Z Genome Lab — Technical Guide (Functional Units)

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Version: Final — Based on Z\_Genome\_Lab\_Checkbox\_Interface

This document outlines the core functionalities, technical logic, and medical potential of each module in the Z Genome Lab simulation system.

# 3D Genomic Viewer

\*\*File:\*\* z\_3d\_genomic\_viewer.py

\*\*Description:\*\* Visualizes DNA sequences in an interactive 3D plot based on base mappings (A, T, G, C).

\*\*Main Functionalities:\*\*

- Converts genome letters to coordinates

- Generates dynamic 3D visualization with Plotly

- Used for educational and diagnostic pattern recognition

\*\*Typical Use Case:\*\* Explore genomic spatial patterns, visualize DNA topologies for mutations and variations.

# AI Research Suggestions

\*\*File:\*\* z\_ai\_auto\_suggestions.py

\*\*Description:\*\* Provides AI-generated research ideas based on known genes and mutations using internal logic.

\*\*Main Functionalities:\*\*

- Uses gene names (BRCA1, TP53...) to trigger suggestions

- Ideal for researchers exploring unexplored directions

- Completely customizable mutation-suggestion engine

\*\*Typical Use Case:\*\* Boosts innovation in genomic research by offering mutation-driven research paths.

# AI Medical Diagnosis

\*\*File:\*\* z\_ai\_medical\_diagnosis.py

\*\*Description:\*\* Analyzes known gene mutations and predicts clinical implications using AI logic.

\*\*Main Functionalities:\*\*

- Maps mutations to associated diseases

- Provides medical risk summary and clinical recommendations

- Ideal for clinicians and predictive diagnosis

\*\*Typical Use Case:\*\* Used to simulate AI-driven diagnosis tools in genomic medicine.

# AI Mutation Risk Predictor

\*\*File:\*\* z\_ai\_prediction.py

\*\*Description:\*\* Predicts mutation effects and assigns risk levels using AI pattern logic.

\*\*Main Functionalities:\*\*

- Reads gene mutation type and computes severity

- Outputs recommendations and risk levels

- Helps guide genomic risk assessments

\*\*Typical Use Case:\*\* Integrated into clinical workflows for AI-powered mutation prognosis.

# Biomarker Discovery Lab

\*\*File:\*\* z\_biomarker\_discovery\_lab.py

\*\*Description:\*\* Identifies the most relevant biomarkers in omics datasets using Random Forest feature importance.

\*\*Main Functionalities:\*\*

- Accepts CSV datasets with class labels

- Trains RandomForest model on data

- Ranks and displays top biomarkers visually

\*\*Typical Use Case:\*\* Used for biomarker-driven therapy and patient stratification.

# Clinical Pathway Mapper

\*\*File:\*\* z\_clinical\_pathway\_mapper.py

\*\*Description:\*\* Maps the clinical decision process for a patient based on genetic data and medical indicators.

\*\*Main Functionalities:\*\*

- Allows the user to define symptoms, diagnostics, and outcomes

- Builds visual representation of clinical decision pathways

- Supports patient-specific treatment modeling

\*\*Typical Use Case:\*\* Used by medical professionals to simulate treatment paths and decision impact.

# CRISPR Simulation Unit

\*\*File:\*\* z\_crispr\_simulator.py

\*\*Description:\*\* Simulates CRISPR gene editing on target DNA sequences, highlighting possible off-targets.

\*\*Main Functionalities:\*\*

- Accepts DNA sequence and CRISPR guide RNA input

- Simulates editing and displays visual mutation effects

- Estimates off-target risks using symbolic logic

\*\*Typical Use Case:\*\* Perfect for educational or research-level exploration of gene editing outcomes.

# Gene Input Handler

\*\*File:\*\* z\_gene\_input.py

\*\*Description:\*\* Interface that allows researchers or users to input gene sequences or names into the system.

\*\*Main Functionalities:\*\*

- Supports gene symbol input (BRCA1, CFTR, etc.)

- Validates against known genomic databases

- Passes the gene data to connected analysis modules

\*\*Typical Use Case:\*\* Essential for input validation and dataset consistency in genomic simulations.

# Predictive Risk Estimator

\*\*File:\*\* z\_predictive\_risk\_estimator.py

\*\*Description:\*\* Calculates statistical or machine learning-based risk estimates from genetic and clinical data.

\*\*Main Functionalities:\*\*

- Uses logistic regression or pre-trained ML models

- Combines gene, age, symptom data

- Outputs detailed risk profile per condition

\*\*Typical Use Case:\*\* Clinics and researchers use it to assess patient risk before further testing.

# Protein Synthesis & Folding Simulator

\*\*File:\*\* z\_protein\_synth\_folding.py

\*\*Description:\*\* Predicts how a genetic mutation affects protein synthesis and folding, crucial for functional outcome predictions.

\*\*Main Functionalities:\*\*

- Simulates translation of gene to protein

- Visualizes basic protein structure

- Highlights folding abnormalities caused by mutations

\*\*Typical Use Case:\*\* Used to understand mutation impact at the protein functionality level.

# RNA Simulation & Transcription Mapper

\*\*File:\*\* z\_rna\_simulation.py

\*\*Description:\*\* Simulates the transcription process from DNA to mRNA and models structural RNA behavior.

\*\*Main Functionalities:\*\*

- Converts DNA sequences into mRNA codons

- Highlights RNA structural elements (loops, stems)

- Visualizes mRNA output for translation simulation

\*\*Typical Use Case:\*\* Used in transcriptomics education and RNA therapy simulation pipelines.

# DNA Methylation Mapper

\*\*File:\*\* z\_methylation\_mapper.py

\*\*Description:\*\* Simulates methylation patterns on CpG sites of DNA sequences and visualizes epigenetic states.

\*\*Main Functionalities:\*\*

- Detects CpG islands

- Applies synthetic methylation states

- Renders epigenetic heatmaps

\*\*Typical Use Case:\*\* Supports epigenetic analysis and cancer research by showing gene silencing effects.

# Genome Comparator Engine

\*\*File:\*\* z\_genome\_comparator.py

\*\*Description:\*\* Compares multiple DNA sequences to detect similarities, mutations, and alignments.

\*\*Main Functionalities:\*\*

- Accepts FASTA-like input sequences

- Performs symbolic or base-pair comparison

- Outputs detailed mutation points and similarity scores

\*\*Typical Use Case:\*\* Used for patient-to-reference genome alignment in clinical diagnostics.

# Genomic Mutation Tracker

\*\*File:\*\* z\_mutation\_tracker.py

\*\*Description:\*\* Tracks and visualizes accumulation of mutations across a genome over time or generations.

\*\*Main Functionalities:\*\*

- Records mutations from input datasets

- Builds visual mutation maps

- Supports longitudinal genomic studies

\*\*Typical Use Case:\*\* Powerful in cancer genomics or hereditary disease progression analysis.

# Genome Data Loader

\*\*File:\*\* z\_genome\_data\_loader.py

\*\*Description:\*\* Provides structured loading and parsing of uploaded genomic data files in CSV or FASTA-like format.

\*\*Main Functionalities:\*\*

- Validates file structure and contents

- Parses sequences and metadata

- Feeds modules with standardized inputs

\*\*Typical Use Case:\*\* Ensures clean data ingestion for all Z Genome modules.

# AI-Powered Suggestion Engine

\*\*File:\*\* z\_ai\_auto\_suggestions.py

\*\*Description:\*\* Analyzes existing genomic data to propose new experiments or potential gene targets using machine learning.

\*\*Main Functionalities:\*\*

- Scans datasets for significant patterns

- Uses AI to suggest research paths or target genes

- Generates textual recommendations

\*\*Typical Use Case:\*\* Used by researchers to guide hypothesis generation or new studies in genomics.

# AI-Based Medical Diagnosis Assistant

\*\*File:\*\* z\_ai\_medical\_diagnosis.py

\*\*Description:\*\* Provides preliminary diagnosis suggestions from genomic profiles using pre-trained clinical models.

\*\*Main Functionalities:\*\*

- Processes gene-based symptoms

- Returns potential conditions with probability scores

- Assists physicians in differential diagnosis

\*\*Typical Use Case:\*\* Can be used in clinical settings as a second opinion system for rare diseases.

# 3D Genomic Data Visualizer

\*\*File:\*\* z\_3d\_genomic\_viewer.py

\*\*Description:\*\* Transforms sequence and structure data into interactive 3D genomic representations for enhanced understanding.

\*\*Main Functionalities:\*\*

- Plots helix-like views of gene sequences

- Visualizes mutation zones and interaction regions

- Supports rotation, zoom, and gene labeling

\*\*Typical Use Case:\*\* Ideal for educational platforms or advanced genomic data exploration.

# Genomic Report Generator

\*\*File:\*\* z\_gene\_report\_generator.py

\*\*Description:\*\* Compiles results from multiple modules into a unified report for export as PDF or visual formats.

\*\*Main Functionalities:\*\*

- Collects outputs from various Z Genome modules

- Formats findings into clinical-style reports

- Exports to PDF and includes 3D snapshots if available

\*\*Typical Use Case:\*\* Used by medical researchers or genetic counselors for formal patient reports or case studies.

# AI Ethics & Genomic Compliance Auditor

\*\*File:\*\* z\_ethics\_ai\_audit.py

\*\*Description:\*\* Evaluates the ethical alignment and data protection of any AI/genomic activity within the platform.

\*\*Main Functionalities:\*\*

- Checks compliance with GDPR, HIPAA, and local laws

- Flags risks in AI model usage and data retention

- Suggests ethical improvement paths

\*\*Typical Use Case:\*\* Useful for institutional deployment of the lab in hospitals or research labs to ensure compliance.

# Biomarker Discovery Lab

\*\*File:\*\* z\_biomarker\_discovery\_lab.py

\*\*Description:\*\* Applies machine learning to identify significant genomic biomarkers associated with specific diseases or traits.

\*\*Main Functionalities:\*\*

- Trains ML models on labeled datasets

- Ranks genes based on importance scores

- Exports top biomarker candidates

\*\*Typical Use Case:\*\* Essential for early disease detection, especially in cancer or rare disorders.

# Genome Compression Tool

\*\*File:\*\* z\_genome\_compression\_tool.py

\*\*Description:\*\* Compresses large genomic datasets for storage, transmission, and computational optimization.

\*\*Main Functionalities:\*\*

- Applies symbolic and standard compression algorithms

- Reduces genomic file sizes up to 90%

- Supports decompression and integrity checks

\*\*Typical Use Case:\*\* Ideal for genomic cloud platforms and low-bandwidth environments.

# Genome Annotation Tool

\*\*File:\*\* z\_genome\_annotation\_tool.py

\*\*Description:\*\* Allows users to annotate DNA sequences with genes, regulatory regions, or custom notes.

\*\*Main Functionalities:\*\*

- Interactive interface to add labels or gene IDs

- Supports import/export of GFF/BED-like formats

- Visual genome navigation

\*\*Typical Use Case:\*\* Useful for research teams tracking functional areas of specific genomes.

# AI Prediction Module

\*\*File:\*\* z\_ai\_prediction.py

\*\*Description:\*\* Uses trained models to predict outcomes based on genomic features such as mutation types or sequence patterns.

\*\*Main Functionalities:\*\*

- Loads data into trained model (e.g., XGBoost)

- Outputs risk categories or probabilities

- Includes feature interpretation

\*\*Typical Use Case:\*\* Supports personalized medicine and genomic risk profiling.

# Gene Input Handler

\*\*File:\*\* z\_gene\_input\_handler.py

\*\*Description:\*\* Processes user-inputted gene symbols or sequences and prepares them for analysis across modules.

\*\*Main Functionalities:\*\*

- Validates and formats gene symbols

- Fetches reference metadata (e.g., Entrez, Ensembl)

- Feeds into analytical pipelines

\*\*Typical Use Case:\*\* Ensures user-friendly entry point into the Z Genome platform.