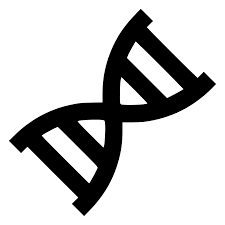
**DNA Analyzer User Manual**

**Running the Application**

1. **Launching the Application**:
   * click on the **DNA analyzer application**
   * or run the script using Python: **DNA script.py**.
2. **Setting Input and Output Folders**:
   * Use the "Select Input Folder" button to choose the folder containing your XML and TXT files.
   * Use the "Select Output Folder" button to choose where you want to save the results. If not specified, the output will be saved in the same folder as the input folder.
3. **Setting Match Sensitivity**:
   * Enter a value between 0 and 1 in the "Match Sensitivity" field. This determines the threshold for DNA matches. A higher value means more matching allele values will define a match.
4. **Starting the Process**:
   * Click the "Start Processing" button to begin. The application will scan the input folder for XML and TXT files, process the data, and save the results in the output folder.

**Notes**

1. **Duplicate Files**:
   * If two identical copies of one file exist under different names, they will appear twice in the table and will show a full match since the table doesn't drop duplicates.
2. **Resetting Result Files**:
   * To reset the result files, you can delete them in the output folder or select a new output folder for a new analysis of the input folder.

**Viewing Results**

1. **Sequencing Summary**:
   * The consolidated sequencing data is saved in **sequencing\_summary.csv**.
   * The final processed data is saved in **final\_DNA\_sequencing\_summary.csv**.
2. **DNA Matches**:
   * Matches are saved in **DNA\_matches.csv**.
   * The results include specimen IDs, match scores, and the latest match time.
3. **Settings**:
   * The settings, including the sensitivity and scanned files, are saved in **settings.csv**.

**Technical Support**

For further questions or technical support, please contact: **eitanfass1996@gmail.com**

**Additional information**

**App Functionality**

1. **File Processing**:
   * The application will automatically scan the input folder for XML and TXT files.
   * XML files will be processed according to their format (CODIS or NIEM).
   * TXT files will be parsed to extract allele data.
2. **Data Consolidation**:
   * Extracted data from all files will be consolidated into a single DataFrame.
   * The data will be saved in **sequencing\_summary.csv** in the output folder.
3. **Formatting the Data**:
   * The application will pivot the data to consolidate rows into a single line per specimen, with loci as columns.
   * The processed data will be saved in **final\_DNA\_sequencing\_summary.csv** in the output folder.
4. **Finding Matches**:
   * The application will compare specimens to find matches based on the set sensitivity.
   * Existing matches will be loaded and new matches will be appended.
   * The matches will be saved in **DNA\_matches.csv** in the output folder.

**Sample Matching Methodology**

1. **Loading Existing Matches**:
   * Existing matches from **DNA\_matches.csv** will be loaded to ensure that previously matched specimens are not reprocessed.
2. **Sensitivity Use**:
   * The sensitivity value determines how stringent the matching criteria are. A higher value (closer to 1) requires more loci to match exactly.
   * Matches are found by comparing alleles for each locus. If the alleles match exactly, the locus is considered a match. Example 24/26 allels are identical matches then the sensitivity score is 24/26=0.92
3. **Finding New Matches**:
   * Specimens are grouped by LocusName, and alleles are compared to identify matches.
   * Only specimens not previously matched are considered.
   * Matches with a score above the sensitivity threshold are saved.