1. Project Description

Objective:  
The goal of this project is to develop an application that tracks the processing of biological samples in a laboratory setting addressing the need for an organized and efficient system that minimizes errors in tracking sample data and ensures compliance with laboratory protocols. The application will manage the steps involved in DNA sample processing, including extraction, quantification, and dilution. This application will serve as a laboratory information management tool in research settings.

Data Description:  
The application will store various types of data, including:

* Sample Information: sample type, collection kit info, sample ID, volumes
* Extraction Data:  Run IDs, batch numbers, sample volume, reagent volumes, DNA extract volume
* Quantification Results: Concentration values, quantification instrument
* Dilution Records: Information on concentrations before and after dilution.

The data involved is quantitative, qualitative, and categorical.

Functionality:  
The Tkinter application will provide the following key functionalities:

* User Management: Account creation and sign in to track activity of sample processor
* User Interface for Data Entry: Forms to enter new extraction data, quantification results, and dilution details
* Database Operations: Ability to query, and add new records.

2. Database Schema Design

ER Model Description:

* Entities:
  + Samples- Represents individual DNA samples being processed.
  + Extraction- Contains details about the extraction process for each sample.
  + Quantification- Records data obtained from the Qubit quantification process
  + Dilution- Tracks the dilution steps for samples prior to PCR analysis.
* Relationships:
  + A Sample can have one associated Extraction (one-to-one).
  + A Sample can have one quantification record (one-to-one).
  + Each Sample can have none or more associated Dilution records (one-to-many).

Keys and Attributes:

* Primary Keys:
  + *SampleID* (Samples)
  + *ExtractionID* (Extraction)
  + *QuantificationID* (Quantification)
  + *DilutionID* (Dilution)
* Foreign Keys:
  + *SampleID* in Extraction references Samples.
  + *SampleID* in Quantification references Samples.
  + *SampleID* in Dilution references Samples.
* Attribute Data Types:

| Entity | Attribute | Data Type |
| --- | --- | --- |
| Samples | Sample\_ID | VARCHAR(255) (Primary Key) |
|  | Sample\_type | VARCHAR(255) |
|  | Collection\_Kit\_Type | VARCHAR(255) |
|  | Collection\_Date | DATE |
|  | Sample\_Volume | FLOAT |
| Extraction | Batch | INT |
|  | Extraction\_ID | INT (Primary Key) |
|  | Extraction\_Date | DATE |
|  | Sample\_ID | VARCHAR(255) (Foreign Key) |
|  | Extraction\_Buffer\_Volume | FLOAT |
|  | 100%\_EtOH\_Volume | FLOAT |
|  | Elution\_Buffer\_Volume | FLOAT |
|  | Elution\_Sample\_ID | VARCHAR(255) |
| Quantification | Quantification\_ID | INT (Primary Key) |
|  | Elution\_Sample\_ID | VARCHAR(255) |
|  | Concentration | FLOAT |
|  | Quantification\_Instrument | VARCHAR(255) |
|  | Quantification\_Date | DATE |
| Dilution | Dilution\_ID | INT (Primary Key) |
|  | Parent\_Sample\_ID | VARCHAR(255) (Foreign Key) |
|  | Dilution\_Sample\_ID | VARCHAR(255) |
|  | Dilution\_Volume | FLOAT |
|  | Dilution\_Concentration | FLOAT |
|  |  |  |

Tools and Implementation

* ER Model Tool:  
  MySQL Workbench's ER Diagram Editor will be used to visually represent the database schema.
* Forward Engineering:  
  The forward engineer feature in MySQL Workbench will convert the ER model into SQL statements that create the necessary database tables on a MySQL server.
* Data Verification:  
  Mock data will be inserted to verify that all tables function correctly and meet the project requirements.