Artificial Intelligence in Genome Calculation

Software Design Document

Ayse Okatan

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Embry-Riddle Aeronautical University

Daytona Beach campus

1 Aerospace Boulevard

Daytona Beach, FL 32114

INTRODUCTION:

This Software Design Document (SSD) describes the functionality and software design of an Artificial intelligence in Genome Calculations (AIGC) game. The Artificial Intelligence in Genome Calculation is a Genetic Algorithms (GA) which is a metaheuristic inspired by the process of natural selection that belongs to the larger class of evolutionary algorithms (EA). Genetic algorithms are commonly used to generate high-quality solutions to optimization and search problems by relying on biologically inspired operators such as mutation, crossover, and selection. By using the concept of a Punnett Square, a diagram is used by biologists to determine the probability of an offspring having a particular genotype. The Punnett square is a tabular summation of possible combinations of maternal alleles with paternal alleles. These tables can be used to examine the genotypical outcome probabilities of the offspring of a single trait (allele), or when crossing multiple traits from the parents. The Punnett square is a visual representation of Mendelian inheritance. It is important to understand the terms "heterozygous," "homozygous", "double heterozygote" (or homozygous), "dominant allele" and "recessive allele" When using the Punnett method.

This document provides a complete description of the Artificial Intelligence Genome in Calculations (AIGC).

PROBLEM DESCRIPTION:

This project showcases the concept of inheritance within user selected parent models. This Genome Calculation (GC) game starts with a user selection of both parents, either randomized or custom made. If selected random, the program will randomly generate and output a Father and Mother figure with Physical Appearance, Physical conditions, and Mental conditions. If the user chose custom, they will be promoted with a series of questions for physical appearance.

Ex. User Trait Selection:

Trait:	**Type:**	**Type:**	**Type:**	**Type:**	**Type:**	**Heterochromia:**	**Selection:**
Eye Color:	Blue	Green	Brown	Hazel	Black	TRUE / FALSE	X or XX

Trait:	**Type:**	**Type:**	**Type:**	**Type:**	**Selection:**
Skin Color:	White	Black	Olive	Brown	X

Trait:	Type:	Type:	Type:	Selection:
Body Type:	Ecto- Morph	Meso-Morph	Endo-Morph	X

User then will then be prompted to select all traits they would like to add to each parent for Physical and Mental Conditions.

Ex. Physical Conditions **Ex. Mental Conditions**

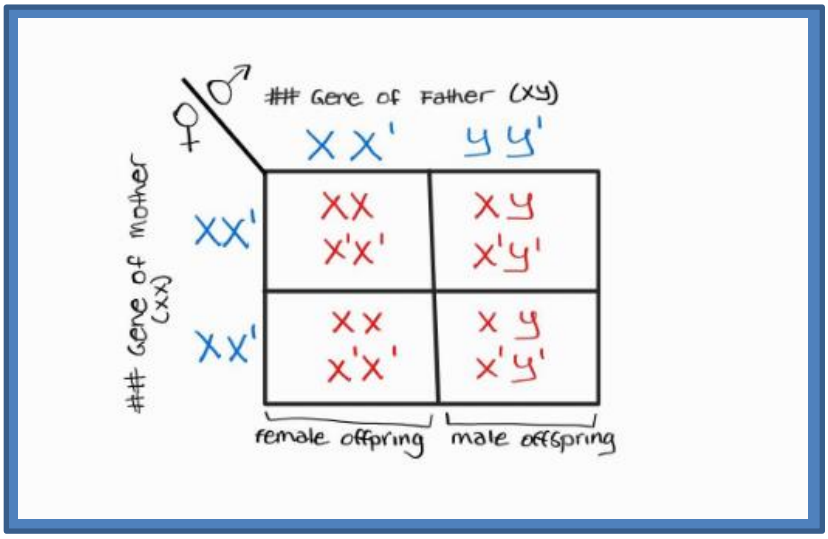
Trait:	Select:	Trait:	Select:
Cancer	X	Down Syndrome	X
Dwarfism	X	ADHD	
Albino		Schizophrenia	X
Back Acne		Depression	
Mutated Toe	X	Cerebral Palsy	
Glaucoma		Alzheimer's	
Scoliosis		Eating Disorder	X
Fetal Alcohol Syndrome		Addiction	
Body Building Aesthetics	X	Multiple Personality	X

Default Albino Characteristics:

Skin:	Eyes:	Hair:	Light Sensitivity
White	Red	White	TRUE

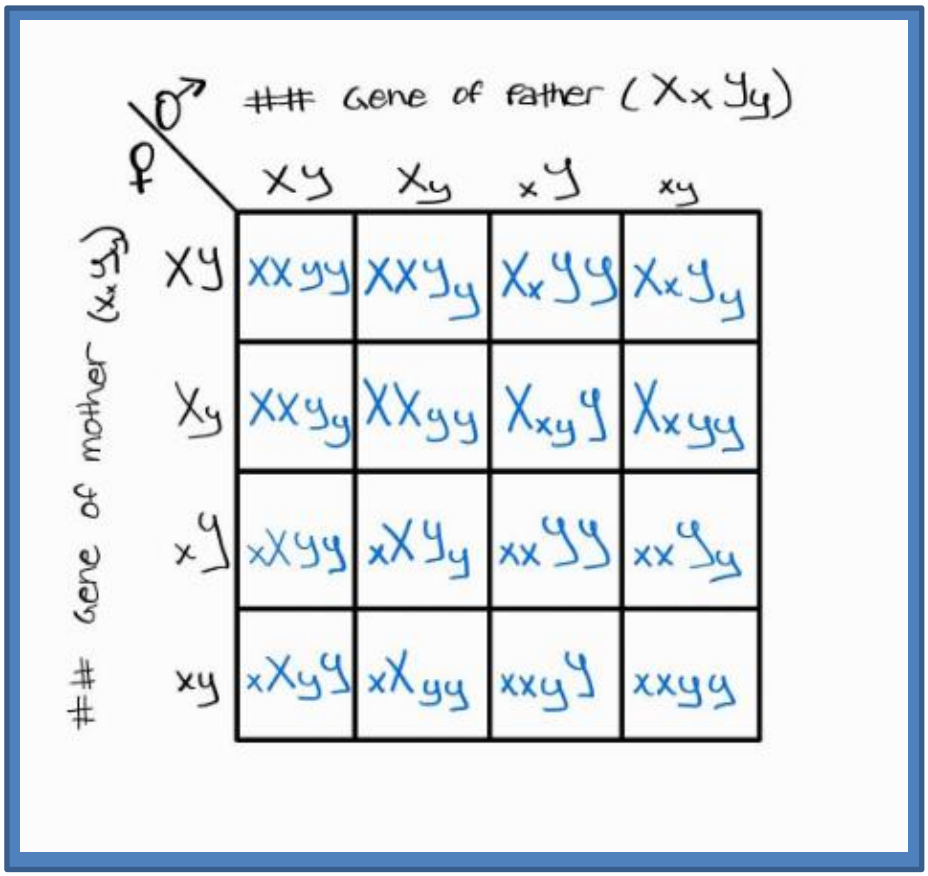
The Genome Calculator (GC) will calculate the trait probability of the first offspring through the concept of the Punnett Square.

Ex. Empty Trait Punnett Square Direct Inheritance



Genetic polymorphism is defined as the inheritance of a trait controlled by a single genetic locus with two alleles, like in Java; polymorphism means "many forms", and it occurs when we have many classes that are related to each other by inheritance. To showcase this in this project, the algorithm shall use a Di-Hybrid Cross to cross two observed traits from the parents that are controlled by two distinct genes. The Genome Calculators AI will determine which selected and or randomized traits depend on each other to create a sub trait, which will then fall into the process of a di-hybrid cross.

Ex. Dy-Hybrid Cross



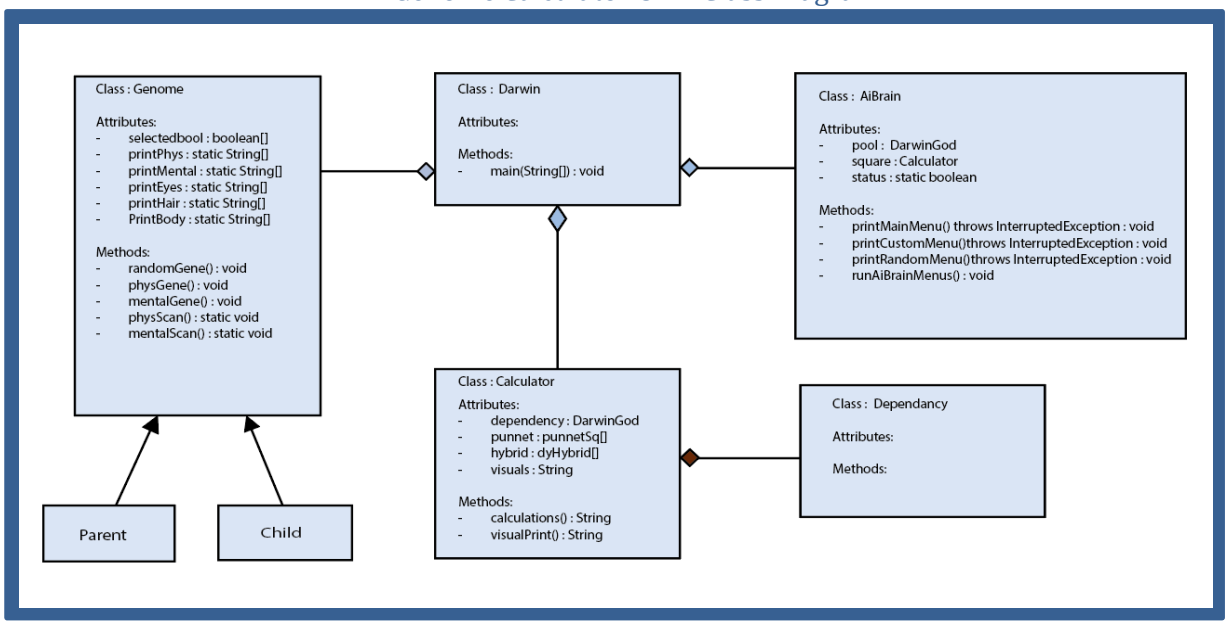
Note:

Capital letter means that the allele is dominant, while a lowercase letter means that it is recessive.

> Alleles are copies of genes that influence hereditary characteristics. Each person inherits at least two alleles for a particular gene—one allele from each parent. The first allele variant is termed dominant and the second recessive. This state of having two different variants of the same gene on each chromosome is originally caused by a mutation in one of the genes, either new (de novo) or inherited. In complete dominance, the effect of one allele in a heterozygous genotype completely masks the effect of the other. The allele that masks is considered dominant to the other allele, and the masked allele is considered recessive.

PROBLEM SOLUTION:

AI Genome Calculator UML Class Diagram



GENOME CLASS –

This class provides the descriptions of every gene type that the user will get to select by initializing each type of characteristic as an array. Each user selected characteristic will be converted into a Boolean array which will then display each true trait.

DARWIN CLASS –

This is the main class where the game will run.

AiBrain Class –

This class serves as a menu class, it provides the Darwin class with the menu's it needs to start the game.

Calculator Class –

This class will calculate the outcome of what the child will be depending on what the chosen parent traits. It will supply each selected trait from the Genome class and assign it with a random dominant or recessive gene which will be used to calculate the child's genetics through the Punnett square algorithm.

Dependency extends Calculator –

This class extension of Calculator determines what trait or genes is dependent to what.

Parents extends Genome –

This extension class inherits the Genome class, it is used to store the data of the parents.

Child extends Genome –

This extension class inherits the Genome class, it is used to store the data of the child.

References:

Wikipedia contributors. Genetic algorithm. Wikipedia, The Free Encyclopedia. October 9, 2022, 21:22 UTC. Available at: https://en.wikipedia.org/w/index.php?title=Genetic_algorithm&oldid=1115108091. Accessed October 25, 2022.

Appendices:

Agile Tracking Sheet (ATS), Requirements and Test Document (RTD).