

Readme for DNA QR Code Web Server

Last modified by Chang Liu on Friday, February 24, 2012

This web server contains five different modules to support the conversion of QR codes and DNA barcode sequences, and QR code based species identification. These functions of these modules are described in more details below.

GetBarcode

This module allows a user to retrieve the consensus sequence and the QR code for a plant and animal species of interest. There are five different DNA barcode marker regions from which the user can retrieve the QR code, which are *rbcL*, *matK*, ITS2 and *psbA-trnH* for plant species, and *CO1* for animal species. The input is a taxid for the species of interest, which can be found from NCBI. To obtain the QR code for an individual sequence or for sequences representing any taxonomic groups such as genus, family, order, class, phylum and etc, please retrieve or construct the sequence first and then use the “Encode” module described below to create the QR code.

Encode

This module allows a user to input a sequence that is retrieved from public database or provided by the user. It will then encode the sequence into the QR code.

Decode

This module allows a user to input a QR code and then will decode the QR code into the original sequence.

IdentifyByBlast

This module takes a QR code as input. The output is the recommended species identity for the input QR code. This module first converts the QR code into its corresponding DNA sequence and then uses BLAST search against the reference database that contains individual-level DNA barcode sequences to determine its species identity. More technical details are provided in the paper describing this web server. Links were provided for the intermediate BLAST results. *It is strongly recommended that the users check the BLAST results carefully before accepting the recommended species identity.*

IdentifyByDistance

Similar to the “IdentifyByBlast” method, this module takes a QR code as input, and output the most likely species identity. This module first decodes the QR code into its corresponding DNA sequence and then performs a BLAST search against the reference database that contains individual-level DNA barcode sequences using

the DNA sequence as input. It will take the top hits from the BLAST results, retrieve the sequences, carry out the alignment of these multiple sequences and then build a phylogenetic tree using the neighbor-join methods. Its identity was determined based on its closest neighbors. More technical details are provided in the paper describing this web server. Links were provided for the BLAST results, the sequences for the top hits and the tree. *It is strongly recommended that the users check the intermediate results carefully before accepting the recommended species identity.*

If you have any questions or suggestions, please write to Dr. Chang Liu at cliu@implad.ac.cn or cliu6688@yahoo.com.