

Supplementary Document

(MTDriverGNN: MTDriverGNN: Multitask Learning Graph Neural Network for Cancer Driver Gene Prioritization)

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Table 1. Comparison of MTDriverGNN with baseline methods across 12 cancer types, evaluated using AUPRC.

Cancer	MTDriverGNN	EMOGI	MTGCN	DGHNN
BRCA	0.7306	0.6482	0.6583	0.6832
BLCA	0.7155	0.5485	0.6568	0.6935
LUAD	0.6653	0.5591	0.6279	0.6410
LIHC	0.5076	0.3845	0.4645	0.4811
THCA	0.3533	0.2587	0.2907	0.3145
LUSC	0.4461	0.2222	0.3099	0.4054
ESCA	0.5027	0.4174	0.4721	0.4763
PRAD	0.7468	0.5233	0.6143	0.7058
STAD	0.7240	0.4604	0.5931	0.6449
COAD	0.5353	0.3459	0.3816	0.4468
UCEC	0.7121	0.4020	0.4954	0.5342
CESC	0.5715	0.5547	0.5972	0.5635

Table 2. Performance of Single-task and Multi-task settings across 12 cancer types, evaluated using AUPRC.

Cancer	Single-task	Multi-task
BRCA	0.6233	0.7110
BLCA	0.7104	0.7028
LUAD	0.6473	0.6508
LIHC	0.4556	0.4863
THCA	0.2435	0.3107
LUSC	0.3054	0.4197
ESCA	0.4000	0.4926
PRAD	0.6577	0.7021
STAD	0.6796	0.6938
COAD	0.3978	0.5136
UCEC	0.5750	0.6837
CESC	0.5098	0.4628

Table 3. Comparison of MTDriverGNN without and with pretraining across 12 cancer types, evaluated using AUPRC.

Cancer	W/O Pretraining	Pretraining
BRCA	0.7110	0.7306
BLCA	0.7028	0.7155
LUAD	0.6508	0.6653
LIHC	0.4863	0.5076
THCA	0.3107	0.3533
LUSC	0.4197	0.4461
ESCA	0.4926	0.5027
PRAD	0.7021	0.7468
STAD	0.6938	0.7240
COAD	0.5136	0.5353
UCEC	0.6837	0.7121
CESC	0.4628	0.5715

Table 4. Summary statistics of feature counts and gene counts across 12 cancer types.

	BRCA	BLCA	LUAD	THCA	LIHC	LUSC	ESCA	PRAD	STAD	COAD	UCEC	CESC
Mutation-derived features	4	4	4	4	4	4	4	4	4	4	4	4
Pathway-derived features	8	6	7	5	11	7	5	8	8	9	8	14
Total features	12	10	11	9	15	11	9	12	12	13	12	18
Driver genes	202	95	179	72	82	26	89	57	94	155	78	18
Passenger genes	2187	2187	2187	2187	2187	2187	2187	2187	2187	2187	2187	2187