

matK-QR Classifier



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1. About *matK*-QR Classifier software

The quick response (QR) code was reported to have the capacity to coding for different alphabets, number, and symbols. With the resolve of the core DNA barcodes for the kingdoms of life, focus would now move towards the practical uses of DNA barcoding technologies. Here we introduced software tool that can represent *matK* gene specific signatures as QR codes library in practical application for taxonomic identification.

2. Contact

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3. Availability

The executable version of *matK-QR* Classifier with sample dataset and user manual are available in Appendix 25.

4. Installation

4.1. System Requirements

1. *matK-QR* Classifier was developed for use on Microsoft Windows® operating systems: Windows XP, 7 and 8 (32-bit).
2. The computer on which *matK-QR* Classifier is installed should meet the following hardware requirements:
 - Windows 7 or 8 (32-bit) is recommended.
 - The minimum computer requirements are at least 1 GB of RAM and 2 GB of available hard disk space with a Pentium® processor.
 - Microsoft .NET Framework 4 is required.
 - The more RAM and faster CPU (processor) supports the faster analysis and less processing time.

4.2. Steps to installation *matK-QR* Classifier on Windows

- i. Unzip '*matK-QR* Classifier' Windows installation package from Appendix 25.
- ii. Extract and Launch the downloaded setup.exe file and follow the Setup wizard by clicking next button as shown in following Figure 1.
- iii. After successful completion of setup, *matK-QR* Classifier icon appeared in Start Menu. User can find at location: (C:\Program files*matK-QR* Classifier). As well as shortcut icon present on Desktop.
- iv. User can click either of the option to open *matK-QR* Classifier software.
- v. If any error message occurred during the uploading files, please provide administrator permission to access C:\ using following steps (Start-Control Panel-User account and family safety-User account-Change user account control settings-Never notify- OK- Restart Computer).

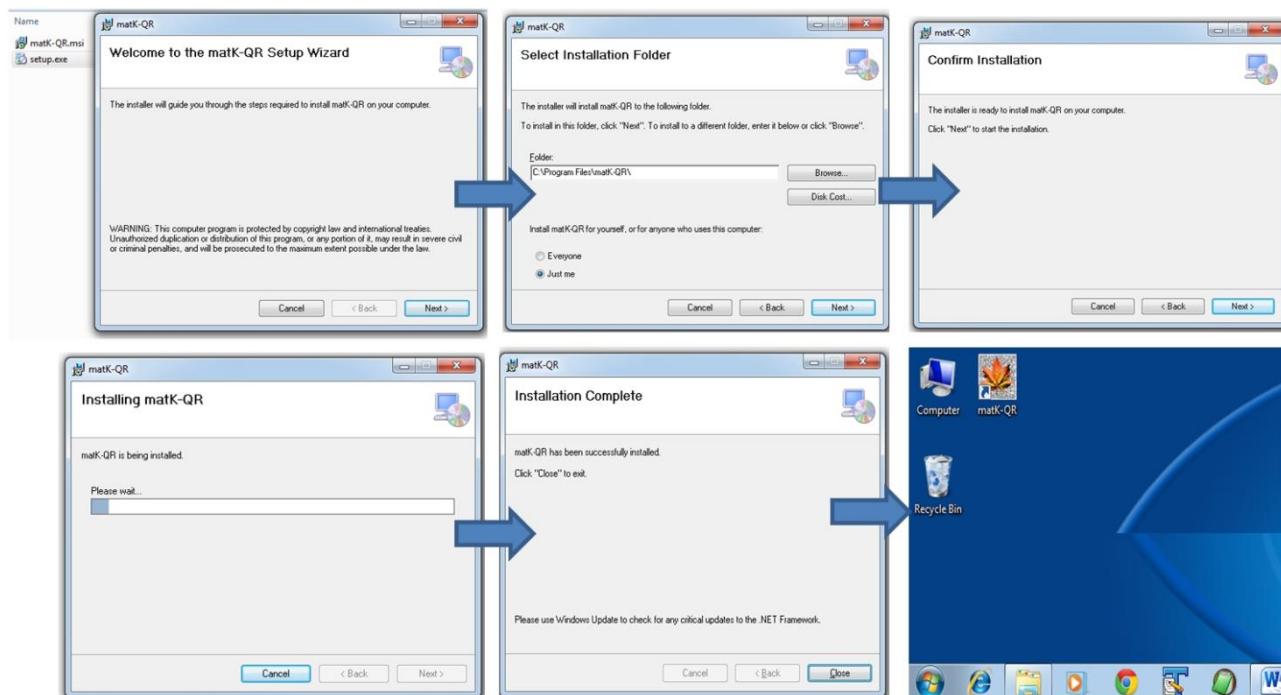


Figure 1: The screenshot of installation steps for *matK-QR* Classifier software.

5. An example of procedure to taxonomic identification

The following are simple steps to perform taxonomic identification:

Step 1: Click on Sequence menu - Open Sequence file – Sample Sequence File (Figure 2a) or Browse file (Figure 2b)

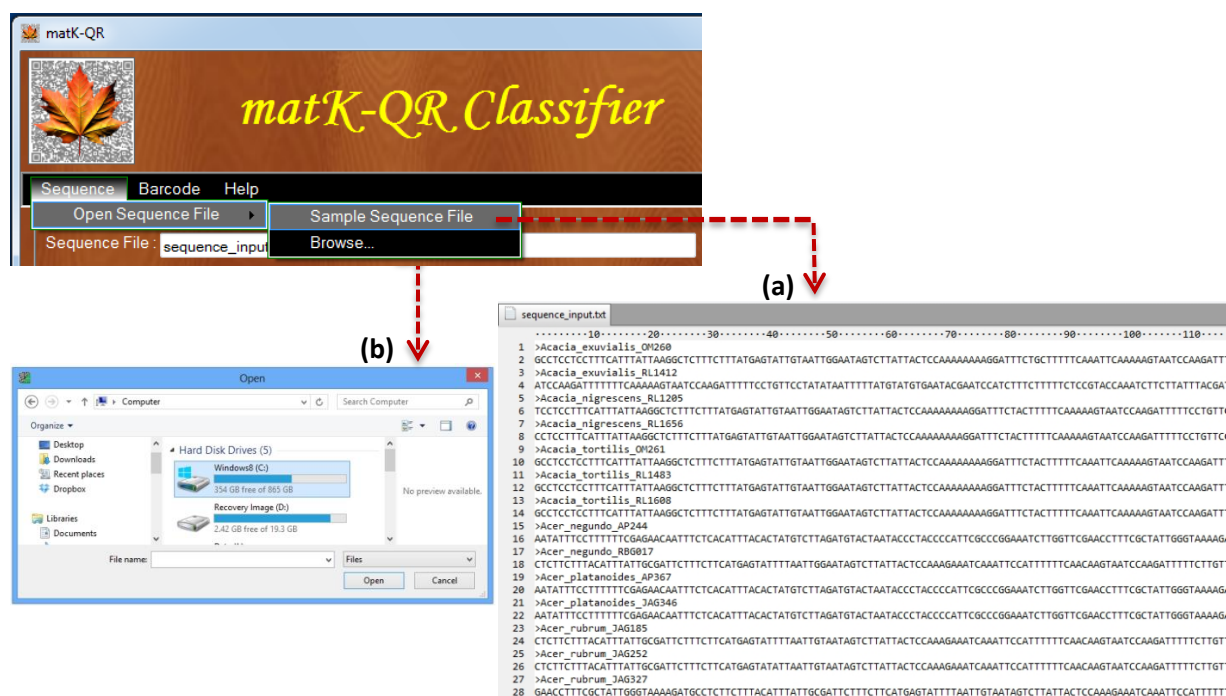


Figure 2: The screenshot of *matK*-QR classifier ‘Sequence’ menu.

Using this menu, user can select either ‘Sample Sequence File’ or upload *matK* sequences file from computer location using ‘Browse’ option as shown in Figure 2. Currently software accepts FASTA format *matK* sequences with .fasta/.txt/.fa/.seq/.fna extension file. Sample sequence file contains 345 studied sample *matK* sequences in this work.

Step 2: Click on Barcode Menu - Open QR DNA barcode – Sample QR DNA Barcode – Acacia (Genus).png (Figure 3a) OR Open Regular Expression (Figure 3b).

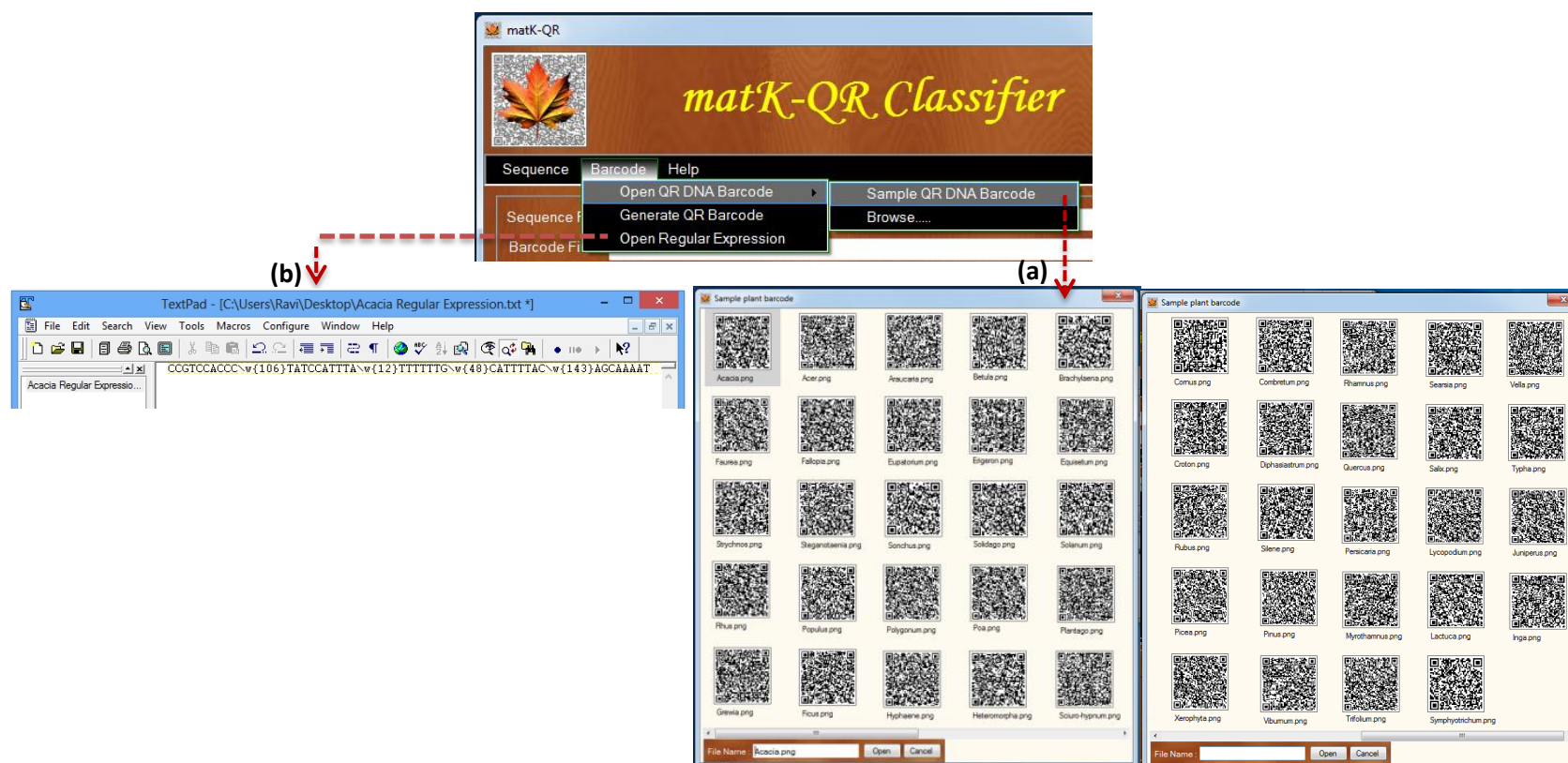


Figure 3: The screenshot of 'Barcode menu' window (a) QR-codes library (b) Regular expression

Using 'Barcode' menu, in 'Open QR DNA Barcode' option, user can select either single QR-code (Ex. Acacia.png as shown in Figure 3a) or open regular expression file (Figure 3b).

Step 3: Click on 'Search Barcodes' and then click on 'OK' show result window (Figure 4).



Figure 4: The screenshot of 'Search Barcode' window.

At this step, after click on 'Search Barcode' button (Figure 4), software perform regular expression based search of QR-code (signature) against *matK* sequences. Once analysis finished, click on OK of show result dialog box in order to view result summery.

Step 4: Click on ‘Export Output’ button and then choose desired folder to save output files (Figure 5).

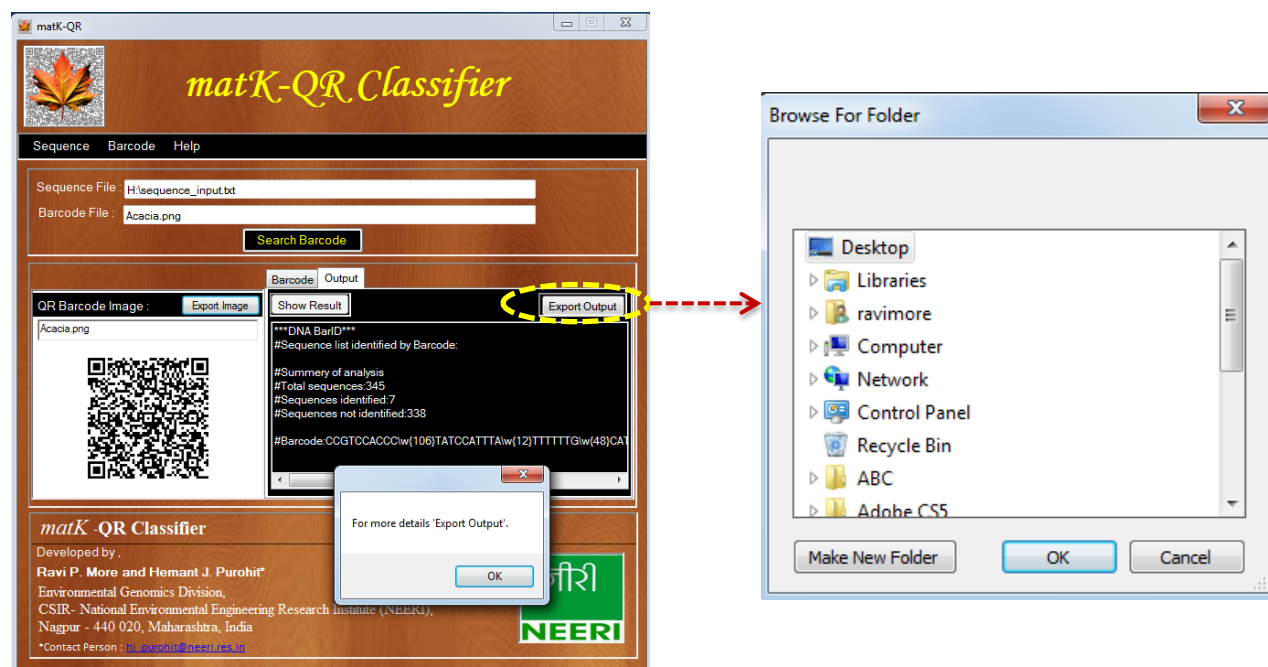


Figure 5: The screenshot of ‘Export Output’ window.

After click on ‘Export Output’ button, user can save output files in desired folder through ‘Browse for folder’ dialog as shown in Figure 5.

Step 5: Open target folder (Ex. Desktop/Result) and open output results files (Figure 6).

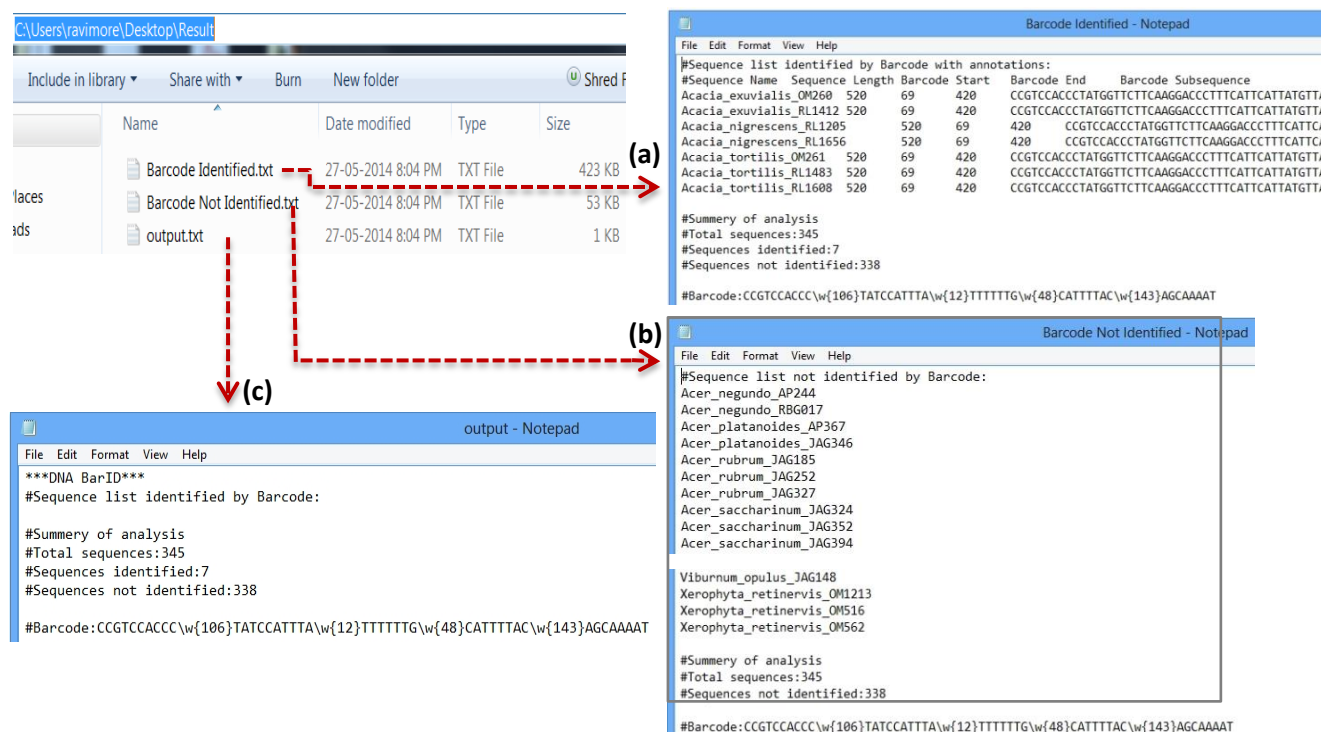


Figure 55: The screenshot of Results output file (a) Barcode Identified.txt (b) Barcode Not Identified.txt (c) output.txt.

Click on 'Barcode Identified.txt' tab-delimited file contains following fields: Sequence Name, Sequence Length, Barcode Start, Barcode End, and Barcode Subsequence (Figure 6a). In 'Barcode Not Identified.txt' file provides not identified sequence name list (Figure 6b). The 'output.txt' file contains the total, identified, not identified sequences list and input Barcode (Figure 6c). User can export these data into the spreadsheet software like Microsoft Excel for making structured database.