

GENERATED: 2/21/2026, 1:41:46 AM
REPORT ID: BRD-ADLY3AWF
REQUIREMENTS: 30

SOURCE: Manual Text Input
STATUS: VERIFIED
ARCH NODES: 8

CONFLICTS: 4

Verified Requirements

PATIENT RECORD MANAGEMENT

[HIGH]

The system shall store and retrieve individual patient records, each uniquely identified by an 'id' field, ensuring data integrity and accessibility.

DIAGNOSTIC CLASSIFICATION STORAGE

[HIGH]

For each patient record, the system shall store a 'diagnosis' field, which can hold one of two categorical values: 'M' for Malignant or 'B' for Benign, indicating the clinical outcome.

MEAN FEATURE DATA STORAGE

[HIGH]

The system shall store a comprehensive set of mean values for various cellular characteristics (e.g., radius, texture, perimeter, area, smoothness, compactness, concavity, concave points, symmetry, fractal dimension) for each patient, representing the average of the measurements.

STANDARD ERROR FEATURE DATA STORAGE

[MEDIUM]

The system shall store a set of standard error values for various cellular characteristics (e.g., radius, texture, perimeter, area, smoothness, compactness, concavity, concave points, symmetry, fractal dimension) for each patient, providing insight into the variability of the measurements.

WORST FEATURE DATA STORAGE

[MEDIUM]

The system shall store a set of 'worst' (largest or most extreme) values for various cellular characteristics (e.g., radius, texture, perimeter, area, smoothness, compactness, concavity, concave points, symmetry, fractal dimension) for each patient, often indicative of more severe conditions.

DATA RECORD INGESTION

[HIGH]

The system must be capable of ingesting structured data records, where each record consists of a unique identifier, a single-character classification label ('B' or 'M'), and a fixed set of approximately 30 numerical feature values.

BINARY CLASSIFICATION

[HIGH]

The system must process the classification label for each record, categorizing it into one of two predefined groups: 'B' (e.g., Benign) or 'M' (e.g., Malignant).

FEATURE EXTRACTION

[MEDIUM]

For each ingested record, the system must extract and store the associated numerical feature values, which are crucial for the classification process.

UNIQUE RECORD IDENTIFICATION

[HIGH]

Each data record must be uniquely identifiable by an integer ID, which is the first field in the record.

DATA FRAGMENT PARSING

[HIGH]

The system must be capable of parsing the provided data fragment, which consists of multiple lines, each representing a record. Each record is delimited by a newline and contains an identifier, a single-character classification label ('B' or 'M'), and a series of floating-point numerical features, all space-separated.

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RECORD IDENTIFICATION

[MEDIUM]

The system must extract the unique identifier for each record, located in the first column, to allow for traceability and individual record management.

CLASSIFICATION LABEL EXTRACTION

[HIGH]

For each parsed record, the system must accurately extract the classification label, which is a single character ('B' for Benign, 'M' for Malignant) located in the second column of each record.

NUMERICAL FEATURE EXTRACTION

[HIGH]

For each parsed record, the system must extract all subsequent numerical values as floating-point features. These features are critical inputs for any subsequent data analysis or machine learning models.

DATA ROW INGESTION

[HIGH]

The system must be capable of ingesting individual data rows, each starting with a unique identifier.

CATEGORICAL TYPE EXTRACTION

[HIGH]

For each ingested data row, the system must extract a single categorical type, represented by a character (e.g., 'B' or 'M').

NUMERICAL FEATURE EXTRACTION

[HIGH]

The system must extract a predefined set of numerical features from each data row, following the categorical type.

DATA AGGREGATION FOR ANALYSIS

[MEDIUM]

The system should aggregate the extracted identifiers, types, and numerical features for subsequent analysis or classification tasks.

DATA FRAGMENT INGESTION

[HIGH]

The system must be capable of ingesting raw tabular data fragments, where each line represents a distinct record.

RECORD PARSING AND IDENTIFICATION

[HIGH]

Each ingested line must be parsed to identify a unique record identifier (e.g., '9010259') at the beginning of the line.

CLASSIFICATION LABEL EXTRACTION

[HIGH]

The system must extract a single-character classification label ('B' or 'M') immediately following the record identifier for each record.

NUMERICAL FEATURE EXTRACTION

[HIGH]

All subsequent floating-point numerical values within each record must be extracted and treated as distinct features associated with that record.

STRUCTURED DATA STORAGE

[MEDIUM]

Processed records, including their identifier, classification, and extracted numerical features, should be stored in a structured format suitable for further analysis or machine learning tasks.

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DATA RECORD INGESTION

[HIGH]

The system must be capable of ingesting raw data fragments, parsing each line as a distinct record. Each record is expected to contain a unique identifier, a single-character classification label ('M' for Malignant, 'B' for Benign), and 30 floating-point numerical features.

CLASSIFICATION LABEL EXTRACTION

[HIGH]

For each ingested record, the system must accurately extract the classification label ('M' or 'B') which serves as the ground truth for the record's type.

NUMERICAL FEATURE EXTRACTION

[HIGH]

For each ingested record, the system must extract the 30 numerical features, ensuring correct data type conversion (e.g., to float) for subsequent analytical processing.

DATA CLASSIFICATION CAPABILITY

[MEDIUM]

The system should support a mechanism to classify new, unlabeled records into 'Malignant' or 'Benign' categories based on their numerical features, leveraging the patterns learned from the provided labeled data.

DATA RECORD INGESTION

[HIGH]

The system shall be capable of ingesting tabular data, where each line represents a distinct data record.

RECORD FIELD PARSING

[HIGH]

For each ingested data record, the system shall parse the fields into a unique identifier, a classification label ('M' or 'B'), and a set of numerical feature values.

CLASSIFICATION LABEL INTERPRETATION

[HIGH]

The system shall interpret the classification label 'M' as Malignant and 'B' as Benign for each record.

NUMERICAL FEATURE PROCESSING

[MEDIUM]

The system shall process and store the extracted numerical feature values for each record, making them available for subsequent analysis or model training.

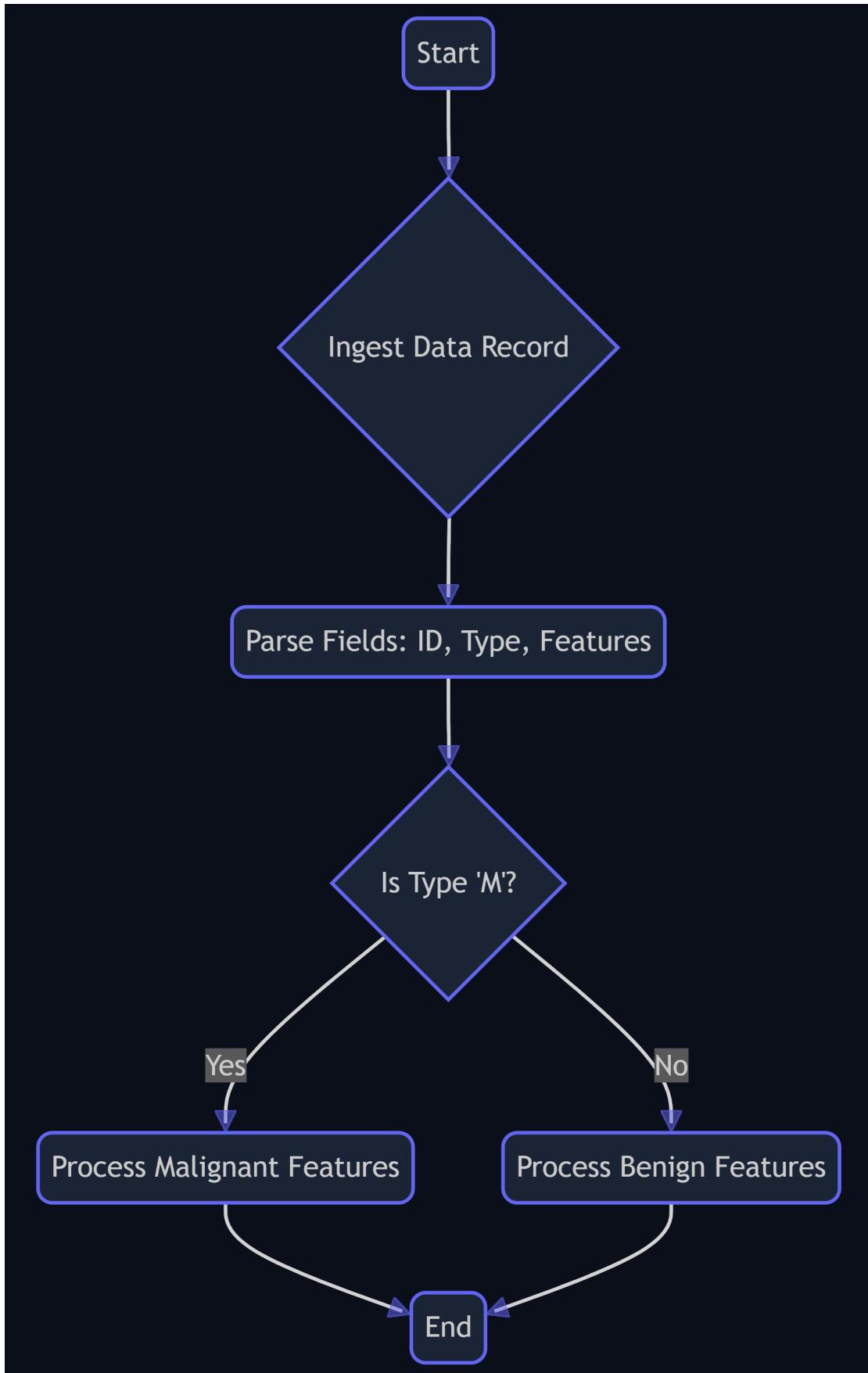
Auditor Redlines (Conflicts)

- ! No logical conflicts are present within this data fragment, as it represents raw observational data rather than conflicting rules or processes.
- ! No logical conflicts were identified within the provided data fragment itself. The data structure and classification labels ('B' and 'M') are consistent.
- ! No logical conflicts or contradictions were identified within this raw data fragment itself, as it represents observations rather than a set of rules or processes.

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- !** The provided data fragment consists solely of raw, structured data points. It does not contain any explicit requirements, rules, or statements that could logically contradict each other. Therefore, no logical conflicts are identified within this specific fragment.

Architecture Map



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DIGITALLY SIGNED BRD REPORT

ISSUER: DK2B Automated Auditor**TIMESTAMP:** 2/21/2026, 1:41:46 AM**INTEGRITY HASH (SHA-256):**

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