Genomics Track results, categorization task — National Library of Medicine - University of Maryland

allele subtask

Run	TP	FP	FN	Precision	Recall	F beta	Utility Factor	Raw	Max	Normalized
NLM2A	292	382	40	0.4332	0.8795	0.5805	17.00	4582	5644	0.8118
aNLMB	312	608	20	0.3391	0.9398	0.4984	17.00	4696	5644	0.8320
aNLMF	176	617	156	0.2219	0.5301	0.3129	17.00	2375	5644	0.4208

expression subtask

Run	TP	FP	FN	Precision	Recall	F beta	Utility Factor	Raw	Max	Normalized
NLM2E	67	167	38	0.2863	0.6381	0.3953	64.00	4121	6720	0.6132
eNLMF	24	162	81	0.1290	0.2286	0.1649	64.00	1374	6720	0.2045
eNLMKNN	25	457	80	0.0519	0.2381	0.0852	64.00	1143	6720	0.1701

go subtask

Run	TP	FP	FN	Precision	Recall	F beta	Utility Factor	Raw	Max	Normalized
NLM1G	280	606	238	0.3160	0.5405	0.3989	11.00	2474	5698	0.4342
NLM2G	293	616	225	0.3223	0.5656	0.4107	11.00	2607	5698	0.4575
gNLMF	314	1350	204	0.1887	0.6062	0.2878	11.00	2104	5698	0.3693

tumor subtask

Run	TP	FP	FN	Precision	Recall	F beta	Utility Factor	Raw	Max	Normalized
NLM1T	13	147	7	0.0813	0.6500	0.1444	231.00	2856	4620	0.6182
NLM2T	13	147	7	0.0813	0.6500	0.1444	231.00	2856	4620	0.6182
tNLMF	11	521	9	0.0207	0.5500	0.0399	231.00	2020	4620	0.4372