

This package mainly includes the following contents:

- 1) **LMMO\_TCBB.m**: the Matlab code that implements the LMMO method for refining motifs, with descriptions of how to use it.
- 2) **demo.m**: an example which uses LMMO to optimize the motif stored in the file named “Initial\_Motif.mat”.
- 3) **roc\_calculation.m**: the Matlab code for evaluating AUROC.
- 4) **Miscellaneous.zip**: the codes used for evaluating and running the compared methods in the LMMO paper, such as:
  1. **dreme.sh**: the shell file for running the DREME algorithm;
  2. **meme.sh**: the shell file for running the MEME algorithm;
  3. **homer2\_denovo.sh**: the shell file for running the HOMER algorithm;
  4. **homer2\_optimize\_PWM.sh**: the shell file for running the DREME+HOMER algorithm;
  5. **batching\_DiMO\_shuffle.R**: the R code for running the DiMO algorithm;
  6. **centriMo-training.sh**: the shell file for performing the Centrimo enrichment analysis;
  7. **shuffle\_1-order\_50-fold.sh**: the shell file for obtaining the negative set by shuffling the positive set using the HMMER package;
  8. **peak2seq\_positive.R**: the R code for obtaining the positive set;
  9. **generate\_positive\_negative\_sequences\_with\_n\_order\_markov\_1\_motif\_1\_decoy.R**: the R code for generating the synthetic data used in Section IV-C of the LMMO paper;
  10. **generate\_positive\_negative\_sequences\_with\_n\_order\_markov\_3\_motifs\_1\_decoy**: the R code for generating the synthetic data used in Section IV-D of the LMMO paper;
  11. **peak2seq\_intergenic\_sequences.R**: the R code for sampling the intergenic regions, which were used to learn the Markov model for generating the synthetic sequences;