



Research article

TYLER, a fast method that accurately predicts cyclin-dependent proteins by using computation-based motifs and sequence-derived features

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Supplementary

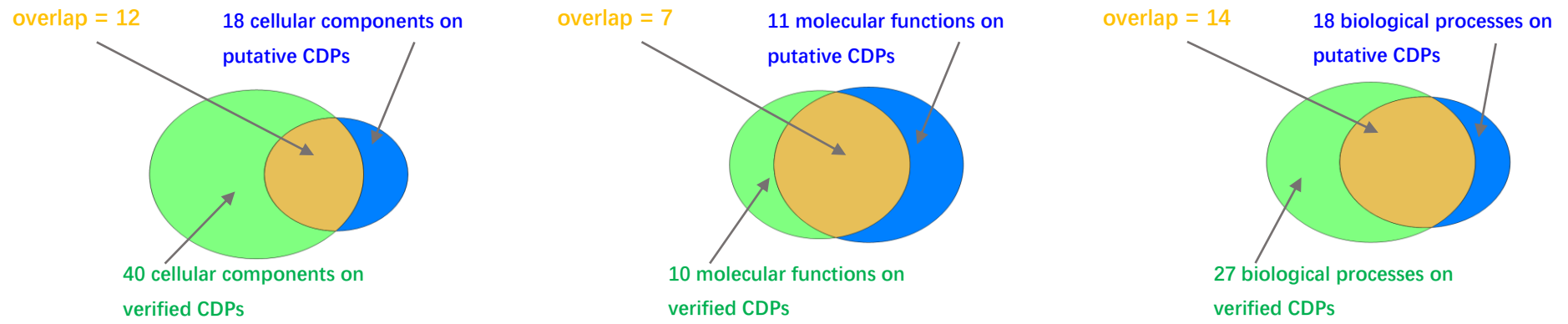


Figure S1. Each set and the overlap of significantly enriched subcellular locations and functions in verified and putative CDPs.

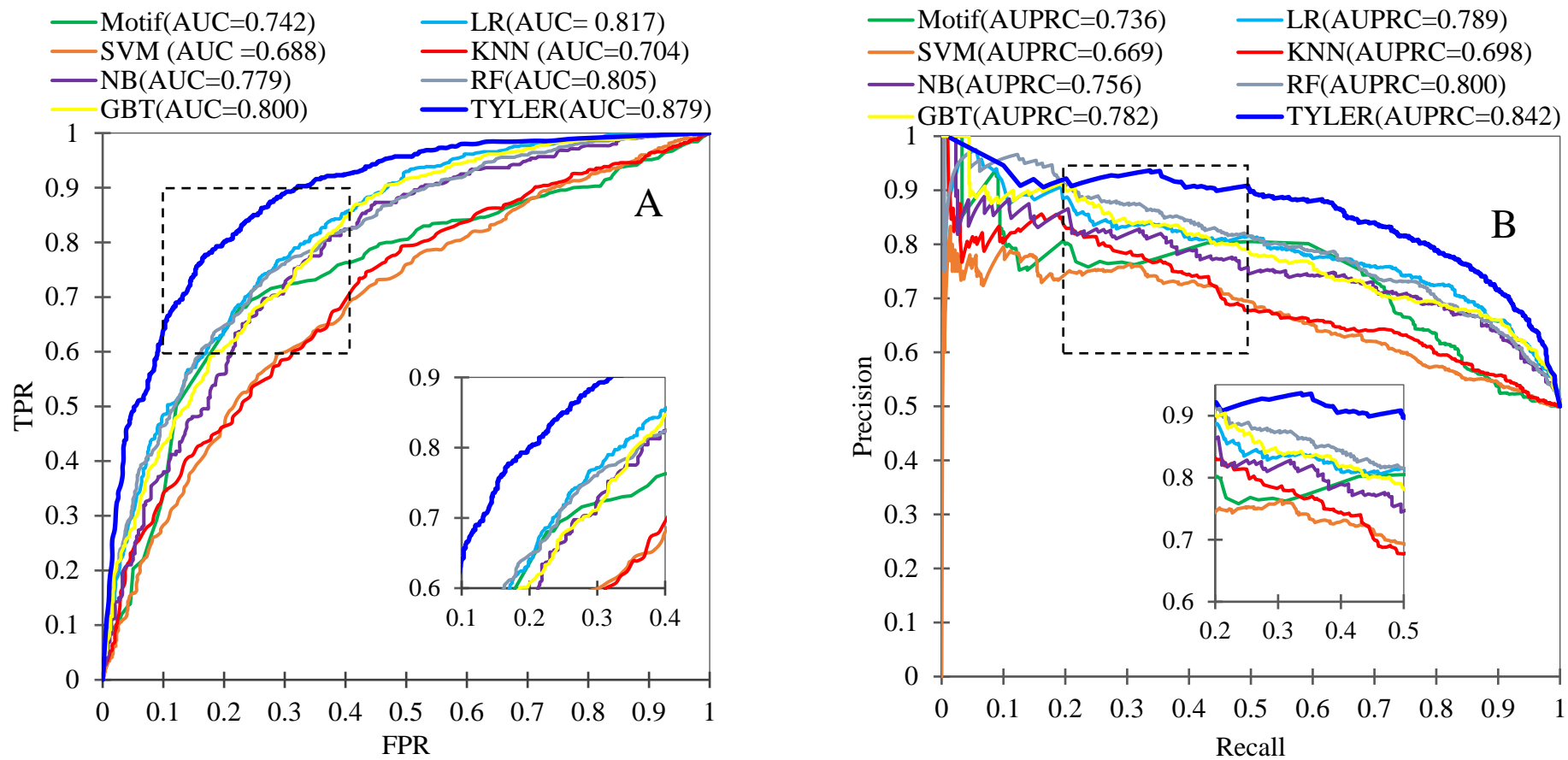


Figure S2. ROC curves and PRC curves for different methods on the TRAINING dataset.

Table S1. Description of features that are utilized for construction of the machine learning model.

Feature type	Description	Number of features	Number of features per feature type
Evolutionary profile	Normalized position-specific substitution scores of hydroxylic residues that substituted by same group of hydroxylic residues	11	121
	Normalized position-specific substitution scores of tiny residues that substituted by same group of tiny residues	11	
	Normalized position-specific substitution scores of small residues that substituted by same group of small residues	11	
	Normalized position-specific substitution scores of acidic residues that substituted by same group of acidic residues	11	
	Normalized position-specific substitution scores of positive residues that substituted by same group of positive residues	11	
	Normalized position-specific substitution scores of polar residues that substituted by same group of polar residues	11	
	Normalized position-specific substitution scores of charged residues that substituted by same group of charged residues	11	
	Normalized position-specific substitution scores of hydrophobic residues that substituted by same group of hydrophobic residues	11	
	Normalized position-specific substitution scores of aromatic residues that substituted by same group of aromatic residues	11	
	Normalized position-specific substitution scores of sulphur residues that substituted by same group of sulphur residues	11	
	Normalized position-specific substitution scores of aliphatic residues that substituted by same group of aliphatic residues	11	
Secondary structure	Fraction of residues located on the helix/sheet/coil of the protein	3	30
	Fraction of helix/sheet/coil segments within the protein	3	
	Fraction of residues in a given secondary structure motif type in the sequence (XHE, XHC, XEH, XEC, XCH, XCE, HEX, HCX, EHX, ECX, EHX, ECX, CHC, CHE, EHC, EHE, HCH, ECH, HCE, ECE, CEC, HEC, CEH, HEH)	24	
Physicochemical Properties	Fraction of {hydroxylic, tiny, small, acidic, positive, polar, charged, hydrophobic, aromatic, sulphur, aliphatic} residues within the protein	11	33
	Fraction of {hydroxylic, tiny, small, acidic, positive, polar, charged, hydrophobic, aromatic, sulphur, aliphatic} residues within longest secondary structure segment	11	
	Fraction of {hydroxylic, tiny, small, acidic, positive, polar, charged, hydrophobic, aromatic, sulphur, aliphatic} residues within longest secondary structure motif	11	
TOTAL			184

Table S2. Selective enriched motifs in CDPs. The motifs are ranked by descending order of IGR.

1	ADFGLAR	16	S-H -[T Q R] S[E Q N]	31	LE-CA	46	GC-I-F
2	YR-PELLL	17	S-FK-S	32	L [I M] [D G] [W H]	47	FESP
3	Y-[D- K-C]	18	RP[S P R Y] [P T S N R] [P T S R]	33	L[A D] [C R] [K F] L	48	EY-R-H
4	W[L- LI-] E-V	19	RLNL	34	L-W-Y-R	49	ES-Q-S
5	W-Y-R-P	20	QSS-P	35	L-KPQ	50	EME-D
6	V -V-V-T-WY -R -P	21	QL-LC	36	K[K L] [I C] [K G]	51	E-S[DP PT]
7	TR-SC	22	Q[K T] [V P] [Q K]	37	K-S[PP TR]	52	E-[E I] W [R P]
8	T- LWY	23	Q-Q-H-H	38	K-R[RI SN]	53	DR[F Y]LS
9	SSH-[S T]	24	P[G L Q] [P K H] [E P Q]	39	K-I-ADFG-AR	54	DI-TN
10	SRRR	25	P-SPK	40	ISP-K	55	DFGL-A
11	SPV-K	26	NNEN	41	IQN-S	56	DEDEE
12	SP-F - P N] K	27	N[I Y]-D[T R]	42	I-D-M-W	57	D-M-W-[S VGC]
13	SN-QN	28	MHRD	43	HS-KR	58	CIF-[A E]
14	SLSS-S	29	LK-PQ	44	H-R-D-L-K	59	C[C L]-[L H]C
15	S-L-SS-S	30	LH-R-D	45	GDDD	60	C-E-FS