Table 1. Detailed information of existing models

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Tool** | **Species** | **Experimental method** | **Sequence**  **length (nt)** | **Featuresa** | **Algorithm** | **Evaluation strategy** | **Year** | **Webserverb** | **Data sizec** |
| iRNA-Methyl | *SC* | m6A-Seq | 51 | PseDNC | SVM | Jackknife | 2015 | http://lin-group.cn/server/iRNA-Methyl | Smet1307 |
| m6Apred | *SC* | m6A-Seq | 21 | CPD | SVM | Jackknife  independent test | 2015 | http://lin-group.cn/server/m6Apred | Smet1307sub |
| pRNAm\_PC | *SC* | m6A-Seq | 51 | PseDNC, AC, CC | SVM | Jackknife | 2016 | decommissioned | Smet1307 |
| RNA-MethylPred | *SC* | m6A-Seq | 51 | DNC, KNN scores | SVM | Jackknife | 2016 | No | Smet1307 |
| M6A-HPCS | *SC* | m6A-Seq | 51 | HPCS | SVM | 10-fold CV | 2016 | decommissioned | Smet1307 |
| TargetM6A | *SC* | m6A-Seq | 21 | PSNP,  PSDP, NC | SVM | Jackknife, independent test | 2016 | decommissioned | Smet1307sub |
| RAM-ESVM | *SC* | m6A-Seq | 51 | PseDNC | Ensemble SVM | 10-fold CV | 2017 | decommissioned | Smet1307 |
| iRNA(m6A)-PseDNC | *SC* | m6A-Seq | 51 | PseDNC | SVM | 10-fold CV | 2018 | http://lin-group.cn/server/iRNA(m6A)-PseDNC.php | Smet1307 |
| M6APred-EL | *SC* | m6A-Seq | 51 | PS(k-mer)NP, RFHC-GACs, AC, CC | Ensemble (SVM) | 10-fold CV | 2018 | decommissioned | Smet1307 |
| DeepM6APred | *SC* | m6A-Seq | 51 | Deep features, NPPS | SVM | 10-fold CV | 2018 | decommissioned | Smet1307 |
| M6A-PXGB | *SC* | m6A-Seq | 51 | PSNP, PSDP, NC | XGBoost | 10-fold CV | 2019 | No | Smet1307 |
| m6A-pred | *SC* | m6A-Seq | 51 | CPD, DNC, TNC | RF | 10-fold CV | 2020 | No | Smet1307 |
| m6A-Finder | *SC* | m6A-Seq | 51 | AC, NC | SVM | Jackknife | 2022 | No | Smet1307 |
| iMethyl-Deep | *SC* | m6A-Seq,  m6A-CLIP, miCLIP | 51 | One-hot | CNN | 10-fold CV, independent test | 2020 | https://github.com/abdul-bioinfo/iMethyl-deep | Smet1307; Smet3270 |
| iMethyl-STTNC | *SC,HSA* | m6A-Seq | 51-41 | PseDNC, PseTNC, STNC, STTNC | SVM | 10-fold CV | 2018 | No | Smet1307;Hmet1130 |
| iRNA-PseColl | *HSA* | m6A-Seq | 41 | CPD | SVM | Jackknife | 2017 | http://lin-group.cn/server/iRNA-PseColl.html | Hmet1130 |
| iRNA-Mod-CNN | *HSA* | m6A-Seq | 41 | K-Gram | CNN | 5-fold CV | 2021 | No | Hmet1130 |
| HMpre | *HSA* | miCLIP | 51 | SLRF, FREI, SNP | XGBoost | Independent test | 2018 | No | 26512: 271214 |
| WHISTLE | *HSA* | m6A-CLIP, miCLIP | unknown | CPD, Genomic features | SVM | 5-fold CV, independent test | 2019 | No | 37899 (1:10) |
| m6Aboost | *HSA* | miCLIP | 21 | Experimental and sequence features | AdaBoost | 5-fold CV, independent test | 2021 | No | 11701:42090 |
| MultiRM | *HSA* | m6A-CLIP, miCLIP | 51 | One-hot | CNN+BiLSTM | Independent test | 2021 | decommissioned | 65178 (1:1) |
| DeepM6ASeq-EL | *HSA* | m6A-CLIP, miCLIP | unknown | One-hot, CPD, Word2vec | Ensemble (CNN+LSTM) | Independent test | 2022 | No | 37899 (1:10) |
| ConsRM | *HSA* | m6A-CLIP, m6A-REF-Seq, miCLIP | 11 | CPD, Genomic features | SVM | 5-fold CV, independent test | 2021 | http://180.208.58.19/conservation/ | 177998 (1:1) |
| MethyRNA | *HSA*, *MMU* | m6A-Seq, MeRIP-Seq | 41 | CPD | SVM | Jackknife | 2016 | http://lin-group.cn/server/MethyRNA | Hmet1130  Mmet725 |
| SRAMP | *HSA*, *MMU* | miCLIP | W | One-hot, SPE, KNN scores, PSSP | RF | 5-fold CV, independent test | 2016 | http://www.cuilab.cn/sramp/ | 57433, mRNA; 68083, full transcripts (1:10); |
| RNAMethPre | *HSA*, *MMU* | MiCLIP-seq, m6A-CLIP | 101 | One-hot, NC, SLS | SVM | 5-fold CV, independent test | 2016 | decommissioned | *HSA:* 29547, mRNA; 31728, full transcripts (1:1)  *MMU*:22740, mRNA; 24705, full transcripts (1:1) |
| iRNA-3typeA | *HSA*, *MMU* | m6A-Seq, MeRIP-Seq | 41 | CPD | SVM | Jackknife | 2018 | http://lin-group.cn/server/iRNA-3typeA.php | Hmet1130; Mmet725 |
| Gene2vec | *HSA*, *MMU* | MiCLIP-seq, m6A-CLIP | 1001 | One-hot, NMSE, word embedding | CNN+ensemble | 10-fold CV, independent test | 2019 | decommissioned | 495572 (1:10) |
| M6ATH | *At* | m6A-seq | 25 | CPD | SVM | Jackknife | 2016 | http://lin-group.cn/server/M6ATH | Amet394 |
| AthMethPre | *At* | m6A-seq, MeRIP-seq | 41 | One-hot, PIkmer | SVM | 5-fold CV, independent test | 2016 | decommissioned | 5081 (1:1) |
| RAM-NPPS | *SC*, *HSA*, *At* | m6A-Seq,  PA-m6A-seq | 51 | NPPS | SVM | 10-fold CV | 2017 | decommissioned | Smet1307; Hmet8366; Amet394 |
| m6A-word2vec | *SC*, *HSA*, *At* | m6A-Seq,  PA-m6A-seq | 51 | word embedding | CNN | 10-fold CV | 2020 | No | Smet1307; Hmet1130; Amet394 |
| m6AGE | *SC*, *HSA*, *At* | m6A-Seq,  PA-m6A-seq | 21-41-25-101 | Graph embedding, Sequence-Derived features (CTD, PseKNC, NPS, NPPS, CPD, EIIP, BPB) | CatBoost | 5-fold CV | 2021 | https://github.com/bokunoBike/m6AGE | Smet1307; Hmet1130; Amet394; Amet2518 |
| DeepM6ASeq | *HSA,* *Mouse,* *ZF* | miCLIP-Seq | 101 | One-hot | CNN+BiLSTM | 5-fold CV, independent test | 2018 | https://github.com/rreybeyb/DeepM6ASeq | *HSA*: 49050; *Mouse*: 37716; *ZF*: 22108 (1:1) |
| iN6-Methyl (5-step) | *SC, HSA,* *MMU* | m6A-seq, MeRIP-seq | 51-41-41 | word embedding | CNN | 10-fold CV | 2019 | decommissioned | Smet1307; Hmet1130;Mmet725 |
| Chong et al. | *SC, HSA,* *MMU* | m6A-seq, MeRIP-seq | 51-41-41 | k-mer | CNN | 10-fold CV | 2021 | No | Smet1307; Hmet1130; Mmet725 |
| MM-m6APred | *SC, HSA,* *MMU* | m6A-seq, MeRIP-seq | 51-41-41 | Probability matrix | Second-order Markov | 10-fold CV | 2021 | decommissioned | Smet1307; Hmet1130; Mmet725 |
| M6AMRFS | *SC, HSA,* *MMU*, *At* | m6A-seq, MeRIP-seq | 51-41-41-101 | One-hot; LPSDF | XGBoost | 5-fold CV, independent test | 2018 | decommissioned | Smet1307; Hmet1130; Mmet725*;* Amet2100 |
| bCNN-Methylpred | *SC, HSA,* *MMU*, *At* | m6A-seq, MeRIP-seq, miCLIP-seq | 51-41-41-101 | Circular encoding, One-hot, NCP | CNN | 10-fold CV | 2021 | https://github.com/Naeem-jbnu/RNA\_Modification\_Sites | Smet1307; Hmet1130; Mmet725*;* Amet1000 |
| m6A-NeuralTool | *SC, HSA,* *MMU*, *At* | m6A-seq, MeRIP-seq | 51-41-41-101 | One-hot | Ensemble (CNN, SVM, NB) | 10-fold CV, independent test | 2021 | http://nsclbio.jbnu.ac.kr/tools/m6A-NeuralTool/ | Smet3270; Hmet1130; Mmet725*;* Amet2100 |
| TL-Methy | *SC, HSA,* *MMU*, *Rice* | m6A-seq, MeRIP-seq | 51-41-41-41 | NAC, DNC, TNC, PSTNP, BPB, One-hot, CPD | Ensemble (SVM, KNN, LR, DA) | 10-fold CV | 2022 | https://github.com/LDWang-dlmu/N6-methyladenine | Smet1307; Hmet1130;Mmet725*;* Rmet880; |
| M6A-BiNP | *SC, HSA, MMU*, *Rat,* *At* | m6A-seq, MeRIP-seq, miCLIP-seq, m6A-REF-seq | 51-41-41-41-25 | PSP-PMI, PSP-PJMI | SVM | 10-fold CV | 2021 | https://github.com/Mingzhao2017/M6A-BiNP | Smet1307; Hmet1130; Mmet725*;* Amet394; Species/tissues-specific datasets; Human51  (1:1) |
| M6A-GSMS | *SC, HSA,* *MMU*, *At, DM* | m6A-seq, MeRIP-seq | 51-41-41-101-41 | NMBAC, PC-PseDNC-General, PseDPC, One-hot, K-mer | Ensemble (RF, ET, SVM, LGBM, Bagging, Adaboost) | 10-fold CV | 2021 | https://github.com/Wang-Jinyue/M6A-GSMS | Smet1307; *HSA*:5100; *MMU:725;* *At*:2100; DM:300  (1:1) |
| MASS | *HSA*, *MMU*, *Chim*, *Rhesus*, *Pig*, *Rat*, *ZF* | m6A-Seq, MeRIP-Seq, m6A-CLIP, miCLIP-seq | 101 | One-hot, Phylogenetic tree | CNN+BiLSTM | 5-fold CV | 2021 | https://github.com/mlcb-thu/MASS | *HSA:*305644;  *MMU*:317702; *Chim:*26248; *Rhesus:*27059; *Pig:*81501; *Rat:*41735; *ZF:*19834 (1:10) |
| iRNA-m6A | *HSA*, *MMU*, *Rat* | m6A-REF-seq | 41 | AC, CC, CPD, One-hot | SVM | 5-fold CV, independent test | 2020 | http://lin-group.cn/server/iRNA-m6A/ | TSdata |
| im6A-TS-CNN | *HSA*, *MMU*, *Rat* | m6A-REF-seq | 41 | One-hot | CNN | 5-fold CV, independent test | 2020 | No | TSdata |
| Jia et al. | *HSA*, *MMU*, *Rat* | m6A-REF-seq | 41 | One-hot, Sequence feature, KNFR | Ensemble (CNN+capsule+BiGRU) | 5-fold CV, independent test | 2022 | No | TSdata |
| DNN-m6A | *HSA*, *MMU*, *Rat* | m6A-REF-seq | 41 | One-hot, TNC, ENAC, KSNPFs, CPD, PseDNC, PSNP, PSDP | DNN | 5-fold CV, independent test | 2021 | https://github.com/GD818/DNN-m6A | TSdata |
| TS-m6A-DL | *HSA*, *MMU*, *Rat* | m6A-REF-seq | 41 | One-hot | CNN | 5-fold CV, independent test | 2021 | http://nsclbio.jbnu.ac.kr/tools/TS-m6A-DL/ | TSdata |

aPseDNC: pseudo dinucleotide composition; DNC: dinucleotide composition; AC: Auto-covariance; CC: cross-covariance; HPCS: heuristic nucleotide physical-chemical property selection; KNN scores: K-nearest neighbor encoding; PIkmer: Position-independent k-mer frequency; PSNP: Position-specific nucleotide propensity; PSDP: Position-specific dinucleotide propensity; NC: Nucleotide composition; PS(k-mer)NP: position-specific k-mer nucleotide propensity; NCP: Nucleotide Chemical Property; CPD: Chemical Property with Density, RFHC-GAC: a method integrating by CPD, AC and CC; NPPS: nucleotide pair position specificity; PseTNC: Pseudo-Trinucleotide-Composition; STNC: Split-Trinucleotide-Composition; STTNC: Split-Tetranucleotide-Composition; PSSP: predicted secondary structure pattern; Spectrum encoding: Nucleotide pair spectrum encoding; SLS: Stability of the local structure; One-hot: Binary encoding; SPE: Spectrum encoding, SLRF: site location related features, FREI: features related to entropy information, SNP: single nucleotide polymorphism features; LPSDF: Local Position-Specific Dinucleotide Frequency; MMSE: Neighboring methylation state encoding; KSNPFs: K-Spaced Nucleotide Pair Frequencies.

bdecommissioned—the webserver/tool is no longer available; no—the publication has no webserver or tool.

cSmet1307: a dataset of m6A sites in the *S. cerevisiae* genome, consisting of 1307 positive samples and 1307 negative samples with 51 nucleotides; Smet1307sub: a subset of Smet1307, of which the 832 m6A sites with distances to the detected m6A-seq peaks less than 10 bp were selected as positive samples; Hmet1130: a dataset of m6A sites in the *H. sapiens* genome, consisting of 1130 positive samples and 1130 negative samples with 41 nucleotides.