Validation Of DNAFIDs Model Through Finite State Machine

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Abstract

The assurance of quality and reliability of process models and workflows is essential for model driven software development. There are numerous ways to achieve these objectives. One is model checking through which it can be verified that a model satisfies specific logical rules. The model to be checked is usually given as finite state machine. Rules have to be specified at the level required by the model checker. In this work, we develop a model for validating the DNA profiling through finite state.. This enables the research/business process professionals to use model checking techniques and to produce higher quality research/business models for subsequent software development. The approach is demonstrated by validating event-driven process chains.

Keywords: DNAFIDs, FSM, Class Diagram, State Diagram, Transition Table

I. Introduction

Model checking permits confirming the grouping of dynamic communications in a model naturally. While the utilization of model checking in equipment related areas is wide-spread and has effectively modern importance, the use of this proper technique in the space of programming items, in any case, is as yet in its beginnings. Albeit model checking is an extremely encouraging method, it has three general issues:

Initially, model checking isn't valuable for the confirmation of a wide range of programming models and code. Particularly at source code level the model development, including information in the state depictions of the state-change framework, prompts the state blast issue. At the plan stage it must be applied for explicit confirmation errands again because of the state blast issue. Furthermore, to utilize model checking, we need to develop the issue to be approved (the conceivable conduct of the framework) in a proper model. This model development issue is considerably more hard to manage programming when contrasted with equipment frameworks. Thirdly, to acquire the advantages of model checking e. g. with regards to business measure displaying, the approval rules must be reasonable for business measure engineers. Right now the fleeting rationale rules must be indicated as text on the low level of the model checker model (rule determination issue).

Numerous ebb and flow research action centres around the decrease of states to keep away from the state blast issue. A few methodologies manage the model development issue, however there has been almost nothing done to tackle the third issue. A first methodology was the meaning of frequently utilized details in property designs. Nonetheless, these examples are as yet text based and fair and square of the model checker model.

A Unified Modeling Language is utilized here for planning the state chart of the proposed DNAFIDs model and this model is approved by carrying out it in Finite State Machine. Consequently UML is a notable displaying language which gives a ton of demonstrating devices and graphical documentations for taking care of complex the item arranged issues in the field of programming. It additionally gives normalization in indicating, recording, composing outline and imagining the ancient rarities of programming escalated framework a work in progress. UML gives a bunch of documentations to portraying the condition of any item through the state talk charts which is perhaps the most flexible apparatuses for depicting the existence pattern of an article from its instatement to end. State outline charts address the powerful conduct of any product framework in graphical structure, which shows every one of the ways through which an item changes its state during as long as its can remember and these ways further graphically addressed by the utilization of the idea of Finite State Machine (FSM).

FSM gives a computational model for dynamic as well as static behaviour of any software system. It is an abstract machine that produces a finite number of states and it produces one state at a time by reading input symbols. The working of FSM is started from the initial state and end on the final state and it can accept any length of string; if an automaton reaches its final state by reading input symbols one by one otherwise it rejects the string. The input is a finite set of alphabets. The finite-state automata can accept or reject an input string.

II. Background

Singh et al [1] have broken down DNA fingerprinting based recognizable proof and planned a DNA fingerprinting based ID model alongside DNA information base administration framework for 360 degree interlinking for example all administrations and advances will be advanced by DNAFIDs and data set. Saxena and Kumar [2] have introduced a way to deal with approve the UML class model through FSM is portrayed with a production of the progress table. Rafi et al [3] have reviewed for Interlinking of DNA Models with Aadhaar Real-Time Records for Enhanced Authentication. Chaturvedi [4] has examined carries out and future works in bioinformatics with Hadoop and furthermore considered the MapReduce calculation from calculation lay by point and exhibit the appropriates of our methodology by following and breaking down productive MapReduce calculations for arranging and recreation issue of equal calculations indicated in the assistance of categorize rule. Singh and Sharma [5] have explored DNA based cryptography for information covering up. Mishra [6] has presented an AAdhar based smartcard framework which will help the South Asian nations in emerging from defilements and working on their economies. O'Keefe et al [7] have introduced a microfluidic stage for atom by-particle recognition of heterogeneous epigenetic examples of uncommon tumor-inferred DNA by exceptionally parallelized computerized liquefy appraisal. Baans and Jambek [8] possess investigated the computational energy for this microarray picture handling. The outcomes show that the force extraction burns-through larger part of the generally computational time. Padmavathi et al [9] have proposed robotization in apportion appropriation utilizing brilliant card dependent on Aadhar card innovation. In this framework, they utilized a model dependent on ATM machine. Mhamane and Shriram [10] have proposed ticket checking is managed without human mediation. Prakasha et al [11] have meant to conquer this downside of manual distinguishing proof and verification of client and accomplish client ID and confirmation through a robotized technique utilizing the Aadhar card. Aadhar project is created by the Unique Identification Authority of India by consolidating biometrics and digitization. Vishal et al [12] have managed the web based democratic framework that will make the democratic framework keen. OVS(online casting a ballot system)is got and it have straightforward plan.

III. Methodology

I. UML Class Diagram and Sequence Diagram For DNAFIDs

a) UML Class Diagram

The UML Class diagram for DNA Profiling or DNAFIDs is presented here. There are ten major classes with their attributes are represented in figure 1.1which is developed by Singh et al [1]. The model shows the complete process of DNA profiling. The Information_Cofigurationhas multiple associations with the Sample_Collection class because it collects the many DNA samples from the information_configuration class whilesample_collection class has single associate with the Audit_database class that has two types of databases like sample fingerprinting database and local fingerprinting database, both these database and the Audit_Database class is directly connected the main DNA Fingerprinting database to access all the audit reports regarding both databases. The SSR_Analysis class is directly connected to the DNA Fingerprinting Database to store and fetch the analysis data for Fingerprinting _Web Services. The Gene_Mapper class, Gene_Excel and Gene_Zip_Packageare the main classes that involved in experiment of DNA fingerprinting are directly connected to the DNA Fingerprinting Database and Experimental Fingerprinting Database because the result of experimental DNA fingerprinting is stored in it after developing the DNA fingerprinting that is accessed by the main DNA fingerprinting database.

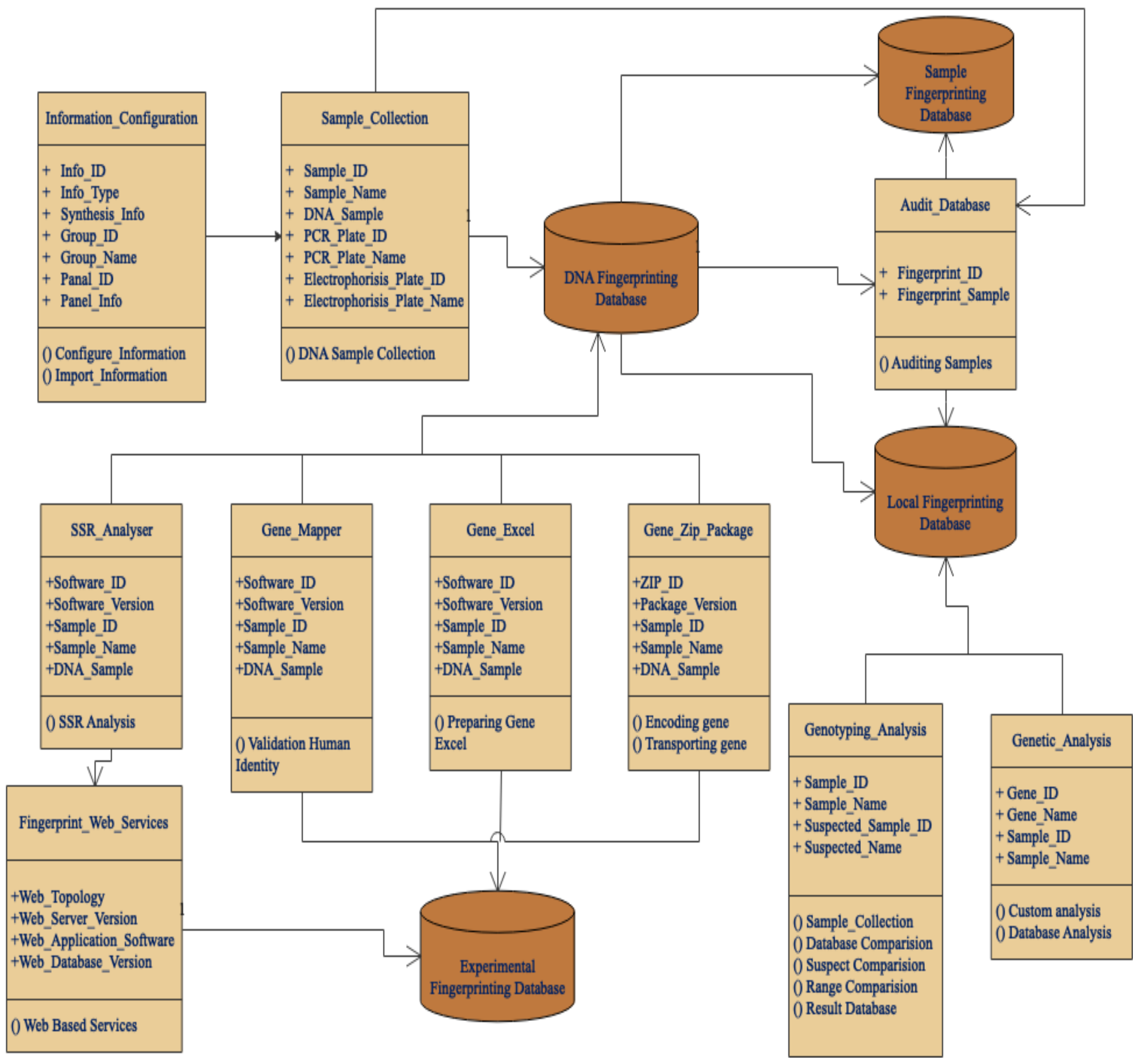

Figure 1.1: UML *Class Diagram for DNA Profiling/DNAFIDs*

b) Sequence Diagram

A sequence diagram is designed here to represent the dynamic behavior of the DNA profiling or DNA fingerprinting from the figure 1.2 it shows the complete process of DNA profiling where six major objects like Sample_Collection, DNA_Isolation, PCR, Gel_Electrophoresis, Blotting and Sanger_Sequencing. The objects are communicated between each other through the massages that is shown along with the solid arrows while the reply message shown by the dotted arrow and the life line of the object is shown by the vertical dotted lines. Therefore itis shown in the sequence diagram that the DNA sample is collected in DNA_Sample collection center and then it is send to the DNA_Isolation point where the DNA is extracted by including some solution in it. After extracting the DNA it is send to the PCR point where the DNA is fragmented and transferred to Electrophoresis station where DNA is separated through the agarose gel during the electrophoresis technique.As the DNA fragment is separated the based pattern is transformed to nylon membrane through southern blotting technique. The radioactive DNA probes binds to specific DNA sequences on the membrane for DNA_Sequencing. As the DNA sequencing is prepared an x-ray film is developed to make visible the DNA pattern after detecting the radioactive pattern, this is known as DNA profiling or DNA fingerprinting.

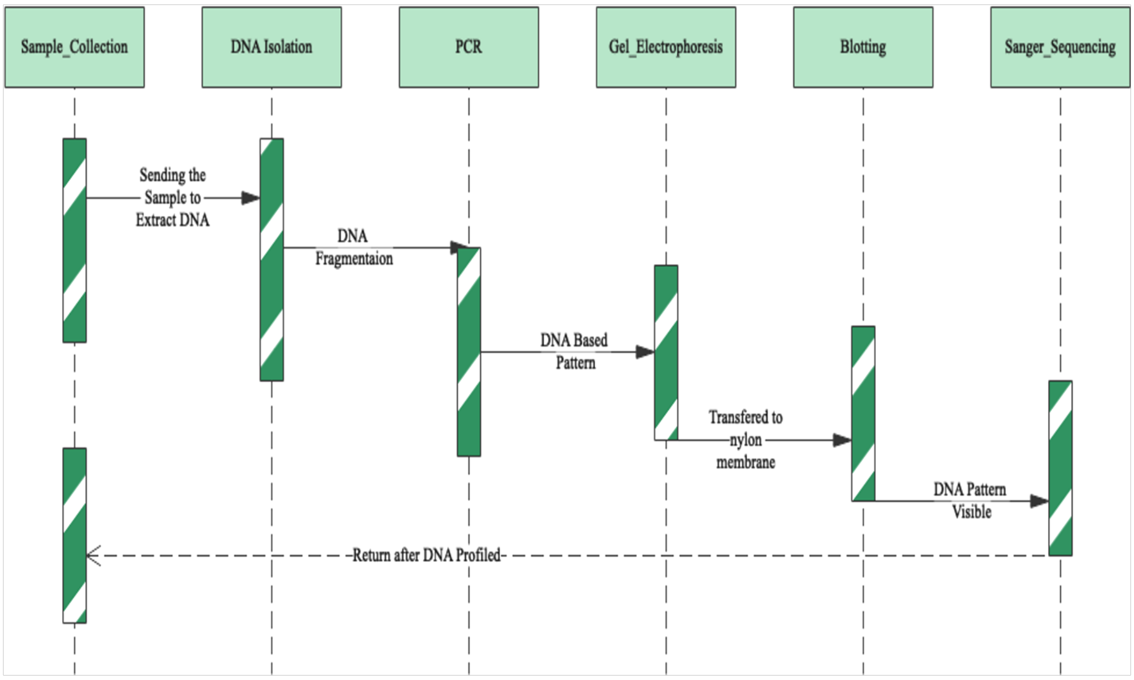

Figure 1.2: UML *Sequence Diagram for DNA Profiling/DNAFIDs*

II. State Transition Diagram For DNAFIDs and Convection Into Finite State Machine

The state transition diagram is illustrated for DNA profiling which is shown below in the figure 2.1:

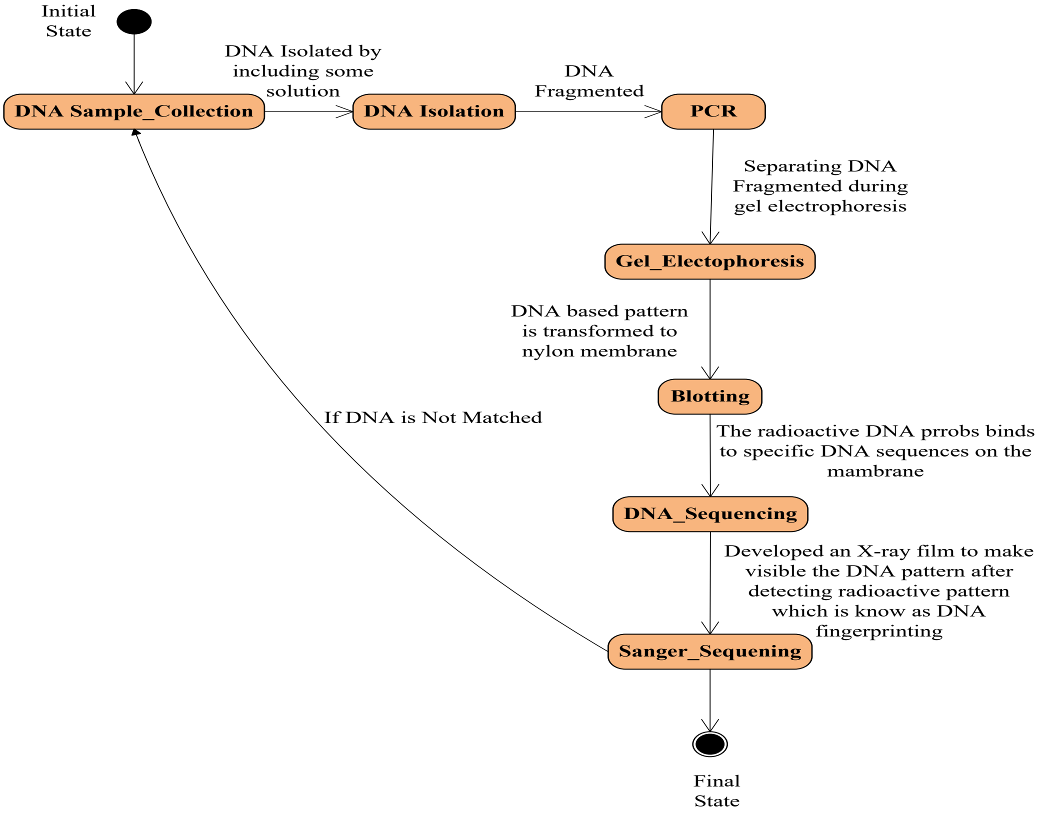
Initial State
DNA Sample_Collection
DNA Isolated by including some solution
DNA Isolation
DNA Fragmented
PCR
Separating DNA Fragmented during gel electrophoresis
Gel_Electophoresis
DNA based pattern is transformed to nylon membrane
Blotting
If DNA is Not Matched
The radioactive DNA prrobs binds to specific DNA sequences on the mambrane
DNA_Sequencing
Developed an X-ray film to make visible the DNA pattern after detecting radioactive pattern which is know as DNA fingerprinting
Sanger_Sequening
Final State

Figure 2.1: State Transition Diagram for DNA Profiling

From the above state transition diagram, it is assumed that the DNA sample is collected at the state of DNA Sample_Colletion it is the initial state which is equivalent to “q_0” and the sample send to the DNA_Isolation state it is equivalent to “q_1” where the DNA is separated by including some separation gel say “a”. At the PCR state which is equivalent to “q_2” the DNA is Fragmented say “b” and this fragmented DNA is send to the Gel_Eletrophoresis state where DNA is Separated from the fragment though the electrophoresis gel say “c” this state is equivalent to “q_3“. After separating the DNA from the fragments a new state is appear which is equivalent to “q_4“ where a DNA based pattern is transformed to the nylon membrane say “d” named as Blotting. At the DNA-Sequencing state (“q_5“) the radioactive DNA probs binds to specific DNA sequences on the membrane say “e” and a DNA sequence is found. An x-ray film is developed to make visible the DNA pattern which is known a DNA fingerprinting say “f” at the final state Sanger_Sequening it is equivalent to “q_6“. If the DNA matches the process is in final state i.e. “q_6“ and if the DNA is not matches then the process went to initial state i.e. “q_0“.

The finite state machines for DNA profiling through the set of these states equivalencies can be drawn as shown in the figure 2.1. The equivalent finite state machine of the above UML state diagram is as shown in figure 2.2:

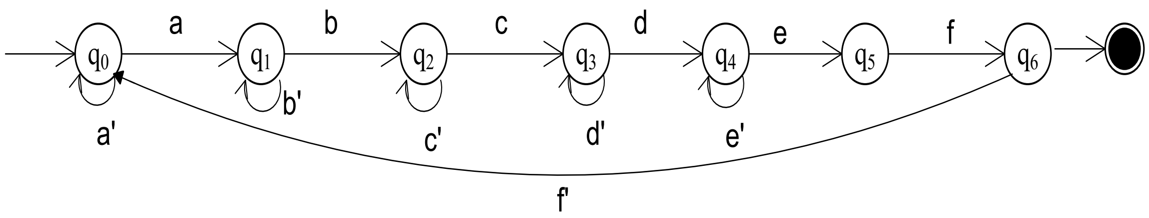

Figure 2.2: UML *Finite State Machine for DNA Profiling/DNAFIDs*

The transformation of one state to another state is done on the basis of {a, a’, b, b’, c, c’, d, d’, e, e’, f, f’} inputs which is considered as terminals and the set of states {q_0, q_1, q_2, q_3, q_4, q_5, q_6 }are the non-terminals states where q_0 is the initial state and q_6 is the final state. There are several production can be induced for the above finite state machine and the corresponding transition table is as shown below in table 2.2:

Table 1: *Transition Table for DNA Profiling/DNAFIDs*

	Inputs										
States	‘a’	a'	‘b’	b′	‘c’	c'	‘d’	d'	‘e'	‘f’	f'
→q0	q1	q0	-	-	-	-	-	-	-	-	-
q1	-	-	q2	q1	-	-	-	-	-	-	-
q2	-	-	-	-	q3	q2	-	-	-	-	-
q3	-	-	-	-	-	-	q4	q3	-	-	-
q4	-	-	-	-	-	-	-	-	q5	q4	-
q5	-	-	-	-	-	-	-	-	-	q6	-
q6	-	-	-	-	-	-	-	-	-	-	q0

III. Test Cases For Validating DNAFIDs Model

From the above work there are some test cases are generated to validate the designed model and described below in brief:

Test case 1:

The DNA is fragmented after isolation by including some solution in collected sample.

$\rightarrow q_0 \rightarrow aq_1$

$q_1 \rightarrow bq_2$

Test case 2:

The radioactive DNA probes binds the specific DNA sequence on Membrane by DNA pattern is transformed to nylon membrane.

$q_2 \rightarrow cq_3$

$q_3 \rightarrow dq_4$

$q_4 \rightarrow eq_5$

Test case 3:

An X-ray film is made to visible the DNA pattern and matched it, if the DNA matched the final state occurs if not then initial state occurs.

$q_5 \rightarrow fq_6$

$q_6 \rightarrow f'q_0$

IV. Result & Discussion

From the above work, it is concluded that UML is a powerful modelling language for modelling the various kinds of the research problems and one can depict the static as well as the dynamic behaviour of the system. The above work is based upon the of validation technique through FSM for the designed DNAFIDs model which show the complete process of DNA profiling. The proposed model for DNA profiling/DNAFIDs is validated through various test cases drawn from the FSM.

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