection of STR loci as genetic markers in forensic analysis including their sequence length (Weber and May, 1989), independent inheritance (Tracey, 2001), polymorphic nature (Weber and May, 1989), and amenability to amplification by the PCR (Yamamoto et al., 1997; Lazaruk et al., 1998; Wenz et al., 1998). The STRs were found to be highly polymorphic consisting of short, repetitive sequence elements of 2 to 7 base pairs each. The overall sequence length is normally less than 400 base pairs which is amenable to amplification by PCR. The number of alleles and consequently the degree of polymorphism is usually high when compared with other non-STR genetic markers such as the human leukocyte antigen (HLA DQA) region and the polymorphic markers including LDLR, GYPA, HBGG, D7S8 and Gc (Hayes et al., 1995; Woo and Budowle, 1995; Yasin et al., 1999; Hamad et al., 2001).

The polymorphic nature of each STR genetic locus which is a reflection of the allelic window for each locus has characterized these short sequences with a highly discriminating power that is useful in human individualization and identification. This power is defined as the probability that two individuals chosen at random will possess different genotypes for the marker being tested. However, studies have shown that the allelic window. In other words the polymorphic nature of STRs, differs among the

human populations indicating a certain degree of genetic variation in the human race when it comes down to these short repetitive sequences (Hayes et al., 1995; Woo and Budowle, 1995; Tahir et al., 1997; Yasin et al., 1999; Hamad et al., 2001). Thus, and since the allelic window is used for determining the power of discrimination for each STR genetic locus, it is expected that the variation in the polymorphic nature of STRs is also exhibited to a certain degree in their inter-ability to discriminate between human individuals from different human populations. In other words, because of this the power of discrimination for any STR genetic locus could differ from one human population to the next. Indeed, earlier studies have shown demonstrable variation in the allelic windows and also a certain degree of significant differences in the allelic frequency distributions for some of the forensic STR genetic loci among different human populations (Edwards et al., 1992; Gamero et al., 2000; Hamad et al., 2001; Yasin, 2002). These findings might shed some doubt on the efficacy of implementation of the same set of STR genetic loci in the forensic arenas for all human populations. they prompt to search for a tangible method for determining the efficacy of implementation of a certain genetic locus in all human populations.

In this study, the concept of computational biology has been implemented in order to design computer software capable of defining our biological investigation, generating biological values, and analyzing the data. Three new biocomputational-based concepts depending on the allelic window for each STR genetic locus to determine the efficacy of implementation of a certain genetic locus in all human populations for forensic use were incorporated into our computer software.

The first concept is termed Maximum Virtual Target Power of Discrimination  $(VTP_D)_{max}$  which requires the generation of all virtual genotypes for each genetic locus. The concept assumes that in any human population all alleles comprising the allelic

window for any STR genetic locus are present in the population. Therefore, the number of all genotypes that could possibly exist or emerge in the population can be determined and listed.

The computer software would randomly generate observed numbers for each genotype; and then, determine the allelic frequencies distribution for each allele in the STR allelic window. These allelic frequencies are then used to calculate the power of discrimination at each random generation of observed number for each genotype of a STR genetic locus. The computer software would determine the maximum possible power of discrimination that could result. This power of discrimination is then termed the  $(VTP_D)_{max}$  which will be used to determine the applicability of a STR genetic locus in forensic arenas in any human population. The power of discrimination based upon the allelic frequency distributions present in the human population would be compared to the  $(VTP_D)_{max}$ . The closest the power of discrimination to the  $(VTP_D)_{max}$ , the STR genetic locus is most applicable in forensic arenas for that human population. This is due to that higher power of discrimination values indicates a greater individualization potential because a large portion of the population can be excluded.

In view of the computer-generated  $(VTP_D)_{max}$  seen in this study (Table 121), our designed computer software was able to randomly generate virtual allelic frequencies for all listed alleles per each genetic locus using the gene counting method. These allelic frequencies were then used to generate the  $(VTP_D)_{max}$  value for each genetic STR locus. These data were considered to be the target in the process for evaluating the use of any genetic STR locus for human identification. The  $(VTP_D)_{max}$  values ranged from 0.99833 for the FGA genetic locus to 0.95213 for the FES/FPS genetic locus which indicates that all of the seventeen genetic STR loci possess an astonishing virtual target

discriminatory power that can be applied in determining the efficacy of each respective genetic locus for forensic applications.

The second concept comprises the generation of Maximum Virtual Observed Heterozygosity values  $(VH_{Obs})_{max}$ . Based on the allelic window for each of the seventeen STR genetic loci, the computer software was designed to generate all the virtual genotypes for each genetic locus, hence, calculating what is to be termed the maximum  $VH_{Obs}$  value for each STR genetic locus. The  $(VH_{Obs})_{max}$  values for the seventeen STR genetic loci were considered to be the reference values for determining the applicability of any genetic STR locus in human identification settings. The results show that the  $(VH_{Obs})_{max}$  for the seventeen STR genetic loci ranged from 0.949 for the FGA STR genetic locus to 0.713 for the FES/FPS STR genetic locus.

In order to evaluate the efficacy of forensic implementation of each of the seventeen STR genetic loci in the Jordanian population, the previously determined allelic and genotypic windows for the Jordanian population (Hamad et al., 2001; Yasin, 2002; Salem et al., 2003) were applied into our computer software. The various forensic parameters including the real  $P_D$  value and the real  $H_{Obs}$  for each STR genetic locus were recalculated, compared with previously published data and analyzed in comparison with the respective  $(VTP_D)_{max}$  and  $(VH_{Obs})_{max}$  values for each STR genetic locus (see table 121).

Data analysis showed that all previously published forensic parameters are identical to these generated by our computer software. In this work, attention was paid for the real  $P_D$  and real  $H_{Obs}$  values for all of the seventeen STR genetic loci. The real  $P_D$  ranged from 0.97640 for the Penta E genetic locus to 0.82840 for the TPOX genetic locus as shown in table 121. The real  $H_{Obs}$  values ranged from 0.88 for the D18S51 STR genetic locus to 0.45 for the TPOX STR genetic locus. All computer-generated real  $P_D$



and real  $H_{Obs}$  values were identical to these published earlier for the Jordanian population (Hamad et al., 2001; Yasin, 2002; Salem et al., 2003).

Statistical comparison of the  $(VTP_D)_{max}$  values with the real  $P_D$  values showed significant differences ( $p < 0.05$ ) at twelve genetic STR loci, namely, TPOX, vWA, CSF1PO, FGA, F13A1, D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, and D21S11, see table 121. Absence of significant differences was demonstrated for the TH01, Penta D, Penta E, FES/FPS, and D18S51 STR genetic loci ( $p > 0.05$ ). Though, the data demonstrated in Table 121 indicate that the real  $P_D$  values for the seventeen genetic loci are high enough to enable them to show a high discriminatory power among Jordanian individuals. Twelve of these STR genetic loci could be excluded from the STR genetic loci panel used for forensic investigations. In other words, the remaining five STR genetic loci are forensically viable for the Jordanian population with a combined  $P_D$  of 0.999999692 (Combined  $P_I = 0.000000308$ ). Thus, combining these five STR genetic loci should yield satisfactory levels of population resolution and individual identification in Jordanians considering the small size of the Jordanian population, which does not exceed 5.5 million according to the latest Jordanian census bureau data.

Comparison between the  $(VH_{Obs})_{max}$  values and the real  $H_{Obs}$  values. Table 121 shows statistically significant differences ( $p < 0.05$ ) at six STR genetic loci, namely, TPOX, Penta E, CSF1PO, FGA, D8S1179, and D21S11. The presence of significant level of differences between the  $(VH_{Obs})_{max}$  values and the real  $H_{Obs}$  values of these six STR genetic loci indicates that the exhibited level of  $H_{Obs}$  for the six STR genetic loci in the Jordanian population is theoretically not accepted. Accordingly, these STR genetic loci can be excluded from any forensic STR set used for human identification or individualization in the Jordanian population. No significant differences ( $p > 0.05$ ) were

shown for the TH01, vWA, Penta D, FES/FPS, F13A1, D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, and D18S51. This demonstrates that these eleven STR genetic loci exhibit high heterozygosity levels. Hence high genetic variability in the Jordanian population indicating their applicability in forensic investigation in Jordan. These eleven STR genetic loci show an exceptionally high combined  $P_D$  of 0.9999999999891 (Combined  $P_I = 1.0914 \times 10^{-12}$ ).

Combining both concepts of  $(VTP_D)_{\max}$  and  $(VH_{\text{Obs}})_{\max}$  can greatly enhance the selection of the forensic STR genetic loci panel used for human identification and individualization in a population. In Jordanian population, the forensic STR genetic loci panel could comprise four STR genetic loci, namely, the TH01, Penta D, FES/FPS, and D18S51. The combined Power of Discrimination for these four loci was calculated at 0.999987 (Combined  $P_I = 0.000013$ ). This is a relatively high discriminatory power considering the population size of Jordan. However, it remains for the forensic authorities in the world to evaluate the applicability of any forensic genetic loci in their respective populations taking in consideration the population size. It is possible that higher population size could require increasing the number of STR genetic loci to achieve significantly higher discriminatory power.

The third concept, which is termed Impossible Genotypes ( $I_G$ ). The  $I_G$  assumes dependence on the percentage allelic representation, which is the ratio of the number of alleles present in the human population to that of total number of alleles possibly exist in the allelic window. Though STR genetic loci are highly polymorphic markers that exhibit high number of alleles when compared to non-STR genetic markers. The percentage allelic representation is less than 100% irrespective of the human population in which they are tested (Budowle et al., 1999; Hamad et al., 2001; Yasin, 2002).

In general, the percentage allelic representation tends to precipitously decrease as the total number of alleles comprising the locus increase (Hamad and Yasin, 2005, Yasin et al., 2005). Additionally, it is often the case that different allelic profiles are present for the same locus in different human populations. By definition, reduced percentage allelic representation for many of these marker systems leads to reduced percentage genotype representation that is the possible number of genotypes that can occur in the population decreases. The absence of at least one member of an allelic pair required to produce a genotype will omit the resultant genotypes from the population leading to what it is to be termed  $I_G$ . Additionally, some of the possible genotypes for a certain marker are usually absent from different human populations due to a diverse set of factors influencing the pattern of allelic dispersion in different human populations. Therefore, a percentage genotype representation of less than 100% is the rule rather than the exception when using this class of loci for DNA typing purposes. It is thus a forgone conclusion that a reduced percentage allelic distribution will differentially minimize potential heterozygosity in different human populations. In this context, a high number of  $I_G$  could be considered as an index for reduced percentage genotype representation. Thus,  $I_G$  could be used as an indicator of variation in the heterozygosity of the population. That is the number of individuals carrying dissimilar alleles of one or more genes, and hence an indicator of the variation in the genotypic pool of the population. Hence, reduced number of  $I_G$  could indicate a relatively high heterozygosity of the population. In this study, the concept of  $I_G$  and its effect on the heterozygosity of the STR forensic loci in the Jordanian population was examined by implementing the  $I_G$  formula into our computer software to calculate locus- $I_G$  values for each of the seventeen genetic STR loci.

Table 121 shows that the  $I_G$  values for the seventeen STR genetic loci ranged from theoretically zero for both FES/FPS and F13A1 STR genetic loci (100% genotypic representation) to 637 for the FGA STR genetic locus (9.388% genotypic representation). In contrast, the TPOX STR genetic locus showed the lowest  $H_{obs}$  value of 0.45 (60% Allelic Representation, 38.182% Genotypic Representation) while the D18S51 STR genetic locus showed the highest  $H_{obs}$  value of 0.88 (44.828% Allelic Representation, 20.92% Genotypic Representation).

Statistical analysis using the linear and exponential regression models has shown that the  $I_G$  values of all the seventeen STR genetic loci have exhibited a significant correlation with their respective forensic parameters. Among the parameters, the  $H_{obs}$ ,  $P_D$ , PIC, PAR and PGR. Using the linear regression model, the  $I_G$  values of the seventeen STR genetic loci tested against their respective  $H_{obs}$  ( $R = 0.612556$ ),  $P_D$  ( $R = 0.606$ ), PIC ( $R = 0.608$ ) have shown a linear relationship. This indicates that as the STR genetic locus- $I_G$  value increases, the values of the  $H_{obs}$ , the  $P_D$ , and PIC of the STR genetic locus increase linearly. In addition, the  $I_G$  values of the seventeen STR genetic loci were compared using the exponential regression model with the values obtained for the PAR ( $R = 0.9477$ ) and PGR ( $R = 0.9651$ ). The results indicate that a significantly exponential relationship exists between the  $I_G$  values of the seventeen STR genetic loci and their respective PAR and PGR. Furthermore, linear regression analysis of the  $I_G$  values of the seventeen STR genetic loci with their respective  $H_{obs}$  values has shown a weak but direct correlation ( $R = 0.4655$ ). That is as the  $I_G$  values of the seventeen STR genetic loci increase, the  $H_{obs}$  values increase in a linear fashion. The results of the statistical analysis of the data contradict our assumptions with regard to the effect of the  $I_G$  on the heterozygosity of the STR genetic markers in a population, that is, increased  $I_G$  values would mean decreased heterozygosity of the STR genetic markers in a

population, hence the power of discriminations of these STR genetic loci is affected inversely. However, the analysis of the  $I_G$  values against the values of the  $H_{obs}$  of the seventeen STR genetic loci in the Jordanian population gave support to our assumption.

The contradiction between our assumption and the results of this study indicated that the STR genetic loci though they lacked certain percentage of their genotypic window in the Jordanian population are still highly polymorphic and the remaining genotypic window is still informative. Furthermore, this is a clear indication of the vast genetic variability of the Jordanian population which comprises different ethnic groups. However, these results require more investigations to elucidate the different factors that affect the distribution of a STR genetic alleles and hence its genotypes in the genetic pool of the Jordanian population. Therefore, the concept of  $I_G$  as an indicator for the selection of the proper STR genetic locus to be used in forensic STR panels as a genetic marker for the Jordanian population is excluded pending further investigations that would consider the population size, the allelic-window size, and other factors that would affect the allelic and genotypic frequency distributions in the population.

In summary, in this study we were able to design computer software capable of DNA profile-processing, analyzing, and calculating forensic parameters essential for human identification and individualization. Furthermore, based on the concepts of  $(VTP_D)_{max}$  and  $(VH_{obs})_{max}$ , we were able to determine and select the most viable STR genetic loci for the Jordanian population. Further investigation of the  $I_G$  concept is essential to elucidate its forensic and genetic importance for any population.

## CONCLUSIONS AND FUTURE WORKS

Several concluding remarks can be drawn from this study. These include:

1. A computer software model for human identification and individualization in forensic settings was designed, validated and experimented.
2. Three new biological concepts, namely the Maximum Virtual Target Power of Discrimination  $(VTP_D)_{max}$ , the Maximum Virtual Observed Heterozygosity  $(VH_{Obs})_{max}$ , and the Impossible Genotypes ( $I_G$ ) were implemented in the computer software model. The affect of  $(VTP_D)_{max}$  and  $(VH_{Obs})_{max}$  on the inclusion of a STR genetic locus into a forensic STR set was noticeable.
3. For the Jordanian population, both concepts of  $(VTP_D)_{max}$  and  $(VH_{Obs})_{max}$  greatly enhanced the selection of the forensic STR genetic loci panel (TH01, Penta D, FES/FPS, and D18S51) to be used for human identification and individualization.
4. The affect of the biological concept of  $I_G$  on various forensic and genetic parameters such as the power of discrimination and heterozygosity requires more investigation to elucidate the kind of correlation that could exist.
5. Investigate the concept of impossible genotypes.
6. Apply this study on other populations.
7. Attempt to reduce the number of required genetic loci to identify the human in a population.
8. Investigate the study results to distinguish a population from another.

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(STR)

:

- 1- Maximum Virtual Target Power of Discrimination ( $VTP_D$ )<sub>max</sub>
- 2- Maximum Heterozygosity ( $VH_{obs}$ )<sub>max</sub>
- 3- Number of Impossible genotype ( $I_G$ )

TPOX, D16S539, Penta D, Penta E, vWA, ) 17  
 FGA, CSF1PO TH01, D21S11, D18S51, D13S317, D8S1179, D7S820,  
 TH01,) 4 (D5S818, D3S1358, F13A1, FES/FPS,  
 (Penta D FES/FPS, D18S51

0.999987

. 5.5