

Genomics Track results, categorization task — Rutgers University (DIMACS team)

allele subtask

Run	TP	FP	FN	Precision	Recall	F beta	Utility Factor	Raw	Max	Normalized
aDIMACSG9md	294	358	38	0.4509	0.8855	0.5976	17.00	4640	5644	0.8221
aDIMACSG9w	289	303	43	0.4882	0.8705	0.6255	17.00	4610	5644	0.8168
aDIMACSI9md	301	482	31	0.3844	0.9066	0.5399	17.00	4635	5644	0.8212
aDIMACSI9w	298	386	34	0.4357	0.8976	0.5866	17.00	4680	5644	0.8292

expression subtask

Run	TP	FP	FN	Precision	Recall	F beta	Utility Factor	Raw	Max	Normalized
eDIMACSG9md	77	412	28	0.1575	0.7333	0.2593	64.00	4516	6720	0.6720
eDIMACSG9w	88	272	17	0.2444	0.8381	0.3785	64.00	5360	6720	0.7976
eDIMACSI9md	76	645	29	0.1054	0.7238	0.1840	64.00	4219	6720	0.6278
eDIMACSI9w	95	374	10	0.2026	0.9048	0.3310	64.00	5706	6720	0.8491

go subtask

Run	TP	FP	FN	Precision	Recall	F beta	Utility Factor	Raw	Max	Normalized
gDIMACSG9md	326	963	192	0.2529	0.6293	0.3608	11.00	2623	5698	0.4603
gDIMACSG9w	309	813	209	0.2754	0.5965	0.3768	11.00	2586	5698	0.4538
gDIMACSI9md	340	1062	178	0.2425	0.6564	0.3542	11.00	2678	5698	0.4700
gDIMACSI9w	346	1066	172	0.2450	0.6680	0.3585	11.00	2740	5698	0.4809

tumor subtask

Run	TP	FP	FN	Precision	Recall	F beta	Utility Factor	Raw	Max	Normalized
tDIMACSG9md	20	340	0	0.0556	1.0000	0.1053	231.00	4280	4620	0.9264
tDIMACSG9w	20	262	0	0.0709	1.0000	0.1325	231.00	4358	4620	0.9433
tDIMACSI9md	19	569	1	0.0323	0.9500	0.0625	231.00	3820	4620	0.8268
tDIMACSI9w	20	430	0	0.0444	1.0000	0.0851	231.00	4190	4620	0.9069