
Procedure for the Use of COSTaR

1.0 Purpose – This procedure specifies the steps for the use of the COSTaR Excel workbook to generate CODIS eligible DNA profiles, to assist in the evaluation of candidate matches from CODIS, and to generate STRmix compatible reference profiles when needed.

2.0 Scope – This procedure applies to Forensic Scientists in the Forensic Biology Section who generate DNA profiles for entry into CODIS.

3.0 Definitions – See Section Definition List

4.0 Equipment, Materials, and Reagents

- COSTaR
- STRmix Software
- CODIS Software

5.0 Procedure

5.1 Overview

5.1.1 COSTaR is an Excel workbook that uses macros to assist in accomplishing various CODIS related functions.

5.1.1.1 COSTaR is a tool used to modify DNA profiles produced by STRmix deconvolutions for CODIS entry. STRmix deconvolution of mixtures may produce multiple genotype possibilities for a single contributor to a mixture and these genotypes must be evaluated for CODIS entry.

5.1.1.1.1 Full, single source evidence profiles (Forensic Unknowns) may be exported directly from GMIDx or COSTaR may be used for CODIS entry.

5.1.1.1.2 All other profiles being entered into CODIS shall be ran through COSTaR. This includes mixtures that are almost fully deconvoluted by STRmix.

5.1.1.2 COSTaR can also be used to assist in the evaluation of matches that occur as the result of CODIS searches using the STRmix DB Creator workbook. COSTaR creates a STRmix searchable database from a list of candidate matches from CODIS.

5.1.1.3 The Reference File Maker workbook of COSTaR can be used to generate STRmix compatible reference files for comparison.

5.1.2 COSTaR was designed primarily as a tool for analyzing STRmix deconvolution data and developing profiles for entry into CODIS. It consists of five main tabs:

5.1.2.1 STRmix Data sheet – where data from STRmix is added

5.1.2.2 Contributors sheet – contains information for each contributor from STRmix data

5.1.2.3 Allele Weights Summary sheet – lists the possible alleles and allele weights, summed from the genotype weights, for a particular contributor

5.1.2.4 MME sheet – where MME calculations are performed

5.1.2.5 CODIS sheet – contains data for the profile that will be entered into CODIS

5.1.3 COSTaR modifies profiles in an attempt to meet eligibility requirements for the highest level of CODIS possible based on the data that is present. A four-step process is used to create CODIS searchable profiles:

5.1.3.1 Alleles above the user-defined maximum number of alleles allowed in a CODIS profile (NDIS max = 4 alleles and SDIS/LDIS max = 8 alleles) are trimmed.

5.1.3.2 Loci with drop-out possibilities (Q values) above the defined trimming threshold are excluded.

5.1.3.3 Obligate alleles are marked to increase discrimination.

5.1.3.4 Additional alleles are trimmed to meet MME requirements and increase discrimination.

5.1.3.5 COSTaR settings for the generation of CODIS eligible profiles:

CODIS Level	Maximum Trimming Threshold	Maximum Number of Alleles per Locus	Number of Original Core Loci Required	MME Threshold
NDIS	13%	4	8	1.00E07
SDIS/LDIS	13%	8	8	1.50E04

5.2 Use of COSTaR for the generation of CODIS eligible profiles

5.2.1 Open COSTaR and click on the “STRmix Data” tab of the COSTaR workbook.



5.2.2 Click “Import Data & Create CODIS Sheets.”



5.2.3 Navigate to the folder that contains your STRmix results for that case and double click the “Results.txt” STRmix results file in the run folder.

5.2.4 The COSTaR macros will run automatically and .xls COSTaR results files will be generated for each contributor. The individual component genotypes and weights will be displayed in the “Contributors” tab.

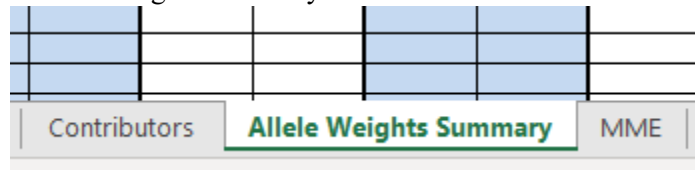


5.2.4.1 The COSTaR files for each contributor will be saved as a separate .xls files in the folder that contains the STRmix results for import.

5.2.4.2 The file name will include the Specimen ID and the level of CODIS eligibility for that contributor of the profile.

5.2.5 Open the COSTaR file for each contributor. The file is named with the contributor number and the level of CODIS entry. Verify the following information:

5.2.5.1 “Allele Weights Summary” tab



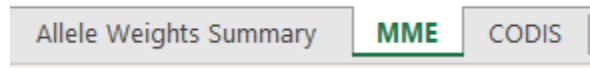
5.2.5.1.1 Verify there are no allele weights greater than 100% - close the workbook and start over if this occurs.

5.2.5.1.2 Verify that trimmed alleles are within the trimming threshold of

13%.

- 5.2.5.1.3** Alleles being entered into CODIS are marked in black.
- 5.2.5.1.4** Obligate alleles are marked in blue – the allele with the highest weight is marked as an obligate when needed to reach the MME value for the highest level of CODIS. If two allele weights are above the threshold (e.g., 1% trimming and two weights are above 99% - 99.8% and 99.2%), the rarer allele is selected by COSTaR.
- 5.2.5.1.5** Q alleles and alleles not used for CODIS are marked red.
- 5.2.5.1.6** When the number of alleles exceeds the maximum level of allowable alleles (e.g., 4 or 8), the number of alleles that are present is indicated below the table in green.
- 5.2.5.1.7** If the allele weight is greater than 1 minus the threshold (e.g., above 99% when trimming is set to 1%), the alleles will be noted in green below the chart. If only one allele meets this requirement, it will be designated as allele, 0.

5.2.5.2 “MME” tab



- 5.2.5.2.1** Do not make any changes to the allele data on this tab. Changes will affect the CODIS sheet and the CODIS import.
- 5.2.5.2.2** Review obligate alleles selected by COSTaR and if any partial locus boxes have been checked.
- 5.2.5.2.3** Verify that CODIS parameters have been met – minimum number of required core loci and MME for the level of entry.
- 5.2.5.2.4** YSTR data that should be included for CODIS entry must be entered on this tab. Once the data is entered, select “Create CODIS Sheet.”

- 5.2.6** For each contributor, click the “CODIS” tab - the case number and item number should automatically populate – the item number will be followed by the contributor number C1, C2, etc.



5.2.6.1 Specimen Category will automatically populate with the eligibility level that the profile will be assigned to in CODIS, however, the category will be automatically set to “Pending” for all import files so that the profiles can be technically reviewed prior to upload.

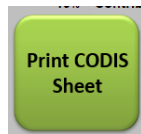
5.2.6.1.1 The following should be considered when verifying that the correct Specimen Category was selected:

Forensic Unknown	Partial Profile - No	All loci in profile or component of mixture deconvoluted to 100% with no complete locus drop-out. No other genotypes or Qs considered during deconvolution.
Forensic Partial	Partial Profile - Yes	At least one core locus being entered deconvoluted <100% with Qs OR complete drop-out at any core loci. No other genotypes considered during deconvolution aside from Qs at all loci being entered.
Forensic Mixture	Partial Profile - No	More than two alleles to be entered at any locus OR multiple genotypes considered in profile/component at any locus entered. Data entered for all loci and no Qs considered during deconvolution.
Forensic Mixture	Partial Profile - Yes	More than two alleles to be entered at any locus OR multiple genotypes considered in profile/component deconvoluted at any locus entered. Data not entered at all loci or Qs considered during deconvolution for loci being entered.

5.2.6.2 Update Source ID to Yes or No.

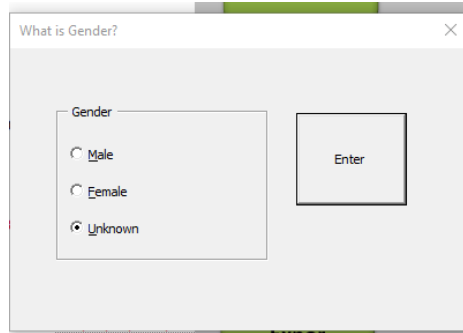
5.2.6.3 Add initials and date below allele values.

5.2.6.4 Click “Print CODIS Sheet.”



5.2.6.4.1 Values for Amelogenin are added when the CODIS sheet is printed by

selecting: Male, Female, or Unknown (no data populated) in the popup.



5.2.6.4.1.1 For COSTaR profiles originating from single source and partial profiles where the gender is clear, the allele values shall be selected.

5.2.6.4.1.2 For COSTaR profiles originating from mixtures where the gender appears to be unclear for the given contributor, it is analyst’s discretion based on the available data whether to update the allele entries for Amelogenin. Allele values shall be selected if the gender is clear.

5.2.6.4.1.3 If there is any potential for dropout at Amelogenin, do not enter any values. Leave the default setting of “Unknown.”

5.2.6.4.2 Save the .pdf file with the following format: COSTaR. All COSTaR files for the case shall be combined and saved in the FA object repository.

5.2.6.5 Click “CODIS Export.”



5.2.6.6 Save the COSTaR Workbook with the CODIS Specimen name within your STRmix results folder.

5.2.6.6.1 If the profile is not eligible for upload due to the profile being

inconclusive based on our STRmix interpretation guidelines, the MME value, or there are an insufficient number of core loci, save the file with “DNE” after the Specimen ID (e.g., R202212345#1-1_C1_DNE). This will be added to the object repository in FA in order to show that an attempt was made for entry. Document the reason why the profile will not be entered in the comments section of the CODIS Sheet.

5.2.6.6.2 If additional information is received (after COSTaR has been used) indicating that the profile is not eligible for upload due the case information not supporting eligibility, save the file with “DNE” after the Specimen ID (e.g., R202212345#1-1_C1_DNE). This will be added to the object repository in FA. Document the reason why the profile will not be entered in the comments section of the CODIS Sheet.

5.2.6.7 Choosing contributors for entry

5.2.6.7.1 COSTaR automatically attempts to generate a CODIS upload profile for each contributor profile generated in STRmix. The contributor profiles may be single source or mixtures.

5.2.6.7.2 To avoid duplicate matches to the same item if mixture profiles are generated for multiple contributors, the CODIS profiles for each contributor shall be compared to see if both contributors are represented in a single mixture that can be uploaded. The Specimen ID must reflect the contributors present (e.g., C1C2, etc) and the contributors being represented shall be entered in the comments section.

5.2.6.7.2.1 Any contributor profiles not being entered shall be saved with “DNE” after the Specimen ID and documentation that this contributor is fully represented in the mixture profile being entered shall be added to the comments section.

5.2.6.7.3 If there is any question as to a contributor being fully represented, both contributor profiles shall be entered.

5.3 Use of COSTaR for CODIS match evaluation

5.3.1 The COSTaR STRmix DB Creator workbook will be used to create a database from candidate matches from CODIS that can be searched against the target profile’s STRmix deconvolution settings file using the STRmix Database search to generate likelihood ratios for the matches. This

tool will be used when a mixture or partial profile matches to multiple known samples and/or when traditional match evaluation would be aided by the use of a LR.

5.3.2 Open CODIS Analyst Workbench Software and then open Match Manager.

5.3.2.1 In order to correctly export the samples for comparison, create a match view for COSTaR by using the “Edit an Existing Match View” icon. The forensic mixture or partial samples for the RCL or WRL ORI’s must be the Target Specimen on the left. The known, single-source samples must be the Candidate specimen on the right. This order is necessary for compatibility with downstream macros in COSTaR.

5.3.2.1.1 On the General Tab:

5.3.2.1.1.1 Match Date: = date of interest

5.3.2.1.2 On the Target Criteria Tab:

5.3.2.1.2.1 Agency: My Agency

5.3.2.1.2.2 Index: Forensic Mixture, Forensic Partial (additional forensic indices may be selected if needed)

5.3.2.1.3 On the Candidate Tab:

5.3.2.1.3.1 Index: Arrestee, Forensic, Offender, Suspect

5.3.2.2 Highlight the matches that are not easily resolved using traditional match evaluation criteria to create a DB file for mixture or partial profiles. Use of this tool is at the CODIS Administrator’s discretion.

5.3.2.3 Select Print Preview for the short version of the Match Details Report. Note: the STRmix Database workbook has a maximum of 1000 matches.

5.3.2.3.1 Click the first icon “Export Report.”

5.3.2.3.2 Change the “Save as (file) type:” to a .csv file and save the file as “Date_Candidates.”

5.3.2.3.3 An “Export completed” message will appear when done. Click OK.

5.3.3 Open the “STRmix DB Creator” workbook of COSTaR

5.3.3.1 On the “CODISData” tab, press the “Select File and Create Database” button.



5.3.3.2 Navigate to the Candidates .csv file that was created from CODIS (Date_Candidates) and click “Open.” The STRmix Database tool will automatically create a STRmix compatible database file from the samples selected in Match Manager

5.3.3.2.1 Click OK in pop up.

5.3.3.2.2 Change the “Save as (file) type:” to a .csv file and save file with the naming convention “Date_Database.”

5.3.3.2.3 Click OK in pop up.

5.3.3.2.4 This file is compatible for use with the Database Search function within STRmix.

5.3.4 STRmix Database Search

5.3.4.1 In the “Investigation” module of STRmix, click on the “Database Search” module.

5.3.4.2 PREVIOUS INTERPRETATION: Click the “Browse” button for Previous Interpretation and navigate to the STRmix deconvolution folder of the target specimen and select the “config.xml” file. Click Open. Alternatively, you can drag and drop the entire deconvolution folder into the Previous Interpretation box.

5.3.4.3 DATABASE FILE: Click the “Browse” button to locate the .csv file created with the STRmix DB Creator workbook (Date_Database). Click Open. Alternatively, you can drag and drop the entire deconvolution folder into the Database File box.

5.3.4.4 DATABASE SEARCH SETUP

5.3.4.4.1 Minimum LR: 50,000

5.3.4.4.2 Population: NIST1036_Comb

5.3.4.4.3 Type of Search: Standard

5.3.4.4.4 FST: 0.0b(1.0,1.0)

5.3.4.4.5 Assign sub-source LR: Y (check the box)

5.3.4.4.6 Extended output: N (do not check)

5.3.4.5 If deconvoluted in STRmix, the specimen information entered during the deconvolution will auto-populate. Add “CODIS_” in front of the name. “-DBSearch” will be added to the end of the name.

5.3.4.6 Click “Start.”

5.3.4.7 Evaluation of results: A “Database Search Report” window will open. Scroll down to the “LR RESULTS” section to see any candidate samples that are returned.

Note: For mixtures, it is important to remember that this search is a comparison to the entire mixture and all of its contributors, not just the contributor targeted in the CODIS search. If any comparisons were done to this sample with a reference standard, the candidate names shall be compared to any listed reference standards to determine if the match should be dispositioned as a Conviction Match.

5.3.4.7.1 If there are no candidates with an LR > 50,000, “No matches found at specified Minimum LR cutoff level” will be seen.

5.3.4.7.1.1 Print the report to .pdf with the naming convention “NM_” and add to the CODIS Matches folder for that day.

5.3.4.7.1.2 Close the report window and click the “Finish” button in the STRmix RESULTS window.

5.3.4.7.1.3 Disposition the matches as “No Matches” in CODIS.

5.3.4.7.2 If there are candidates with an LR > 50,000, they will be listed in the LR RESULTS area with the CASE NUMBER: CODIS, SAMPLE: CODIS Specimen ID, GENDER: if available, and LR result: written as “numberE__”.

5.3.4.7.2.1 If the LR is between 50,000 (5.0000E4) and 20 million (2.000E7), additional evaluation will be performed.

5.3.4.7.2.1.1 If the known candidate sample does not have information at the expanded loci (loci beyond the original 13 core loci), a request will be made for those additional loci to be tested. Once the additional testing is complete, the LR will be ran again with the updated data and the match will be re-evaluated.

5.3.4.7.2.1.2 If it is not possible to get any additional data and the LR is within this range, the candidate profile will be compared to the STRmix output in its entirety for that contributor to determine if there is additional information that can be used to make a match disposition determination.

5.3.4.7.2.2 For each case with an evaluation, print the report to .pdf with the naming convention “CODIS_Case#_Item#-DBSearch” and add the report and STRmix project to the CODIS Matches folder for that day.

5.3.4.7.2.3 Close the report window and click the “Finish” button in the STRmix RESULTS window.

5.3.4.7.2.4 Disposition the matches as appropriate in CODIS.

5.3.4.7.3 If Multiple candidates are returned from the database search of an item because it is a mixture, an LR from previous calculation may be performed with all of the candidates to show if it is possible for all of them to be contributors together. The Reference File Maker workbook is used for this purpose.

5.4 Use of COSTaR for reference profiles

5.4.1 The Reference File Maker is an Excel workbook that will create reference files compatible with the LR from Previous STRmix function from a STRmix database file (to generate an LR to determine which candidate best fits a specific contributor to a mixture) or from a reference sample not within GMID-X (e.g., older samples or samples from another lab). Note: This is not considered re-analysis, it is formatting the profiles into a specific text file so that they can be searched using STRmix.

5.4.1.1 If the known reference sample does not have the information at the expanded loci (loci beyond the original core 13 loci), a request will be made for those additional loci to be tested prior to performing this LR evaluation.

5.4.2 Reference File Maker workbook

5.4.2.1 Import of contributors of mixtures for LR from Previous Calculation

- 5.4.2.1.1** Open the “Reference File Maker” workbook of COSTaR.
- 5.4.2.1.2** In the Sample File column cell A2, enter the candidate sample CODIS specimen ID listed in the Database Search Report and hit Enter.
- 5.4.2.1.3** Click the “Choose Database” button and navigate to the appropriate Candidates.csv file in the folder and click Open.
- 5.4.2.1.4** Change the “Save as file type:” to Text (Tab delimited) .txt file and save as the candidate specimen ID. Click OK in the pop up.

5.4.2.2 Manual Entry for samples for comparison

- 5.4.2.2.1** Open the “Reference File Maker” workbook of COSTaR.
- 5.4.2.2.2** In the Sample File column cell A2, enter the identifier of the sample the STRMix compatible reference profile is being generated for and hit Enter.
- 5.4.2.2.3** Manually enter the DNA profile information for the reference sample appropriately into cells C2:D25 (Allele columns 1 and 2). Do not enter any partial loci.
- 5.4.2.2.4** The allele size will automatically populate for most alleles.
- 5.4.2.2.5** If your allele does not exist in the ladder (microvariant), you will have to interpolate the value from the two closest alleles.
- 5.4.2.2.6** Save as a .txt file that will serve as a reference file for STRmix and will be compatible with the LR from Previous function in STRmix.

5.4.3 STRmix LR from Previous Calculation

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- 5.4.3.1** In the “Investigation” module of STRmix, click on the “LR from Previous” module.
- 5.4.3.2** Navigate to the STRmix deconvolution folder for the mixture. Select the settings file and click Open. Click the “Select” button.
- 5.4.3.3** In the CASE DETAILS window, make the following changes:
- 5.4.3.3.1** Case Number: add “CODIS_” to the specimen ID for the mixture
 - 5.4.3.3.2** Sample ID: add the candidate sample (known) CODIS specimen ID to what is already populated
 - 5.4.3.3.3** Click the “Next” button
- 5.4.3.4** In the PROFILE DATA window, drag and drop the text file into the “Reference Profile Data” box. “_REF.csv” will be added to the name.
- 5.4.3.5** Click the “Start” button.
- 5.4.3.6** An “LR from Previous Report” window will open. Scroll down to the “PER LOCUS LIKELIHOOD RATIOS” section of the report and review the 99% 1-sided lower HPD intervals values.
- 5.4.3.6.1** If the lowest value is < 50,000:
 - 5.4.3.6.1.1** Print the report to .pdf with the naming convention “NM_” and add to the CODIS Matches folder for that day.
 - 5.4.3.6.1.2** Close the report window and click the “Finish” button in the STRmix RESULTS window.
 - 5.4.3.6.1.3** Disposition the matches as “No Matches” in CODIS.
 - 5.4.3.6.2** If the lowest value is > 50,000:
 - 5.4.3.6.2.1** If the LR is between 50,000 (5.0000E4) and 20 million (2.0000E7), additional evaluation will be performed.

5.4.3.6.2.1.1 The candidate profile will be compared to the STRmix output in its entirety for that contributor to determine if there is additional information that can be used to make a match disposition determination.

5.4.3.6.2.2 For each case with an evaluation, print the report to .pdf with the naming convention "CODIS_Case#-DBSearch" and add the report and STRmix project to the CODIS Matches folder for that day.

5.4.3.6.2.3 Close the report window and click the "Finish" button in the STRmix RESULTS window.

5.4.3.6.2.4 Disposition the matches as appropriate in CODIS.

6.0 Limitations – Samples that span the range of what may be encountered in casework were used for the validation of this program; however, not all situations that may occur with casework can be accounted for during a validation. When evidence profiles are modified in order to meet CODIS eligibility requirements, it is possible that data may be removed that will result in the sample not matching to the true contributor even if the person is present in the database. This risk was taken into account versus the risk of not being able to enter the profile at all. The COSTaR Suite is best used to assist in match evaluation of forensic samples that hit to multiple, complete known samples.

7.0 Safety – N/A

8.0 References

COSTaR v5.2 05182021 Instructions; emailed by Brian Burritt; July 30, 2021

9.0 Records – N/A

10.0 Attachments – N/A

Revision History		
Effective Date	Version Number	Reason
05/24/2024	2	5.1, 5.3.1, 5.3.2.2 – update wording to clarify COSTaR use; 5.1.3.5 – update table to match software settings; 5.3.2.3.2, 5.3.3.2.2, 5.3.4.3 – update file names; 5.3.4.7.2.1, 5.3.4.7.2.2, 5.4.1.1, 5.4.3.6.2 – update steps for additional evaluation