

Fibonacci and k -Subsecting Recursive Feature Elimination: Supplementary Material

Dariusz Brzezinski *

Keywords: feature selection, filter-wrapper methods, recursive feature elimination, Fibonacci search

Data Availability

To promote reproducible research, the results presented in this supplement are also available as reproducible R script at https://github.com/dabrze/subsecting_rfe in the **results** folder. The repository also includes experimental scripts, datasets, and result files. The data display items presented in this supplement can be reproduced using scripts provided in the aforementioned source code repository.

A. Supplementary Tables

*Institute of Computing Science, Poznan University of Technology, Poznan, Poland dariusz.brzezinski@cs.put.poznan.pl

A.1. SVM

Table S1. Average number of selected features using wrapped SVM for each dataset. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3-SRFE	RFE ₃	5-SRFE	RFE ₅	10-SRFE	RFE ₁₀
ALLAML	1142	1417	480	1253	568	1170	137	1316
arcene	5340	9198	5760	8852	5773	8585	5825	8482
BASEHOCK	3386	3428	3418	2617	3538	3121	2970	3058
Carcinom	3191	626	2127	605	1687	570	603	526
CLL-SUB-111	3228	3550	2867	1713	1831	1804	1168	1929
COIL20	761	628	571	630	552	636	664	550
colon	510	785	362	491	511	268	445	518
gisette	2952	1990						
GLI-85	2047	15699	1602	16102	1608	16054	2039	16105
GLIOMA	450	1579	222	1198	288	1239	238	874
Isolet	525	529	517	530	510	517	491	516
leukemia	888	3990	449	4352	544	2288	69	2502
lung	791	2017	507	1752	559	1609	578	1546
lung_small	149	174	117	65	119	72	105	97
lymphoma	655	1271	369	1467	647	960	555	1518
madelon	276	20	80	5	6	3	3	5
nci9								
ORL	450	498	348	468	366	472	364	511
orlraws10P	2270	7930	3685	8007	3790	7748	3445	8036
PCMAC	1881	1715	2424	1240	2484	1167	1831	1334
pixraw10P	987	7946	701	8028	714	8066	679	8064
Prostate-GE	979	4013	930	1338	788	1935	1106	1391
RELATHE	3929	3250	3281	3266	3314	2839	3378	3080
TOX-171	2740	2203	2000	2460	2450	1652	2046	2266
USPS	216	173	183	120	160	134	143	115
warpAR10P	988	1023	734	1014	765	1000	629	977
warpPIE10P	982	2048	284	2104	311	2083	315	2100
Yale	931	855	803	882	860	865	868	884

Table S2. Processing time using wrapped SVM for each dataset [s]. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3-SRFE	RFE ₃	5-SRFE	RFE ₅	10-SRFE	RFE ₁₀
ALLAML	6	18	10	49	10	41	15	50
arcene	57	49	191	120	145	107	168	132
BASEHOCK	638	457	1893	1094	1409	900	1378	1116
Carcinom	76	93	156	235	95	207	95	246
CLL-SUB-111	40	49	94	128	65	109	60	134
COIL20	131	95	275	191	215	174	245	211
colon	2	1	4	5	4	6	4	6
gisette	2581	2291	3600	3600	3600	3600	3600	3600
GLI-85	29	39	75	102	60	85	73	96
GLIOMA	3	5	4	15	5	14	6	24
Isolet	139	87	306	142	273	146	273	175
leukemia	9	16	14	45	13	40	15	47
lung	19	28	33	77	41	67	47	79
lung_small	0	0	1	1	1	1	1	1
lymphoma	21	26	30	78	44	68	43	76
madelon	98	101	83	121	75	136	113	181
nci9	3600	3600	3600	3600	3600	3600	3600	3600
ORL	14	13	30	29	24	25	27	28
orlraws10P	49	51	131	126	104	107	139	133
PCMAC	405	357	997	622	924	652	865	837
pixraw10P	20	46	35	123	30	106	44	127
Prostate-GE	12	21	31	59	23	49	32	57
RELATHE	453	254	943	502	792	495	903	608
TOX-171	49	50	145	128	112	108	122	124
USPS	160	112	320	186	250	189	274	226
warpAR10P	20	24	23	62	25	55	25	65
warpPIE10P	27	26	13	59	13	54	22	70
Yale	6	2	8	4	7	4	8	4

Table S3. Average classification accuracy using wrapped SVM for each dataset. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3- SRFE	RFE ₃	5- SRFE	RFE ₅	10- SRFE	RFE ₁₀	All
ALLAML	0.971	0.983	0.971	0.983	0.971	0.983	0.971	0.983	0.983
arcene	0.904	0.904	0.904	0.904	0.904	0.904	0.904	0.904	0.909
BASEHOCK	0.939	0.939	0.942	0.937	0.942	0.939	0.939	0.940	0.941
Carcinom	0.921	0.940	0.939	0.947	0.934	0.941	0.953	0.941	0.927
CLL-SUB-111	0.785	0.766	0.784	0.782	0.775	0.784	0.804	0.766	0.775
COIL20	0.986	0.985	0.988	0.985	0.988	0.988	0.988	0.988	0.987
colon	0.805	0.824	0.824	0.824	0.840	0.824	0.824	0.840	0.807
gisette	0.971	0.973							0.974
GLI-85	0.918	0.907	0.896	0.907	0.896	0.907	0.896	0.907	0.907
GLIOMA	0.769	0.802	0.765	0.794	0.808	0.827	0.794	0.794	0.788
Isolet	0.946	0.945	0.947	0.944	0.944	0.944	0.945	0.945	0.947
leukemia	0.954	0.983	0.983	0.983	0.983	0.983	0.971	0.983	0.967
lung	0.960	0.965	0.960	0.965	0.955	0.965	0.960	0.961	0.965
lung_small	0.886	0.896	0.905	0.896	0.866	0.896	0.896	0.886	0.886
lymphoma	0.975	0.949	0.968	0.948	0.975	0.956	0.968	0.948	0.941
madelon	0.538	0.607	0.580	0.583	0.572	0.582	0.583	0.572	0.500
nci9									
ORL	0.983	0.980	0.985	0.983	0.983	0.983	0.983	0.985	0.980
orlraws10P	0.990	0.980	0.970	0.980	0.970	0.970	0.990	0.980	0.980
PCMAC	0.820	0.829	0.827	0.827	0.819	0.820	0.832	0.829	0.823
pixraw10P	0.990	0.990	0.990	0.990	0.980	0.990	0.980	0.990	0.990
Prostate-GE	0.911	0.911	0.921	0.911	0.901	0.911	0.901	0.911	0.901
RELATHE	0.860	0.858	0.858	0.856	0.854	0.858	0.857	0.853	0.858
TOX-171	0.796	0.797	0.791	0.789	0.791	0.791	0.786	0.796	0.825
USPS	0.957	0.958	0.958	0.960	0.959	0.959	0.958	0.960	0.958
warpAR10P	1.000	1.000	1.000	1.000	0.995	1.000	0.995	1.000	0.990
warpPIE10P	0.990	0.995	0.960	0.995	0.960	0.995	0.955	0.995	0.995
Yale	0.803	0.810	0.797	0.810	0.797	0.810	0.790	0.810	0.817

Table S4. Average macro recall using wrapped SVM for each dataset. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3- SRFE	RFE ₃	5- SRFE	RFE ₅	10- SRFE	RFE ₁₀	All
ALLAML	0.965	0.975	0.965	0.975	0.965	0.975	0.965	0.975	0.975
arcene	0.903	0.903	0.903	0.903	0.903	0.903	0.903	0.903	0.909
BASEHOCK	0.939	0.939	0.942	0.937	0.942	0.939	0.939	0.940	0.941
Carcinom	0.887	0.918	0.917	0.926	0.902	0.914	0.933	0.917	0.896
CLL-SUB-111	0.839	0.826	0.838	0.839	0.833	0.839	0.853	0.826	0.831
COIL20	0.986	0.985	0.988	0.985	0.988	0.988	0.988	0.988	0.987
colon	0.783	0.808	0.808	0.808	0.833	0.808	0.808	0.833	0.796
gisette	0.971	0.973							0.974
GLI-85	0.875	0.858	0.850	0.858	0.850	0.858	0.850	0.858	0.858
GLIOMA	0.746	0.779	0.746	0.771	0.783	0.804	0.771	0.771	0.767
Isolet	0.946	0.945	0.947	0.944	0.944	0.944	0.945	0.945	0.947
leukemia	0.953	0.975	0.975	0.975	0.975	0.975	0.965	0.975	0.950
lung	0.925	0.938	0.925	0.938	0.905	0.938	0.925	0.936	0.938
lung_small	0.829	0.843	0.850	0.843	0.814	0.843	0.843	0.836	0.829
lymphoma	0.961	0.928	0.959	0.913	0.961	0.930	0.959	0.913	0.911
madelon	0.538	0.607	0.580	0.583	0.572	0.582	0.583	0.572	0.500
nci9									
ORL	0.983	0.980	0.985	0.983	0.983	0.983	0.983	0.985	0.980
orlraws10P	0.990	0.980	0.970	0.980	0.970	0.970	0.990	0.980	0.980
PCMAC	0.820	0.829	0.827	0.827	0.819	0.820	0.832	0.829	0.823
pixraw10P	0.990	0.990	0.990	0.990	0.980	0.990	0.980	0.990	0.990
Prostate-GE	0.910	0.910	0.920	0.910	0.900	0.910	0.900	0.910	0.900
RELATHE	0.860	0.857	0.857	0.855	0.853	0.857	0.856	0.852	0.858
TOX-171	0.801	0.801	0.796	0.794	0.796	0.796	0.791	0.801	0.828
USPS	0.953	0.954	0.953	0.955	0.954	0.954	0.953	0.955	0.953
warpAR10P	1.000	1.000	1.000	1.000	0.995	1.000	0.995	1.000	0.990
warpPIE10P	0.990	0.995	0.960	0.995	0.960	0.995	0.955	0.995	0.995
Yale	0.803	0.810	0.797	0.810	0.797	0.810	0.790	0.810	0.817

Table S5. Average Kappa using wrapped SVM for each dataset. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3- SRFE	RFE ₃	5- SRFE	RFE ₅	10- SRFE	RFE ₁₀	All
ALLAML	0.932	0.957	0.932	0.957	0.932	0.957	0.932	0.957	0.957
arcene	0.805	0.805	0.805	0.805	0.805	0.805	0.805	0.805	0.816
BASEHOCK	0.879	0.879	0.885	0.875	0.884	0.879	0.879	0.881	0.883
Carcinom	0.910	0.932	0.930	0.939	0.925	0.933	0.946	0.933	0.916
CLL-SUB-111	0.631	0.599	0.629	0.628	0.615	0.631	0.663	0.599	0.613
COIL20	0.985	0.985	0.987	0.985	0.988	0.988	0.987	0.988	0.987
colon	0.580	0.618	0.618	0.618	0.661	0.625	0.618	0.661	0.592
gisette	0.943	0.947							0.947
GLI-85	0.779	0.746	0.723	0.746	0.728	0.746	0.728	0.746	0.746
GLIOMA	0.677	0.727	0.671	0.708	0.728	0.760	0.709	0.710	0.706
Isolet	0.944	0.943	0.945	0.942	0.941	0.942	0.943	0.943	0.945
leukemia	0.899	0.957	0.957	0.957	0.957	0.957	0.932	0.957	0.914
lung	0.913	0.929	0.913	0.929	0.903	0.929	0.913	0.921	0.929
lung_small	0.855	0.867	0.878	0.867	0.831	0.867	0.867	0.855	0.855
lymphoma	0.966	0.930	0.958	0.924	0.966	0.938	0.958	0.924	0.915
madelon	0.076	0.214	0.161	0.166	0.145	0.165	0.166	0.145	0.000
nci9									
ORL	0.982	0.979	0.985	0.982	0.982	0.982	0.982	0.985	0.979
orlraws10P	0.989	0.978	0.967	0.978	0.967	0.967	0.989	0.978	0.978
PCMAC	0.641	0.657	0.653	0.654	0.639	0.640	0.663	0.657	0.646
pixraw10P	0.989	0.989	0.989	0.989	0.978	0.989	0.978	0.989	0.989
Prostate-GE	0.821	0.821	0.841	0.821	0.801	0.821	0.801	0.821	0.801
RELATHE	0.719	0.714	0.714	0.710	0.706	0.713	0.711	0.704	0.714
TOX-171	0.729	0.729	0.721	0.719	0.721	0.721	0.714	0.728	0.766
USPS	0.952	0.953	0.953	0.955	0.954	0.954	0.953	0.955	0.952
warpAR10P	1.000	1.000	1.000	1.000	0.994	1.000	0.994	1.000	0.989
warpPIE10P	0.989	0.994	0.956	0.994	0.956	0.994	0.950	0.994	0.994
Yale	0.789	0.796	0.782	0.796	0.782	0.796	0.775	0.796	0.804

Table S6. Average G-mean using wrapped SVM for each dataset. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3- SRFE	RFE ₃	5- SRFE	RFE ₅	10- SRFE	RFE ₁₀	All
ALLAML	0.960	0.971	0.960	0.971	0.960	0.971	0.960	0.971	0.971
arcene	0.903	0.903	0.903	0.903	0.903	0.903	0.903	0.903	0.909
BASEHOCK	0.939	0.939	0.942	0.937	0.942	0.939	0.939	0.940	0.941
Carcinom	0.570	0.696	0.696	0.739	0.626	0.707	0.722	0.692	0.595
CLL-SUB-111	0.815	0.800	0.817	0.818	0.810	0.817	0.835	0.800	0.809
COIL20	0.983	0.982	0.985	0.982	0.985	0.986	0.985	0.986	0.985
colon	0.767	0.793	0.793	0.793	0.822	0.790	0.793	0.822	0.777
gisette	0.971	0.973							0.974
GLI-85	0.856	0.832	0.824	0.832	0.829	0.832	0.829	0.832	0.832
GLIOMA	0.386	0.476	0.386	0.454	0.456	0.490	0.453	0.400	0.526
Isolet	0.940	0.938	0.940	0.937	0.937	0.938	0.938	0.938	0.941
leukemia	0.947	0.971	0.971	0.971	0.971	0.971	0.960	0.971	0.941
lung	0.869	0.871	0.869	0.871	0.794	0.871	0.869	0.870	0.871
lung_small	0.582	0.645	0.648	0.645	0.570	0.645	0.645	0.635	0.582
lymphoma	0.824	0.692	0.823	0.673	0.824	0.693	0.823	0.673	0.671
madelon	0.536	0.602	0.554	0.533	0.536	0.502	0.516	0.520	0.498
nci9									
ORL	0.897	0.883	0.910	0.897	0.897	0.897	0.897	0.910	0.883
orlraws10P	0.950	0.900	0.875	0.900	0.875	0.850	0.950	0.900	0.900
PCMAC	0.820	0.827	0.826	0.825	0.819	0.818	0.830	0.828	0.823
pixraw10P	0.950	0.950	0.950	0.950	0.900	0.950	0.900	0.950	0.950
Prostate-GE	0.907	0.906	0.916	0.905	0.896	0.906	0.896	0.905	0.896
RELATHE	0.858	0.855	0.855	0.853	0.850	0.854	0.853	0.850	0.855
TOX-171	0.758	0.759	0.753	0.747	0.753	0.754	0.747	0.758	0.782
USPS	0.952	0.953	0.953	0.955	0.953	0.954	0.953	0.955	0.952
warpAR10P	1.000	1.000	1.000	1.000	0.993	1.000	0.993	1.000	0.950
warpPIE10P	0.987	0.993	0.933	0.993	0.933	0.993	0.931	0.993	0.993
Yale	0.513	0.522	0.503	0.522	0.503	0.522	0.502	0.522	0.532

A.2. Logistic Regression

Table S7. Average number of selected features using wrapped Logistic Regression for each dataset. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3-SRFE	RFE ₃	5-SRFE	RFE ₅	10-SRFE	RFE ₁₀
ALLAML	1558	953	742	911	327	920	67	887
arcene	5166	7445	5671	7338	5921	7703	5695	7405
BASEHOCK	3819	3659	3805	3497	3919	3531	3658	3454
Carcinom	2098	1500	1670	1523	1671	1404	1200	1145
CLL-SUB-111	2527	1494	2488	225	1940	783	960	466
COIL20	702	686	675	706	698	665	644	669
colon	304	855	338	721	326	578	289	545
gisette	2879	934	1842	822	1451	415	1419	391
GLI-85	1565	17218	995	17248	1483	17411	1210	17223
GLIOMA	1910	1860	1550	1543	1484	1846	1100	1408
Isolet	479	457	437	445	403	445	421	429
leukemia	572	1264	41	1280	358	1250	206	1290
lung	983	1999	960	1759	1026	1940	969	1504
lung_small	116	185	91	162	87	198	92	168
lymphoma	1001	1495	889	1404	752	1077	633	1307
madelon	317	1	70	9	1	3	1	1
nci9								
ORL	701	823	588	864	608	866	591	824
orlraws10P	3503	7776	2344	6810	2888	6324	1957	6293
PCMAC	2657	2612	2742	2590	2673	2639	2525	2477
pixraw10P	3540	10000	1748	8116	3093	8146	1877	8160
Prostate-GE	730	2596	617	1947	597	211	661	1941
RELATHE	3250	3615	3161	3489	3321	3450	3355	3364
TOX-171	3202	2748	3021	2304	3491	2932	2524	2226
USPS	233	230	227	228	232	215	214	209
warpAR10P	950	1846	616	1837	615	1881	614	1860
warpPIE10P	183	2277	100	2281	136	2286	90	2282
Yale	866	940	870	962	822	923	812	926

Table S8. Processing time using wrapped Logistic Regression for each dataset [s]. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3-SRFE	RFE ₃	5-SRFE	RFE ₅	10-SRFE	RFE ₁₀
ALLAML	8	17	11	44	10	38	12	47
arcene	21	20	73	47	58	42	65	53
BASEHOCK	44	29	123	56	99	55	110	69
Carcinom	47	114	83	285	75	250	88	291
CLL-SUB-111	17	36	32	85	24	76	25	91
COIL20	221	148	435	274	366	252	327	303
colon	1	2	2	8	1	7	2	6
gisette	238	195	463	473	287	404	354	481
GLI-85	23	42	47	112	46	94	53	104
GLIOMA	3	3	7	7	6	7	6	8
Isolet	221	140	342	212	287	230	330	276
leukemia	5	17	8	42	8	35	12	43
lung	10	14	22	34	19	27	23	35
lung_small	0	0	1	1	1	1	1	1
lymphoma	6	10	15	23	11	19	12	22
madelon	27	25	15	27	15	32	26	42
nci9	3600	3600	3600	3600	3600	3600	3600	3600
ORL	80	53	160	101	129	91	143	110
orlraws10P	44	70	79	178	75	142	78	175
PCMAC	35	24	98	45	78	44	85	55
pixraw10P	42	63	68	152	76	135	75	165
Prostate-GE	6	18	14	49	14	42	18	48
RELATHE	34	25	99	50	79	47	88	59
TOX-171	24	26	56	57	55	50	43	61
USPS	492	258	802	350	740	383	910	539
warpAR10P	11	11	21	27	18	23	22	28
warpPIE10P	9	18	13	42	14	37	19	46
Yale	15	8	34	14	26	13	29	16

Table S9. Average classification accuracy using wrapped Logistic Regression for each dataset. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3- SRFE	RFE ₃	5- SRFE	RFE ₅	10- SRFE	RFE ₁₀	All
ALLAML	0.971	0.983	0.954	0.983	0.954	0.983	0.971	0.983	0.983
arcene	0.904	0.899	0.914	0.909	0.914	0.904	0.914	0.909	0.909
BASEHOCK	0.958	0.958	0.959	0.958	0.958	0.958	0.957	0.958	0.960
Carcinom	0.971	0.953	0.966	0.948	0.966	0.960	0.960	0.962	0.942
CLL-SUB-111	0.794	0.785	0.801	0.829	0.794	0.793	0.811	0.801	0.775
COIL20	0.957	0.954	0.956	0.954	0.955	0.956	0.955	0.957	0.956
colon	0.824	0.838	0.807	0.840	0.807	0.824	0.824	0.840	0.855
gisette	0.976	0.977	0.977	0.975	0.976	0.977	0.976	0.977	0.977
GLI-85	0.885	0.907	0.885	0.907	0.896	0.907	0.885	0.907	0.907
GLIOMA	0.770	0.718	0.737	0.635	0.785	0.751	0.770	0.668	0.785
Isolet	0.953	0.951	0.953	0.952	0.953	0.951	0.953	0.953	0.950
leukemia	0.967	0.983	0.971	0.983	0.983	0.983	0.971	0.983	0.983
lung	0.960	0.960	0.960	0.955	0.960	0.960	0.960	0.950	0.955
lung_small	0.897	0.897	0.886	0.897	0.877	0.897	0.888	0.897	0.886
lymphoma	0.940	0.923	0.940	0.923	0.940	0.933	0.930	0.923	0.906
madelon	0.560	0.616	0.605	0.607	0.614	0.612	0.614	0.615	0.565
nci9									
ORL	0.978	0.973	0.975	0.975	0.978	0.975	0.978	0.975	0.978
orlraws10P	0.970	0.960	0.960	0.960	0.960	0.960	0.960	0.960	0.970
PCMAC	0.862	0.859	0.862	0.861	0.863	0.860	0.859	0.860	0.864
pixraw10P	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.990
Prostate-GE	0.911	0.921	0.941	0.920	0.921	0.911	0.930	0.930	0.921
RELATHE	0.887	0.887	0.889	0.887	0.889	0.888	0.888	0.884	0.888
TOX-171	0.779	0.779	0.778	0.785	0.772	0.785	0.766	0.780	0.784
USPS	0.943	0.943	0.943	0.943	0.944	0.943	0.943	0.944	0.943
warpAR10P	0.990	0.980	0.975	0.980	0.975	0.990	0.975	0.980	1.000
warpPIE10P	0.977	1.000	0.968	1.000	0.982	1.000	0.988	1.000	1.000
Yale	0.850	0.843	0.850	0.837	0.837	0.830	0.837	0.830	0.843

Table S10. Average macro recall using wrapped Logistic Regression for each dataset. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3- SRFE	RFE ₃	5- SRFE	RFE ₅	10- SRFE	RFE ₁₀	All
ALLAML	0.965	0.975	0.953	0.975	0.953	0.975	0.965	0.975	0.975
arcene	0.904	0.898	0.914	0.908	0.914	0.904	0.914	0.908	0.909
BASEHOCK	0.958	0.958	0.959	0.958	0.958	0.958	0.957	0.958	0.960
Carcinom	0.956	0.933	0.951	0.918	0.951	0.943	0.941	0.935	0.918
CLL-SUB-111	0.846	0.839	0.853	0.873	0.846	0.846	0.858	0.853	0.831
COIL20	0.957	0.954	0.956	0.954	0.955	0.956	0.955	0.957	0.956
colon	0.796	0.808	0.783	0.821	0.783	0.796	0.796	0.821	0.833
gisette	0.976	0.977	0.977	0.975	0.976	0.977	0.976	0.977	0.977
GLI-85	0.833	0.858	0.833	0.858	0.850	0.858	0.833	0.858	0.858
GLIOMA	0.746	0.692	0.713	0.600	0.758	0.708	0.746	0.633	0.758
Isolet	0.953	0.951	0.953	0.952	0.953	0.951	0.953	0.953	0.950
leukemia	0.963	0.975	0.965	0.975	0.975	0.975	0.965	0.975	0.975
lung	0.925	0.925	0.925	0.915	0.925	0.925	0.925	0.895	0.915
lung_small	0.843	0.843	0.829	0.843	0.814	0.843	0.829	0.843	0.829
lymphoma	0.901	0.882	0.901	0.882	0.901	0.899	0.885	0.882	0.857
madelon	0.560	0.616	0.605	0.607	0.614	0.612	0.614	0.615	0.565
nci9	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
ORL	0.978	0.973	0.975	0.975	0.978	0.975	0.978	0.975	0.978
orlraws10P	0.970	0.960	0.960	0.960	0.960	0.960	0.960	0.960	0.970
PCMAC	0.862	0.859	0.862	0.861	0.863	0.860	0.858	0.860	0.864
pixraw10P	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.990	0.990
Prostate-GE	0.910	0.920	0.940	0.920	0.920	0.910	0.930	0.930	0.920
RELATHE	0.886	0.886	0.887	0.886	0.888	0.886	0.886	0.883	0.886
TOX-171	0.784	0.784	0.784	0.789	0.778	0.790	0.771	0.785	0.789
USPS	0.936	0.936	0.936	0.936	0.936	0.936	0.936	0.936	0.936
warpAR10P	0.990	0.980	0.975	0.980	0.975	0.990	0.975	0.980	1.000
warpPIE10P	0.977	1.000	0.968	1.000	0.982	1.000	0.988	1.000	1.000
Yale	0.850	0.843	0.850	0.837	0.837	0.830	0.837	0.830	0.843

Table S11. Average Kappa using wrapped Logistic Regression for each dataset. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3- SRFE	RFE ₃	5- SRFE	RFE ₅	10- SRFE	RFE ₁₀	All
ALLAML	0.932	0.957	0.899	0.957	0.899	0.957	0.932	0.957	0.957
arcene	0.806	0.796	0.827	0.816	0.827	0.806	0.827	0.816	0.817
BASEHOCK	0.916	0.917	0.918	0.916	0.916	0.916	0.914	0.916	0.920
Carcinom	0.967	0.946	0.962	0.941	0.962	0.954	0.954	0.957	0.934
CLL-SUB-111	0.647	0.631	0.660	0.709	0.647	0.647	0.676	0.660	0.613
COIL20	0.955	0.952	0.954	0.952	0.953	0.954	0.953	0.955	0.954
colon	0.609	0.637	0.566	0.652	0.577	0.609	0.609	0.652	0.680
gisette	0.952	0.954	0.954	0.949	0.953	0.953	0.952	0.954	0.953
GLI-85	0.696	0.746	0.696	0.746	0.723	0.746	0.696	0.746	0.746
GLIOMA	0.671	0.591	0.621	0.489	0.691	0.648	0.671	0.539	0.691
Isolet	0.951	0.949	0.951	0.950	0.951	0.949	0.951	0.951	0.948
leukemia	0.924	0.957	0.932	0.957	0.957	0.957	0.932	0.957	0.957
lung	0.913	0.913	0.913	0.903	0.913	0.913	0.913	0.894	0.903
lung_small	0.868	0.868	0.855	0.868	0.843	0.868	0.856	0.868	0.855
lymphoma	0.913	0.889	0.913	0.889	0.913	0.905	0.898	0.889	0.866
madelon	0.121	0.232	0.211	0.214	0.228	0.223	0.228	0.231	0.129
nci9									
ORL	0.977	0.972	0.974	0.974	0.977	0.974	0.977	0.974	0.977
orlraws10P	0.967	0.956	0.956	0.956	0.956	0.956	0.956	0.956	0.967
PCMAC	0.724	0.718	0.723	0.722	0.726	0.720	0.717	0.720	0.727
pixraw10P	0.989	0.989	0.989	0.989	0.989	0.989	0.989	0.989	0.989
Prostate-GE	0.821	0.841	0.881	0.840	0.841	0.821	0.860	0.860	0.841
RELATHE	0.772	0.772	0.774	0.772	0.776	0.773	0.773	0.766	0.773
TOX-171	0.705	0.705	0.705	0.714	0.697	0.714	0.688	0.707	0.713
USPS	0.937	0.936	0.937	0.936	0.937	0.936	0.936	0.937	0.936
warpAR10P	0.989	0.978	0.972	0.978	0.972	0.989	0.972	0.978	1.000
warpPIE10P	0.974	1.000	0.965	1.000	0.980	1.000	0.987	1.000	1.000
Yale	0.839	0.832	0.839	0.825	0.825	0.818	0.825	0.818	0.832

Table S12. Average G-mean using wrapped Logistic Regression for each dataset. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3- SRFE	RFE ₃	5- SRFE	RFE ₅	10- SRFE	RFE ₁₀	All
ALLAML	0.960	0.971	0.947	0.971	0.947	0.971	0.960	0.971	0.971
arcene	0.903	0.897	0.913	0.907	0.913	0.903	0.913	0.907	0.909
BASEHOCK	0.958	0.958	0.959	0.958	0.958	0.958	0.957	0.958	0.960
Carcinom	0.799	0.722	0.793	0.696	0.793	0.747	0.743	0.747	0.673
CLL-SUB-111	0.827	0.817	0.837	0.857	0.829	0.826	0.842	0.835	0.811
COIL20	0.934	0.931	0.934	0.931	0.915	0.933	0.932	0.935	0.932
colon	0.777	0.788	0.738	0.806	0.767	0.777	0.777	0.806	0.817
gisette	0.976	0.977	0.977	0.975	0.976	0.977	0.976	0.977	0.977
GLI-85	0.805	0.832	0.805	0.832	0.824	0.832	0.805	0.832	0.832
GLIOMA	0.450	0.363	0.360	0.257	0.462	0.365	0.450	0.266	0.462
Isolet	0.947	0.945	0.948	0.946	0.947	0.946	0.948	0.947	0.944
leukemia	0.957	0.971	0.960	0.971	0.971	0.971	0.960	0.971	0.971
lung	0.869	0.869	0.869	0.856	0.869	0.869	0.869	0.781	0.856
lung_small	0.611	0.611	0.588	0.611	0.567	0.611	0.590	0.611	0.588
lymphoma	0.616	0.546	0.616	0.546	0.616	0.614	0.547	0.546	0.498
madelon	0.560	0.615	0.605	0.606	0.613	0.611	0.613	0.614	0.564
nci9									
ORL	0.865	0.840	0.849	0.856	0.865	0.856	0.865	0.856	0.869
orlraws10P	0.875	0.825	0.825	0.825	0.825	0.825	0.825	0.825	0.875
PCMAC	0.862	0.858	0.861	0.860	0.863	0.860	0.858	0.859	0.863
pixraw10P	0.950	0.950	0.950	0.950	0.950	0.950	0.950	0.950	0.950
Prostate-GE	0.907	0.916	0.938	0.918	0.916	0.906	0.927	0.927	0.918
RELATHE	0.884	0.884	0.885	0.884	0.886	0.885	0.885	0.881	0.885
TOX-171	0.715	0.715	0.718	0.729	0.711	0.722	0.704	0.719	0.721
USPS	0.935	0.935	0.935	0.935	0.935	0.935	0.935	0.935	0.935
warpAR10P	0.950	0.925	0.918	0.925	0.918	0.950	0.918	0.925	1.000
warpPIE10P	0.970	1.000	0.958	1.000	0.976	1.000	0.986	1.000	1.000
Yale	0.556	0.541	0.556	0.540	0.554	0.540	0.532	0.540	0.541

A.3. Random Forest

Table S13. Average number of selected features using wrapped Random Forest for each dataset. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3-SRFE	RFE ₃	5-SRFE	RFE ₅	10-SRFE	RFE ₁₀
ALLAML	5159	4416	2459	5426	2838	5211	2735	5227
arcene	5734	4289	4668	4475	5209	6068	3993	5507
BASEHOCK	3391	1406	2324	1249	3006	845	1894	946
Carcinom	5262	6422	5507	5232	3920	4159	5906	3284
CLL-SUB-111	9583	6309	5557	5967	4922	6410	4106	8284
COIL20	851	806	655	840	744	731	793	810
colon	1245	880	1290	1424	1277	1178	956	1053
gisette	3539	618	1257	1264	900	976	1268	1153
GLI-85	12380	13976	2661	13161	9113	12767	11460	13343
GLIOMA	3406	2492	1692	2586	2227	2542	2229	2739
Isolet	480	462	408	385	338	369	364	374
leukemia	4688	3778	1296	5424	1726	5198	1057	5404
lung	1827	1832	1801	1377	2211	1308	1604	1261
lung_small	159	229	217	212	190	195	211	198
lymphoma	2296	3175	2822	2882	2962	2514	2199	1817
madelon	73	32	16	23	17	18	19	24
nci9								
ORL	905	673	540	762	483	584	535	612
orlraws10P	5504	6073	4391	6118	7572	7750	5556	7761
PCMAC	2113	1349	1290	800	1568	638	1119	702
pixraw10P	3880	7144	4005	8630	2994	8391	3161	8674
Prostate-GE	3514	4643	979	3848	2110	4581	2703	4437
RELATHE	3456	1682	2369	2562	2302	1964	1733	2187
TOX-171	3230	2445	1743	4256	3283	4034	2993	3634
USPS	200	188	201	205	186	201	191	195
warpAR10P	1349	1818	1522	1760	1822	1762	1631	1885
warpPIE10P	1190	1619	1136	1485	1343	1257	1408	1872
Yale	882	751	563	684	637	750	599	750

Table S14. Processing time using wrapped Random Forest for each dataset [s]. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3-SRFE	RFE ₃	5-SRFE	RFE ₅	10-SRFE	RFE ₁₀
ALLAML	51	50	158	116	122	101	138	122
arcene	65	66	181	150	144	125	161	160
BASEHOCK	112	95	193	164	199	167	202	223
Carcinom	94	86	265	189	172	177	256	225
CLL-SUB-111	71	62	181	145	133	115	154	147
COIL20	158	101	320	196	256	172	317	208
colon	42	44	107	80	93	79	115	106
gisette	1525	1273	1768	3064	1206	2445	1480	2945
GLI-85	63	63	186	159	148	134	166	151
GLIOMA	48	48	151	116	115	97	127	115
Isolet	121	86	204	140	175	149	189	174
leukemia	50	51	162	123	123	102	129	113
lung	47	48	133	105	102	90	127	122
lung_small	32	33	79	55	71	59	83	72
lymphoma	45	44	125	91	93	78	118	108
madelon	58	86	129	172	104	143	123	176
nci9	3600	3600	3600	3600	3600	3600	3600	3600
ORL	121	80	204	150	162	144	188	170
orlraws10P	69	69	212	175	174	127	186	163
PCMAC	83	76	191	159	161	151	168	187
pixraw10P	56	59	189	145	134	118	155	139
Prostate-GE	47	46	158	116	118	97	132	116
RELATHE	114	87	212	165	172	152	185	200
TOX-171	57	58	159	131	139	114	138	126
USPS	312	207	504	273	508	325	560	389
warpAR10P	42	42	113	87	88	73	110	100
warpPIE10P	46	47	145	111	111	94	129	114
Yale	41	40	114	85	88	71	96	84

Table S15. Average classification accuracy using wrapped Random Forest for each dataset. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3- SRFE	RFE ₃	5- SRFE	RFE ₅	10- SRFE	RFE ₁₀	All
ALLAML	0.942	0.942	0.971	0.942	0.971	0.971	0.942	0.942	0.938
arcene	0.805	0.799	0.784	0.815	0.779	0.834	0.815	0.805	0.810
BASEHOCK	0.951	0.948	0.946	0.947	0.949	0.948	0.948	0.945	0.950
Carcinom	0.881	0.858	0.873	0.851	0.893	0.848	0.853	0.876	0.883
CLL-SUB-111	0.833	0.766	0.738	0.776	0.826	0.795	0.755	0.797	0.776
COIL20	0.973	0.964	0.967	0.965	0.961	0.965	0.964	0.966	0.964
colon	0.719	0.802	0.786	0.736	0.771	0.802	0.750	0.819	0.802
gisette	0.969	0.971	0.972	0.970	0.970	0.968	0.968	0.968	0.970
GLI-85	0.858	0.872	0.860	0.882	0.859	0.896	0.861	0.906	0.880
GLIOMA	0.790	0.838	0.813	0.817	0.813	0.726	0.765	0.838	0.765
Isolet	0.909	0.906	0.903	0.903	0.912	0.904	0.906	0.901	0.912
leukemia	0.983	0.971	0.988	0.983	0.971	0.983	1.000	0.983	0.971
lung	0.931	0.926	0.941	0.940	0.926	0.931	0.941	0.931	0.931
lung_small	0.885	0.821	0.847	0.810	0.834	0.812	0.812	0.877	0.871
lymphoma	0.877	0.883	0.837	0.885	0.882	0.862	0.862	0.880	0.882
madelon	0.877	0.869	0.885	0.882	0.884	0.885	0.887	0.882	0.817
nci9									
ORL	0.913	0.910	0.910	0.920	0.923	0.910	0.895	0.903	0.918
orlraws10P	0.950	0.970	0.970	0.980	0.950	0.950	0.950	0.980	0.960
PCMAC	0.901	0.902	0.902	0.907	0.904	0.903	0.905	0.907	0.902
pixraw10P	0.990	0.980	1.000	0.990	0.990	0.990	0.980	0.990	0.980
Prostate-GE	0.920	0.920	0.911	0.880	0.930	0.881	0.921	0.900	0.890
RELATHE	0.872	0.878	0.879	0.879	0.879	0.877	0.874	0.879	0.874
TOX-171	0.586	0.653	0.614	0.626	0.625	0.605	0.642	0.559	0.633
USPS	0.953	0.951	0.955	0.952	0.953	0.952	0.953	0.952	0.952
warpAR10P	0.895	0.860	0.910	0.905	0.895	0.885	0.900	0.890	0.885
warpPIE10P	0.920	0.937	0.932	0.903	0.910	0.923	0.922	0.927	0.920
Yale	0.720	0.750	0.713	0.723	0.740	0.723	0.697	0.750	0.730

Table S16. Average macro recall using wrapped Random Forest for each dataset. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3- SRFE	RFE ₃	5- SRFE	RFE ₅	10- SRFE	RFE ₁₀	All
ALLAML	0.917	0.929	0.958	0.929	0.958	0.958	0.917	0.929	0.921
arcene	0.800	0.794	0.776	0.805	0.771	0.828	0.811	0.799	0.802
BASEHOCK	0.951	0.948	0.946	0.947	0.949	0.948	0.948	0.945	0.950
Carcinom	0.834	0.789	0.825	0.773	0.839	0.759	0.792	0.816	0.833
CLL-SUB-111	0.864	0.816	0.807	0.822	0.873	0.836	0.808	0.838	0.824
COIL20	0.973	0.964	0.967	0.965	0.961	0.965	0.964	0.966	0.964
colon	0.675	0.771	0.750	0.688	0.733	0.771	0.700	0.763	0.788
gisette	0.969	0.971	0.972	0.970	0.970	0.968	0.968	0.968	0.970
GLI-85	0.800	0.833	0.800	0.833	0.808	0.842	0.808	0.850	0.808
GLIOMA	0.771	0.829	0.792	0.804	0.804	0.721	0.758	0.829	0.746
Isolet	0.909	0.906	0.903	0.903	0.912	0.904	0.906	0.901	0.912
leukemia	0.975	0.965	0.983	0.975	0.965	0.975	1.000	0.975	0.958
lung	0.833	0.797	0.857	0.844	0.804	0.818	0.834	0.833	0.824
lung_small	0.838	0.746	0.762	0.748	0.770	0.739	0.739	0.831	0.829
lymphoma	0.837	0.820	0.770	0.826	0.841	0.823	0.805	0.841	0.803
madelon	0.877	0.869	0.885	0.882	0.884	0.885	0.887	0.882	0.817
nci9									
ORL	0.913	0.910	0.910	0.920	0.923	0.910	0.895	0.903	0.918
orlraws10P	0.950	0.970	0.970	0.980	0.950	0.950	0.950	0.980	0.960
PCMAC	0.901	0.901	0.901	0.907	0.903	0.903	0.905	0.906	0.901
pixraw10P	0.990	0.980	1.000	0.990	0.990	0.990	0.980	0.990	0.980
Prostate-GE	0.920	0.920	0.912	0.880	0.930	0.882	0.922	0.900	0.890
RELATHE	0.869	0.876	0.877	0.877	0.878	0.875	0.873	0.878	0.873
TOX-171	0.589	0.654	0.616	0.629	0.624	0.608	0.644	0.559	0.636
USPS	0.947	0.945	0.949	0.945	0.947	0.945	0.948	0.946	0.945
warpAR10P	0.895	0.860	0.910	0.905	0.895	0.885	0.900	0.890	0.885
warpPIE10P	0.920	0.937	0.932	0.903	0.910	0.923	0.922	0.927	0.920
Yale	0.720	0.750	0.713	0.723	0.740	0.723	0.697	0.750	0.730

Table S17. Average Kappa using wrapped Random Forest for each dataset. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3- SRFE	RFE ₃	5- SRFE	RFE ₅	10- SRFE	RFE ₁₀	All
ALLAML	0.853	0.867	0.929	0.867	0.929	0.929	0.857	0.867	0.852
arcene	0.603	0.590	0.557	0.618	0.548	0.660	0.622	0.601	0.608
BASEHOCK	0.903	0.896	0.892	0.895	0.898	0.896	0.897	0.891	0.900
Carcinom	0.865	0.838	0.854	0.830	0.878	0.827	0.832	0.859	0.866
CLL-SUB-111	0.712	0.600	0.553	0.613	0.706	0.646	0.579	0.650	0.616
COIL20	0.971	0.962	0.965	0.963	0.959	0.963	0.962	0.965	0.962
colon	0.348	0.558	0.518	0.390	0.488	0.558	0.421	0.565	0.576
gisette	0.938	0.942	0.944	0.939	0.940	0.937	0.937	0.937	0.940
GLI-85	0.632	0.685	0.616	0.691	0.642	0.704	0.630	0.719	0.665
GLIOMA	0.702	0.775	0.738	0.747	0.739	0.620	0.672	0.773	0.668
Isolet	0.905	0.902	0.899	0.899	0.908	0.901	0.903	0.897	0.908
leukemia	0.957	0.932	0.971	0.957	0.932	0.957	1.000	0.957	0.929
lung	0.851	0.839	0.871	0.869	0.839	0.854	0.870	0.851	0.848
lung_small	0.859	0.775	0.802	0.774	0.793	0.738	0.757	0.839	0.842
lymphoma	0.837	0.838	0.778	0.844	0.836	0.816	0.813	0.840	0.835
madelon	0.753	0.738	0.771	0.764	0.768	0.770	0.775	0.763	0.635
nci9									
ORL	0.910	0.908	0.908	0.918	0.921	0.908	0.892	0.900	0.915
orlraws10P	0.944	0.967	0.967	0.978	0.944	0.944	0.944	0.978	0.956
PCMAC	0.802	0.803	0.803	0.814	0.807	0.806	0.810	0.813	0.803
pixraw10P	0.989	0.978	1.000	0.989	0.989	0.989	0.978	0.989	0.978
Prostate-GE	0.840	0.840	0.822	0.760	0.860	0.762	0.842	0.800	0.780
RELATHE	0.740	0.753	0.754	0.755	0.756	0.752	0.746	0.756	0.746
TOX-171	0.447	0.535	0.484	0.499	0.497	0.471	0.520	0.409	0.508
USPS	0.947	0.945	0.949	0.946	0.947	0.946	0.948	0.946	0.946
warpAR10P	0.883	0.844	0.900	0.894	0.883	0.872	0.889	0.878	0.872
warpPIE10P	0.911	0.930	0.924	0.893	0.900	0.915	0.913	0.919	0.911
Yale	0.700	0.732	0.693	0.704	0.721	0.704	0.675	0.732	0.711

Table S18. Average G-mean using wrapped Random Forest for each dataset. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3- SRFE	RFE ₃	5- SRFE	RFE ₅	10- SRFE	RFE ₁₀	All
ALLAML	0.899	0.921	0.952	0.921	0.952	0.952	0.905	0.921	0.910
arcene	0.794	0.788	0.768	0.795	0.763	0.823	0.807	0.794	0.794
BASEHOCK	0.951	0.947	0.945	0.947	0.948	0.947	0.948	0.945	0.949
Carcinom	0.541	0.299	0.417	0.280	0.423	0.283	0.341	0.418	0.397
CLL-SUB-111	0.850	0.792	0.776	0.799	0.850	0.825	0.787	0.815	0.801
COIL20	0.966	0.953	0.957	0.932	0.940	0.950	0.946	0.954	0.953
colon	0.577	0.753	0.712	0.635	0.717	0.753	0.638	0.733	0.771
gisette	0.969	0.971	0.972	0.970	0.970	0.968	0.968	0.968	0.970
GLI-85	0.771	0.814	0.734	0.810	0.786	0.775	0.739	0.789	0.774
GLIOMA	0.522	0.637	0.533	0.520	0.588	0.359	0.442	0.637	0.440
Isolet	0.897	0.893	0.891	0.890	0.900	0.889	0.894	0.887	0.901
leukemia	0.971	0.960	0.982	0.971	0.960	0.971	1.000	0.971	0.952
lung	0.624	0.487	0.642	0.636	0.489	0.572	0.567	0.624	0.564
lung_small	0.524	0.471	0.413	0.424	0.444	0.396	0.410	0.573	0.534
lymphoma	0.484	0.456	0.410	0.500	0.484	0.459	0.433	0.527	0.427
madelon	0.876	0.868	0.885	0.882	0.884	0.885	0.887	0.881	0.817
nci9									
ORL	0.574	0.573	0.557	0.582	0.612	0.563	0.516	0.525	0.600
orlraws10P	0.775	0.850	0.850	0.900	0.813	0.775	0.800	0.900	0.850
PCMAC	0.898	0.898	0.899	0.904	0.900	0.900	0.902	0.904	0.898
pixraw10P	0.950	0.900	1.000	0.950	0.950	0.950	0.900	0.950	0.900
Prostate-GE	0.915	0.915	0.909	0.873	0.927	0.873	0.917	0.895	0.882
RELATHE	0.867	0.874	0.875	0.875	0.876	0.873	0.870	0.876	0.871
TOX-171	0.409	0.555	0.490	0.492	0.457	0.441	0.543	0.389	0.499
USPS	0.946	0.944	0.948	0.944	0.946	0.945	0.947	0.946	0.945
warpAR10P	0.681	0.640	0.712	0.706	0.699	0.618	0.687	0.637	0.656
warpPIE10P	0.903	0.892	0.892	0.822	0.844	0.841	0.854	0.893	0.853
Yale	0.430	0.444	0.408	0.416	0.459	0.407	0.341	0.454	0.449

A.4. Gradient Boosting Machine

Table S19. Average number of selected features using wrapped GBM for each dataset. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3-SRFE	RFE ₃	5-SRFE	RFE ₅	10-SRFE	RFE ₁₀
ALLAML	9	7129	10	7129	61	7129	9	7129
arcene	4656	10000	5319	7050	5127	5094	3761	4100
BASEHOCK	3349	3019	2002	2539	3234	2522	3203	2537
Carcinom	5247	4214			2018		3177	
CLL-SUB-111	7702	11340	2722	4633	3639	10226	2676	5760
COIL20								
colon	10	2000	9	2000	9	2000	9	2000
gisette								
GLI-85	6415	20055	2757	20055	9264	20055	9491	20055
GLIOMA								
Isolet								
leukemia	8	7070	8	7070	8	7070	8	7070
lung	1441	1573	798	1840	1165	1523	998	1875
lung_small	43	239	44	151	36	150	40	182
lymphoma	1186	2884	1264	2515	834	2879	1167	3253
madelon	376	32	333	17	254	16	8	7
nci9								
ORL					590	763		
orlraws10P	2478	8343	2140	6377	2924	7357	2043	7422
PCMAC	2085	2045	2170	2380	2243	2066	1534	1771
pixraw10P	1093	10000	1759	10000	1298	10000	1769	10000
Prostate-GE	2032	5966	687	5966	1014	5966	954	5966
RELATHE	3326	3091	1446	3121	2485	3108	1187	2306
TOX-171	3182	4112	1834	1373	2990	2458	2401	1409
USPS	227	198						
warpAR10P	1029	1236	746	1255	1052	1412	1235	861
warpPIE10P	722	861	498	319	546	826	704	285
Yale	529	478	398	485	395	471	495	474

Table S20. Processing time using wrapped GBM for each dataset [s]. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3-SRFE	RFE ₃	5-SRFE	RFE ₅	10-SRFE	RFE ₁₀
ALLAML	12	25	14	43	15	41	21	51
arcene	196	196	607	465	429	425	406	563
BASEHOCK	99	76	149	156	184	146	210	172
Carcinom	2281	2066	3600	3600	2318	3600	3707	3600
CLL-SUB-111	467	316	426	880	480	682	448	865
COIL20	3600	3600	3600	3600	3600	3600	3600	3600
colon	1	2	3	3	2	3	3	4
gisette	3600	3600	3600	3600	3600	3600	3600	3600
GLI-85	118	169	164	377	338	353	400	397
GLIOMA	3600	3600	3600	3600	3600	3600	3600	3600
Isolet	3600	3600	3600	3600	3600	3600	3600	3600
leukemia	4	7	6	11	6	11	8	13
lung	372	433	518	993	562	833	660	1006
lung_small	3	3	8	7	7	7	9	8
lymphoma	71	86	161	196	122	170	155	189
madelon	202	156	391	275	262	264	145	321
nci9	3600	3600	3600	3600	3600	3600	3600	3600
ORL	3600	3600	3600	3600	4382	3540	3600	3600
orlraws10P	396	714	765	1832	778	1456	825	1719
PCMAC	68	56	160	111	131	101	126	124
pixraw10P	252	555	624	1331	428	1112	783	1434
Prostate-GE	27	31	37	69	38	60	47	70
RELATHE	94	69	160	150	171	134	146	164
TOX-171	431	403	643	1043	819	842	790	1083
USPS	2686	1554	3600	3600	3600	3600	3600	3600
warpAR10P	134	145	333	361	281	274	387	372
warpPIE10P	303	472	658	1332	508	964	777	1326
Yale	159	143	335	318	267	278	311	307

Table S21. Average classification accuracy using wrapped GBM for each dataset. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3- SRFE	RFE ₃	5- SRFE	RFE ₅	10- SRFE	RFE ₁₀	All
ALLAML	0.983	0.983	0.983	0.983	0.983	0.983	0.983	0.983	0.983
arcene	0.810	0.830	0.820	0.825	0.810	0.825	0.835	0.815	0.830
BASEHOCK	0.960	0.959	0.960	0.957	0.959	0.961	0.959	0.957	0.960
Carcinom	0.908	0.910			0.909		0.907		0.898
CLL-SUB-111	0.768	0.778	0.787	0.787	0.769	0.778	0.778	0.778	0.778
COIL20									0.938
colon	0.740	0.757	0.724	0.757	0.676	0.757	0.740	0.757	0.757
gisette									0.981
GLI-85	0.871	0.849	0.871	0.849	0.871	0.849	0.860	0.849	0.871
GLIOMA									0.808
Isolet									0.912
leukemia	0.983	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
lung	0.940	0.935	0.940	0.940	0.935	0.940	0.935	0.940	0.935
lung_small	0.735	0.779	0.702	0.740	0.672	0.748	0.717	0.700	0.765
lymphoma	0.852	0.847	0.852	0.861	0.830	0.839	0.838	0.854	0.847
madelon	0.826	0.846	0.834	0.868	0.835	0.855	0.878	0.869	0.823
nci9									
ORL					0.930	0.935			0.938
orlraws10P	0.980	0.990	0.980	0.990	0.980	0.990	0.980	0.990	0.990
PCMAC	0.904	0.903	0.905	0.908	0.907	0.905	0.904	0.907	0.905
pixraw10P	0.980	0.980	0.970	0.980	0.980	0.980	0.980	0.980	0.980
Prostate-GE	0.891	0.901	0.900	0.901	0.900	0.901	0.891	0.901	0.901
RELATHE	0.881	0.876	0.876	0.877	0.879	0.875	0.882	0.872	0.879
TOX-171	0.684	0.652	0.652	0.668	0.644	0.663	0.651	0.672	0.679
USPS	0.965	0.964							0.965
warpAR10P	0.880	0.880	0.890	0.900	0.880	0.870	0.875	0.890	0.885
warpPIE10P	0.933	0.935	0.922	0.930	0.923	0.940	0.945	0.918	0.935
Yale	0.683	0.663	0.683	0.690	0.693	0.670	0.677	0.693	0.697

Table S22. Average macro recall using wrapped GBM for each dataset. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3- SRFE	RFE ₃	5- SRFE	RFE ₅	10- SRFE	RFE ₁₀	All
ALLAML	0.975	0.975	0.975	0.975	0.975	0.975	0.975	0.975	0.975
arcene	0.808	0.827	0.819	0.822	0.808	0.823	0.834	0.812	0.827
BASEHOCK	0.960	0.959	0.960	0.957	0.959	0.961	0.959	0.957	0.960
Carcinom	0.887	0.900			0.887		0.892		0.881
CLL-SUB-111	0.827	0.836	0.842	0.843	0.830	0.836	0.837	0.837	0.836
COIL20									0.938
colon	0.667	0.692	0.642	0.692	0.629	0.692	0.667	0.692	0.692
gisette									0.981
GLI-85	0.825	0.808	0.817	0.808	0.825	0.808	0.817	0.808	0.825
GLIOMA									0.767
Isolet									0.912
leukemia	0.975	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
lung	0.873	0.853	0.873	0.873	0.853	0.873	0.863	0.873	0.853
lung_small	0.710	0.726	0.654	0.680	0.630	0.687	0.667	0.627	0.696
lymphoma	0.805	0.779	0.805	0.819	0.761	0.768	0.756	0.790	0.779
madelon	0.826	0.846	0.834	0.868	0.835	0.855	0.878	0.869	0.823
nci9									
ORL					0.930	0.935			0.938
orlraws10P	0.980	0.990	0.980	0.990	0.980	0.990	0.980	0.990	0.990
PCMAC	0.904	0.903	0.905	0.908	0.907	0.905	0.904	0.907	0.905
pixraw10P	0.980	0.980	0.970	0.980	0.980	0.980	0.980	0.980	0.980
Prostate-GE	0.892	0.902	0.900	0.902	0.900	0.902	0.892	0.902	0.902
RELATHE	0.880	0.875	0.875	0.876	0.879	0.875	0.881	0.872	0.878
TOX-171	0.689	0.656	0.656	0.673	0.651	0.669	0.659	0.675	0.683
USPS	0.961	0.960							0.961
warpAR10P	0.880	0.880	0.890	0.900	0.880	0.870	0.875	0.890	0.885
warpPIE10P	0.933	0.935	0.922	0.930	0.923	0.940	0.945	0.918	0.935
Yale	0.683	0.663	0.683	0.690	0.693	0.670	0.677	0.693	0.697

Table S23. Average Kappa using wrapped GBM for each dataset. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3- SRFE	RFE ₃	5- SRFE	RFE ₅	10- SRFE	RFE ₁₀	All
ALLAML	0.957	0.957	0.957	0.957	0.957	0.957	0.957	0.957	0.957
arcene	0.614	0.653	0.636	0.644	0.614	0.645	0.666	0.623	0.653
BASEHOCK	0.920	0.919	0.921	0.914	0.918	0.922	0.918	0.914	0.920
Carcinom	0.895	0.898			0.896		0.894		0.884
CLL-SUB-111	0.603	0.621	0.634	0.638	0.606	0.621	0.622	0.622	0.621
COIL20									0.935
colon	0.341	0.398	0.276	0.398	0.252	0.398	0.333	0.398	0.398
gisette									0.962
GLI-85	0.677	0.637	0.670	0.637	0.677	0.637	0.654	0.637	0.677
GLIOMA									0.736
Isolet									0.909
leukemia	0.957	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
lung	0.869	0.860	0.869	0.869	0.860	0.869	0.859	0.869	0.860
lung_small	0.666	0.721	0.620	0.674	0.592	0.681	0.649	0.624	0.704
lymphoma	0.797	0.788	0.797	0.810	0.769	0.778	0.772	0.798	0.788
madelon	0.652	0.692	0.668	0.736	0.669	0.709	0.755	0.738	0.645
nci9									
ORL					0.928	0.933			0.936
orlraws10P	0.978	0.989	0.978	0.989	0.978	0.989	0.978	0.989	0.989
PCMAC	0.808	0.805	0.811	0.816	0.814	0.811	0.807	0.815	0.810
pixraw10P	0.978	0.978	0.967	0.978	0.978	0.978	0.978	0.978	0.978
Prostate-GE	0.782	0.802	0.800	0.802	0.800	0.802	0.782	0.802	0.802
RELATHE	0.759	0.749	0.749	0.751	0.756	0.748	0.761	0.741	0.755
TOX-171	0.578	0.534	0.534	0.556	0.524	0.549	0.534	0.561	0.570
USPS	0.961	0.960							0.961
warpAR10P	0.867	0.867	0.878	0.889	0.867	0.856	0.861	0.878	0.872
warpPIE10P	0.926	0.928	0.913	0.922	0.915	0.933	0.939	0.909	0.928
Yale	0.661	0.639	0.661	0.668	0.671	0.646	0.654	0.671	0.675

Table S24. Average G-mean using wrapped GBM for each dataset. Cells without numbers show cases where the result could not be computed within one hour. Results obtained using stratified 10-fold cross-validation.

	FRFE	RFE _F	3- SRFE	RFE ₃	5- SRFE	RFE ₅	10- SRFE	RFE ₁₀	All
ALLAML	0.971	0.971	0.971	0.971	0.971	0.971	0.971	0.971	0.971
arcene	0.804	0.823	0.815	0.819	0.804	0.820	0.832	0.807	0.823
BASEHOCK	0.960	0.959	0.960	0.957	0.959	0.961	0.959	0.957	0.960
Carcinom	0.575	0.642			0.575		0.620		0.570
CLL-SUB-111	0.812	0.819	0.827	0.830	0.814	0.819	0.821	0.822	0.819
COIL20									0.903
colon	0.488	0.556	0.421	0.556	0.478	0.556	0.488	0.556	0.556
gisette									0.981
GLI-85	0.802	0.791	0.795	0.791	0.802	0.791	0.793	0.791	0.802
GLIOMA									0.449
Isolet									0.902
leukemia	0.971	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
lung	0.713	0.638	0.713	0.713	0.638	0.713	0.700	0.713	0.638
lung_small	0.325	0.337	0.224	0.339	0.286	0.301	0.290	0.299	0.315
lymphoma	0.438	0.368	0.438	0.461	0.357	0.356	0.335	0.392	0.368
madelon	0.826	0.846	0.834	0.868	0.834	0.854	0.878	0.869	0.822
nci9									
ORL					0.651	0.679			0.694
orlraws10P	0.900	0.950	0.900	0.950	0.900	0.950	0.900	0.950	0.950
PCMAC	0.904	0.902	0.905	0.907	0.906	0.905	0.903	0.907	0.904
pixraw10P	0.900	0.900	0.850	0.900	0.900	0.900	0.900	0.900	0.900
Prostate-GE	0.882	0.896	0.891	0.896	0.895	0.896	0.882	0.896	0.896
RELATHE	0.878	0.873	0.873	0.874	0.877	0.873	0.879	0.869	0.876
TOX-171	0.581	0.530	0.523	0.576	0.549	0.529	0.559	0.579	0.580
USPS									0.961
warpAR10P	0.594	0.576	0.601	0.651	0.594	0.551	0.588	0.601	0.594
warpPIE10P	0.920	0.920	0.875	0.917	0.909	0.924	0.931	0.848	0.919
Yale	0.307	0.278	0.303	0.293	0.305	0.283	0.280	0.325	0.322

B. Supplementary Figures

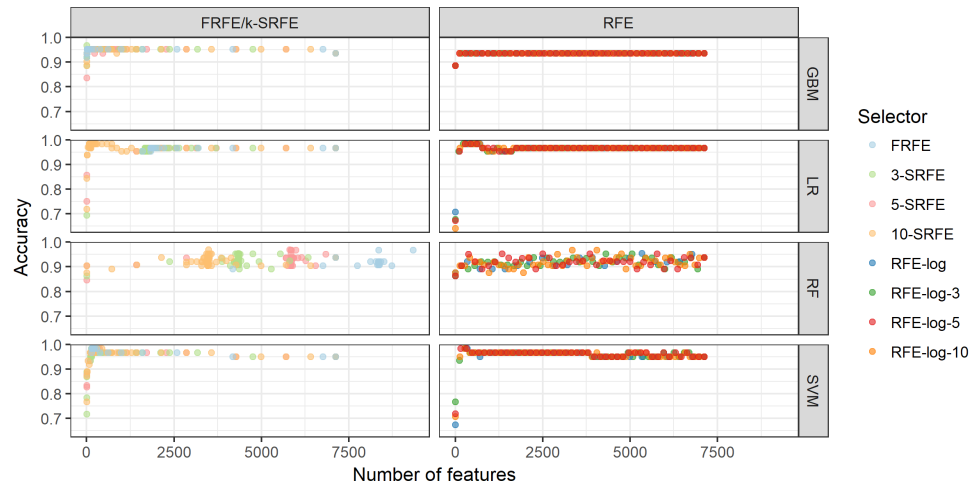


Figure S1. Mean validation scores for a single experiment fold during feature elimination on the ALLAML dataset; plot best viewed online in color.

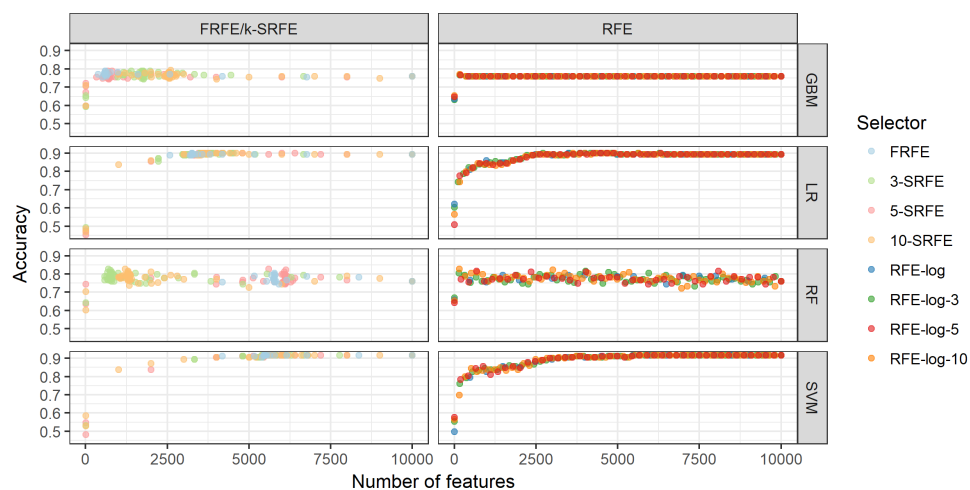


Figure S2. Mean validation scores for a single experiment fold during feature elimination on the arcene dataset; plot best viewed online in color.

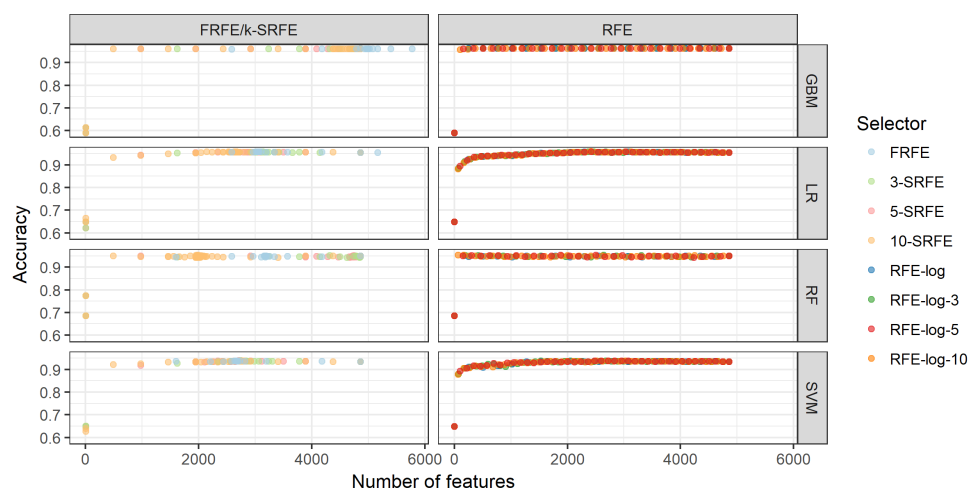


Figure S3. Mean validation scores for a single experiment fold during feature elimination on the BASEHOCK dataset; plot best viewed online in color.

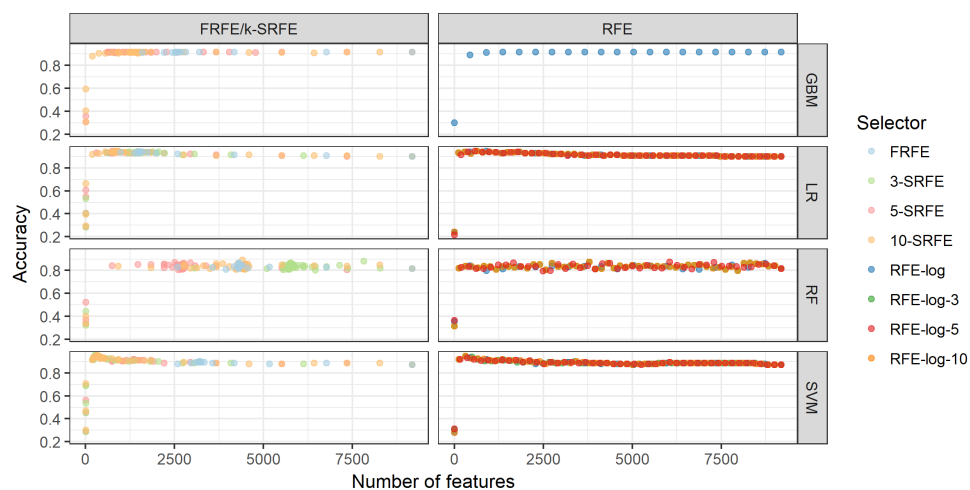


Figure S4. Mean validation scores for a single experiment fold during feature elimination on the Carcinom dataset; plot best viewed online in color.

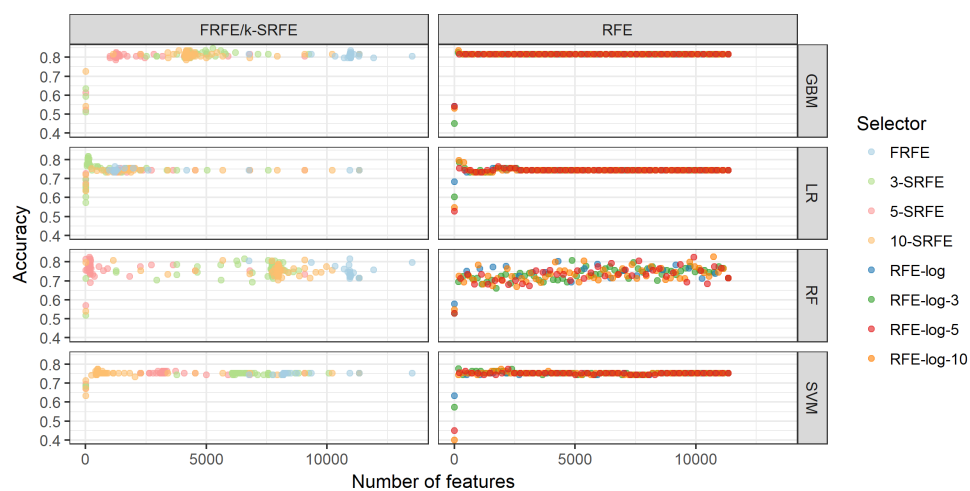


Figure S5. Mean validation scores for a single experiment fold during feature elimination on the CLL-SUB-111 dataset; plot best viewed online in color.

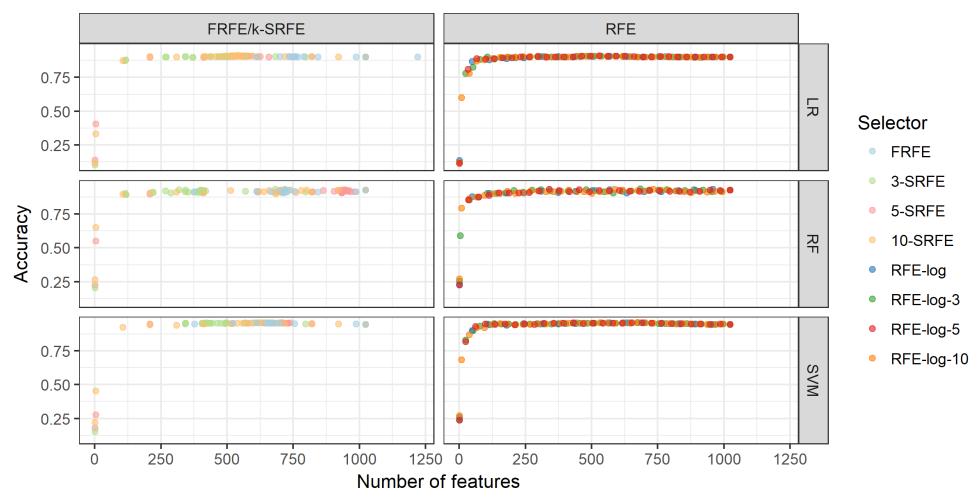


Figure S6. Mean validation scores for a single experiment fold during feature elimination on the COIL20 dataset; plot best viewed online in color.

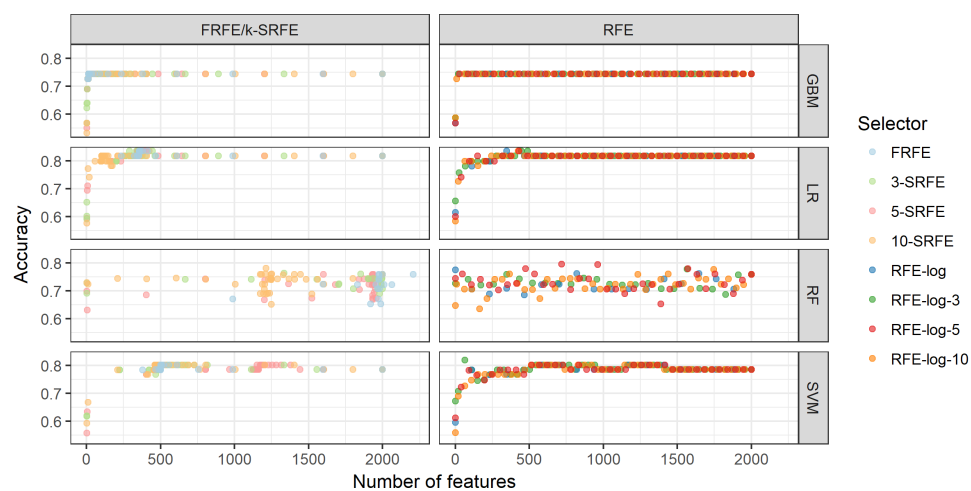


Figure S7. Mean validation scores for a single experiment fold during feature elimination on the colon dataset; plot best viewed online in color.

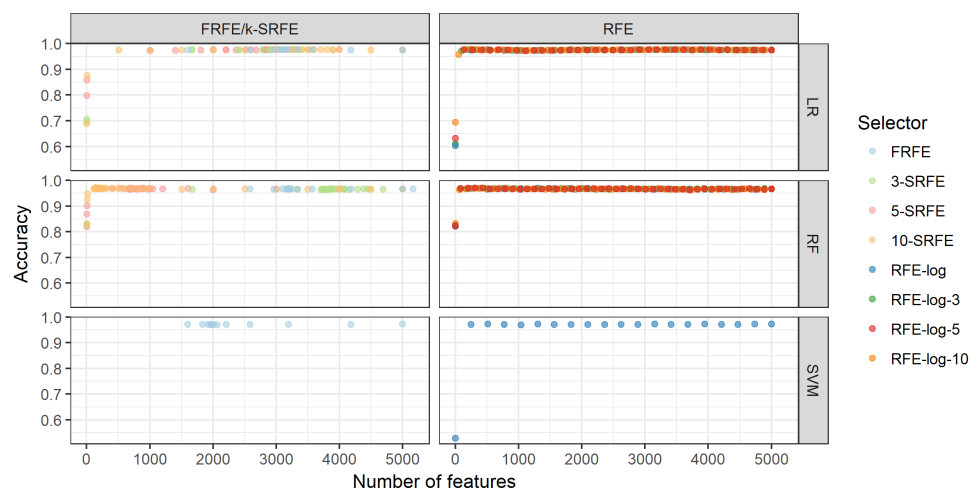


Figure S8. Mean validation scores for a single experiment fold during feature elimination on the gisette dataset; plot best viewed online in color.

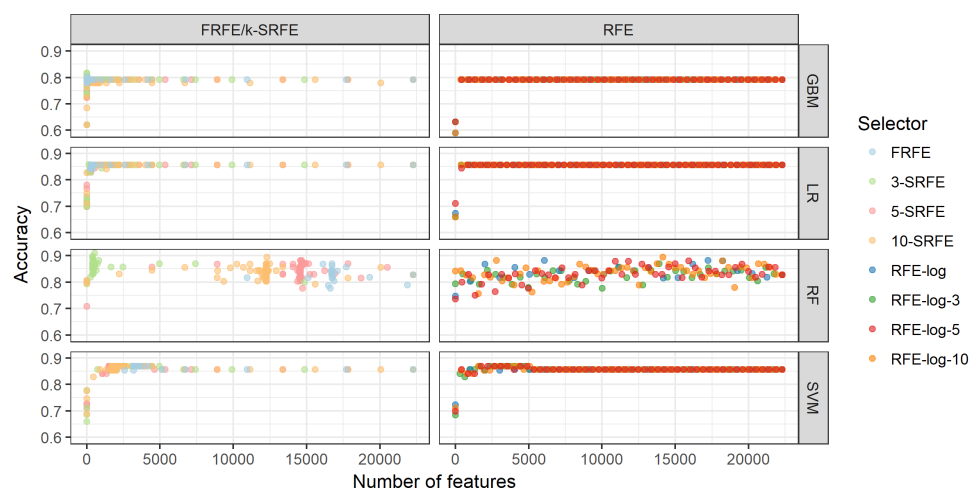


Figure S9. Mean validation scores for a single experiment fold during feature elimination on the GLI-85 dataset; plot best viewed online in color.

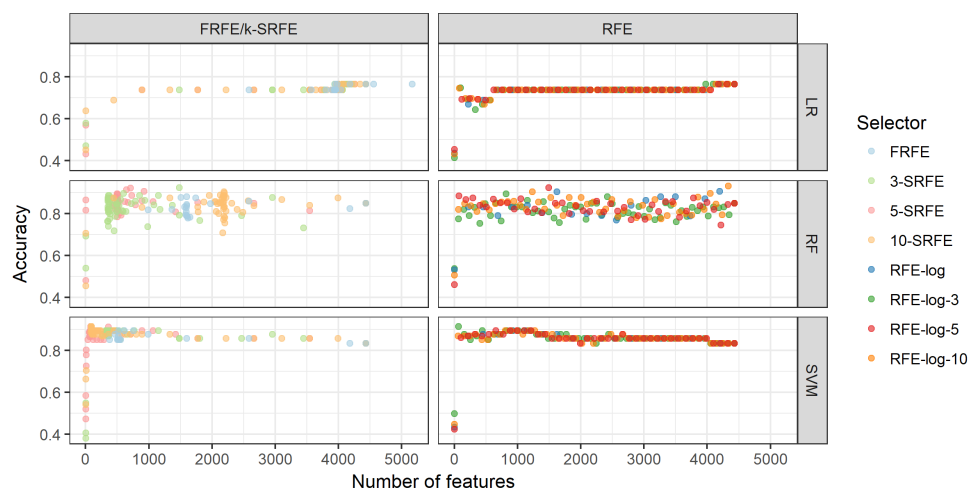


Figure S10. Mean validation scores for a single experiment fold during feature elimination on the GLIOMA dataset; plot best viewed online in color.

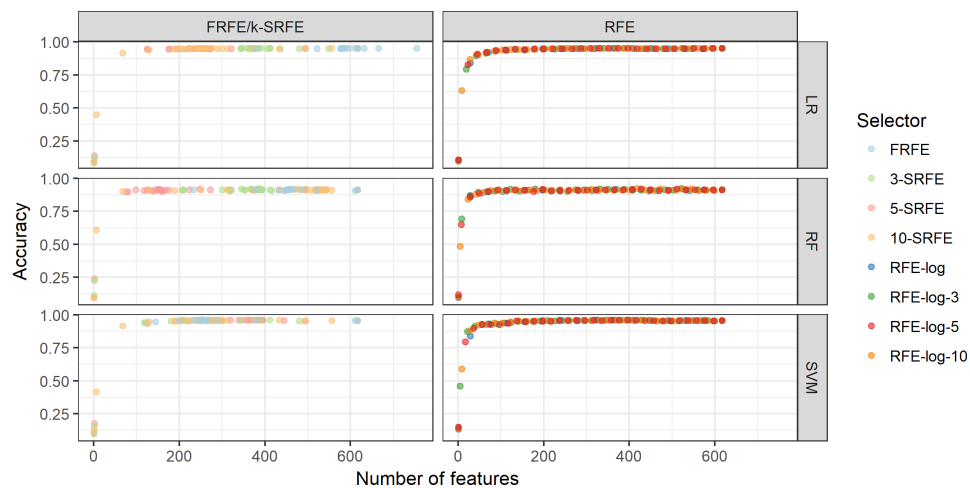


Figure S11. Mean validation scores for a single experiment fold during feature elimination on the Isolet dataset; plot best viewed online in color.

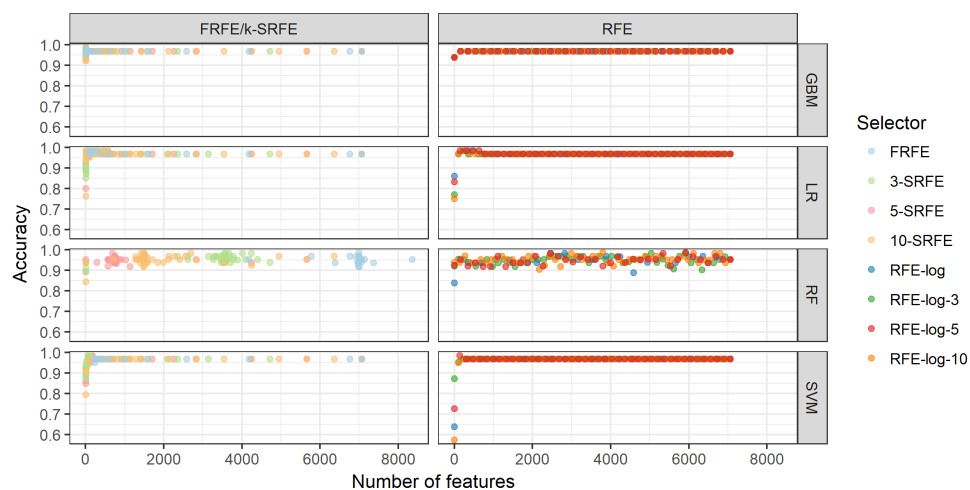


Figure S12. Mean validation scores for a single experiment fold during feature elimination on the leukemia dataset; plot best viewed online in color.

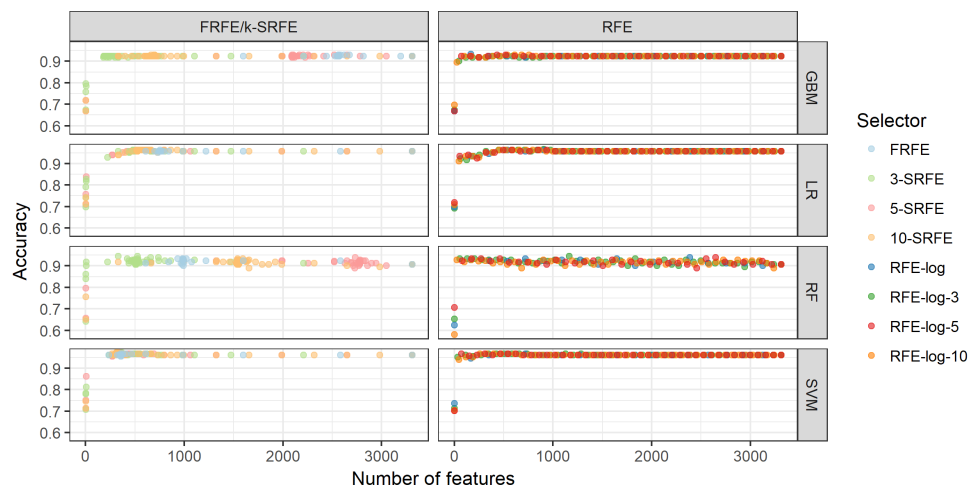


Figure S13. Mean validation scores for a single experiment fold during feature elimination on the lung dataset; plot best viewed online in color.

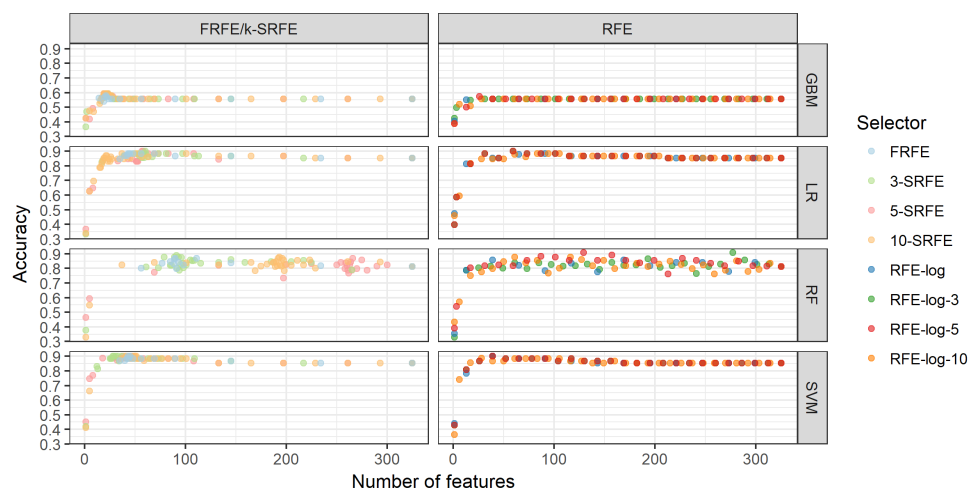


Figure S14. Mean validation scores for a single experiment fold during feature elimination on the lung_small dataset; plot best viewed online in color.

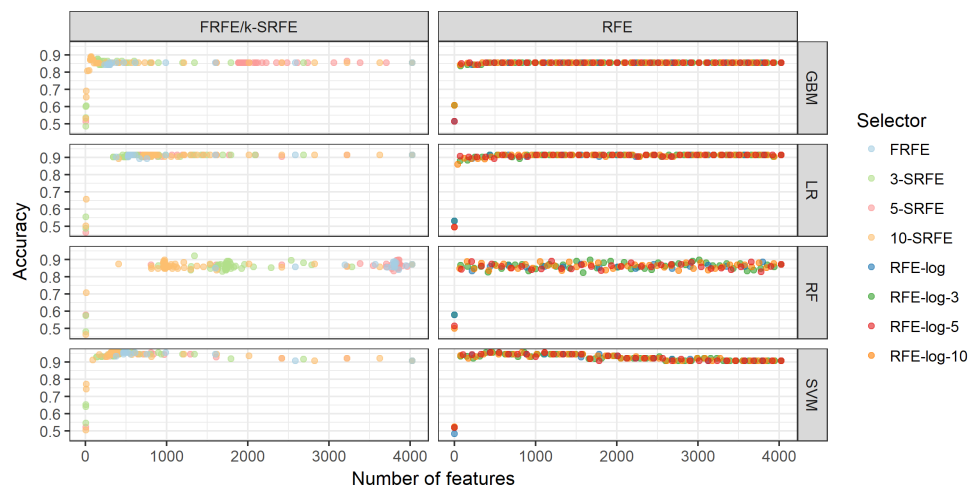


Figure S15. Mean validation scores for a single experiment fold during feature elimination on the lymphoma dataset; plot best viewed online in color.

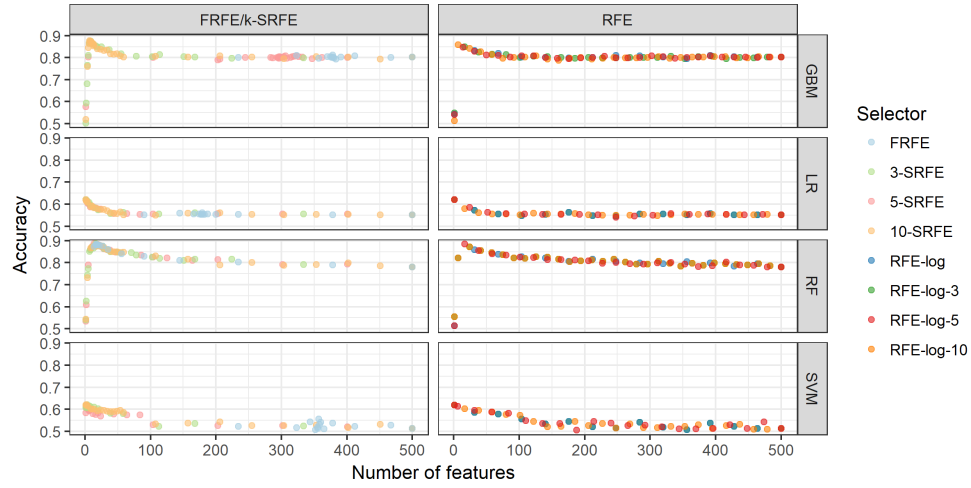


Figure S16. Mean validation scores for a single experiment fold during feature elimination on the madelon dataset; plot best viewed online in color.

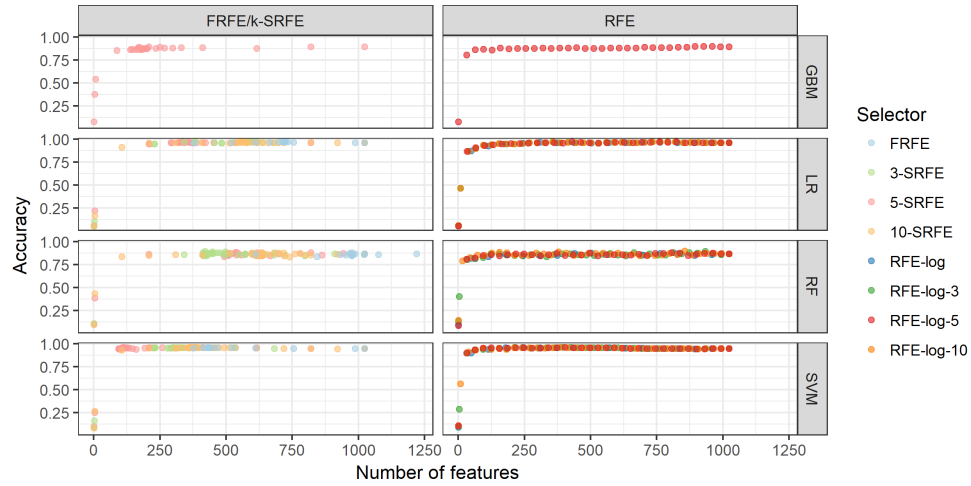


Figure S17. Mean validation scores for a single experiment fold during feature elimination on the ORL dataset; plot best viewed online in color.

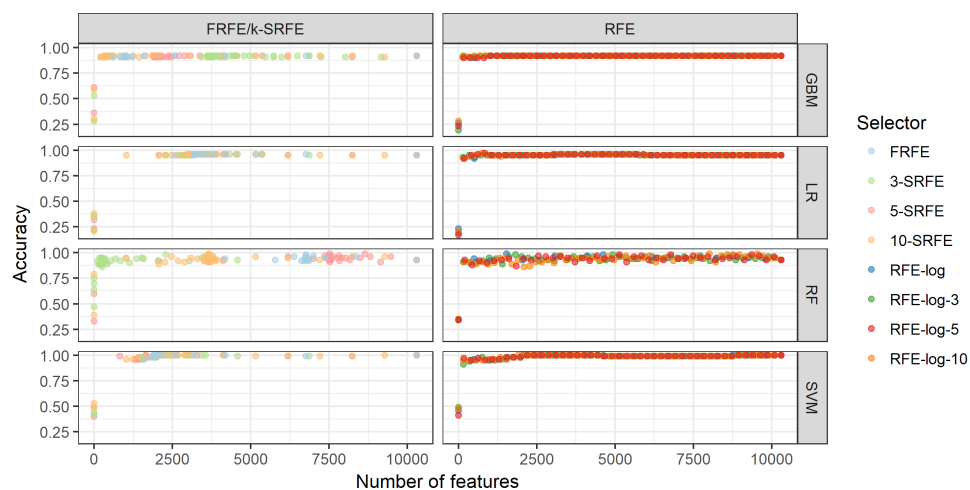


Figure S18. Mean validation scores for a single experiment fold during feature elimination on the orlraws10P dataset; plot best viewed online in color.

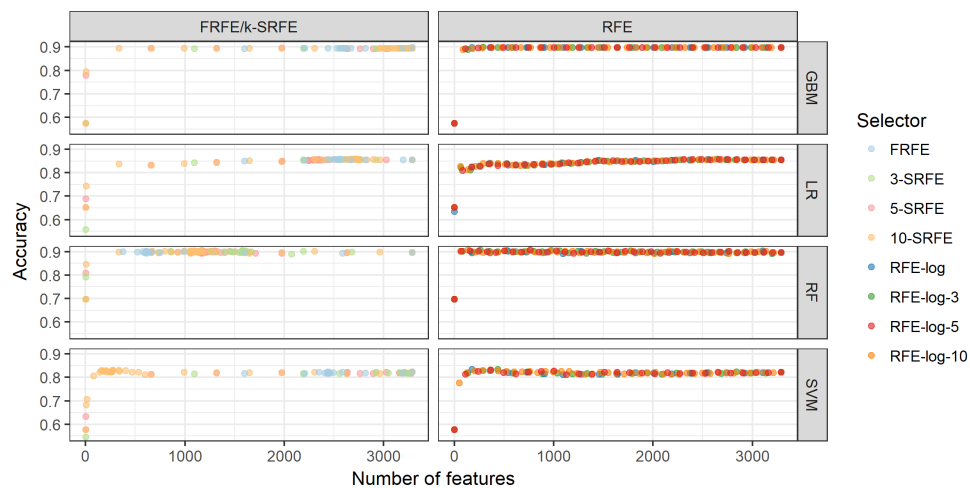


Figure S19. Mean validation scores for a single experiment fold during feature elimination on the PCMAC dataset; plot best viewed online in color.

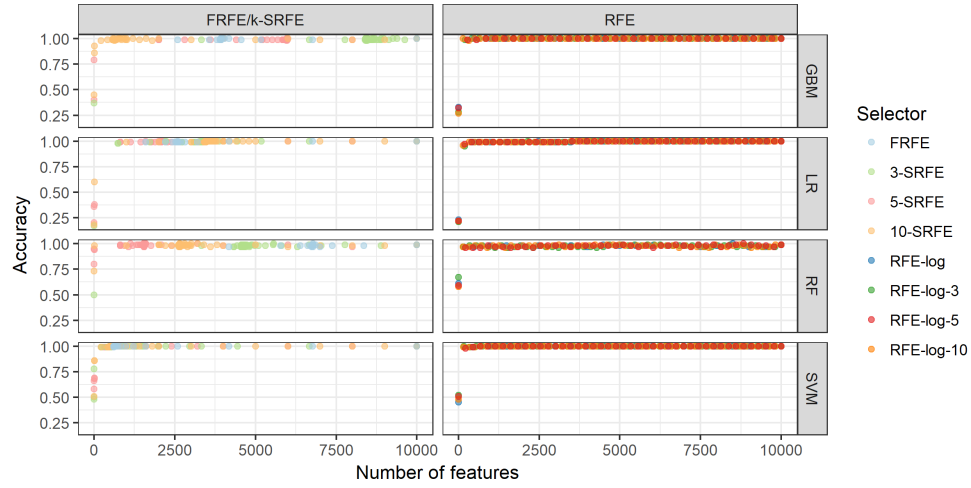


Figure S20. Mean validation scores for a single experiment fold during feature elimination on the pixraw10P dataset; plot best viewed online in color.

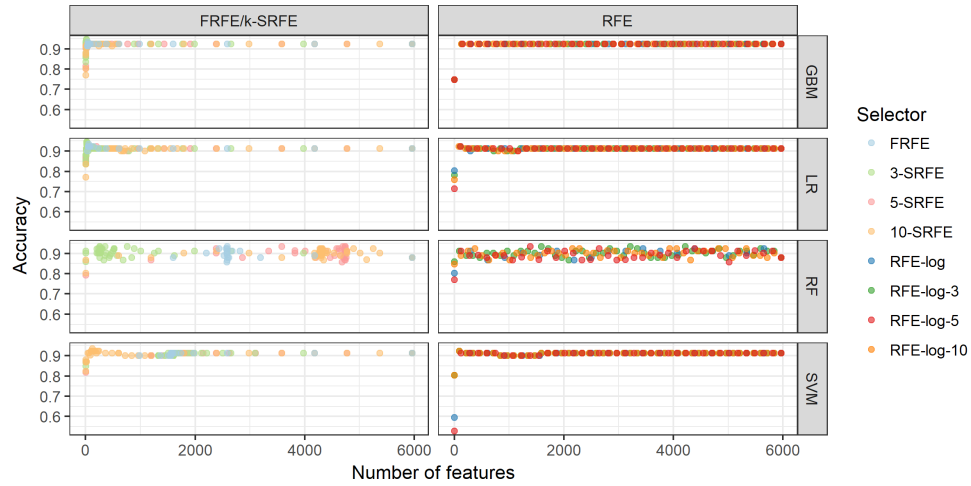


Figure S21. Mean validation scores for a single experiment fold during feature elimination on the Prostate-GE dataset; plot best viewed online in color.

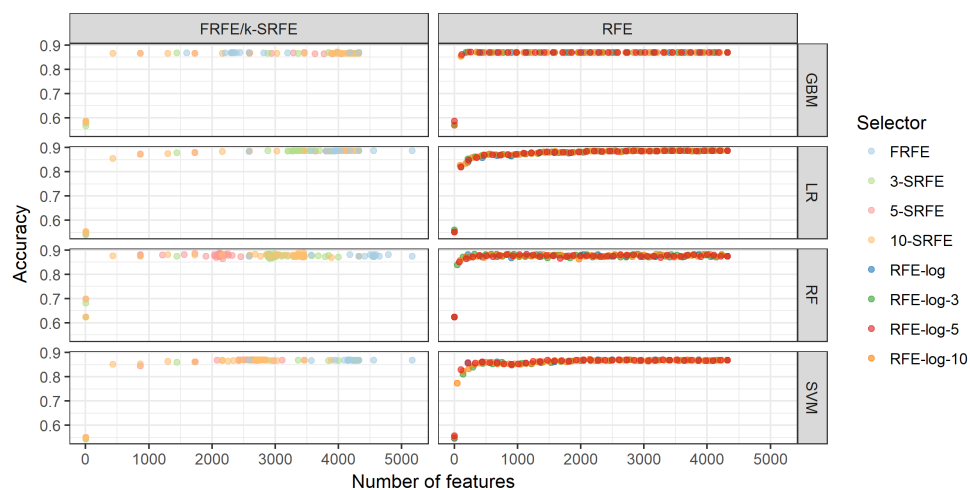


Figure S22. Mean validation scores for a single experiment fold during feature elimination on the RELATHE dataset; plot best viewed online in color.

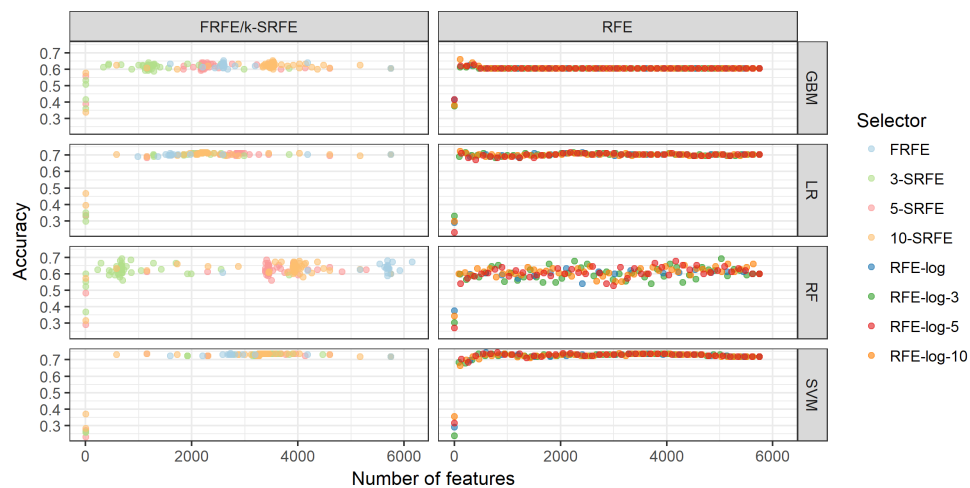


Figure S23. Mean validation scores for a single experiment fold during feature elimination on the TOX-171 dataset; plot best viewed online in color.

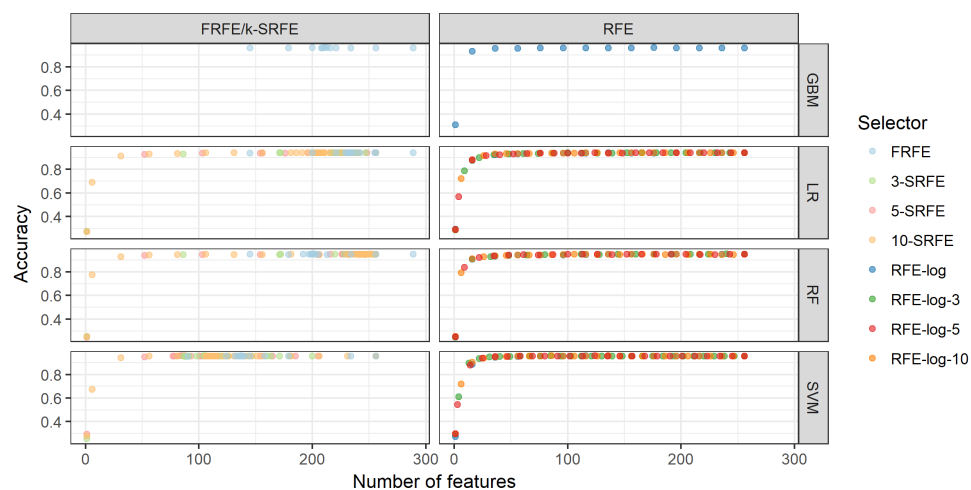


Figure S24. Mean validation scores for a single experiment fold during feature elimination on the USPS dataset; plot best viewed online in color.

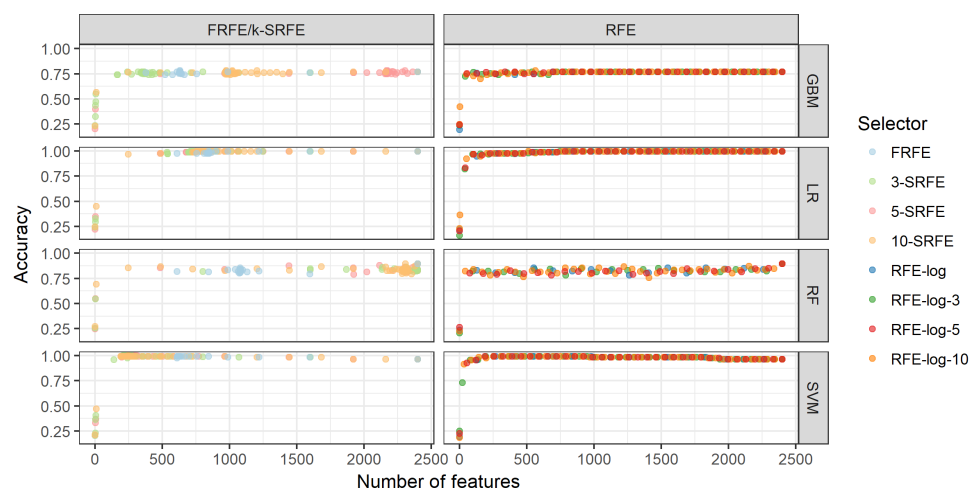


Figure S25. Mean validation scores for a single experiment fold during feature elimination on the warpAR10P dataset; plot best viewed online in color.

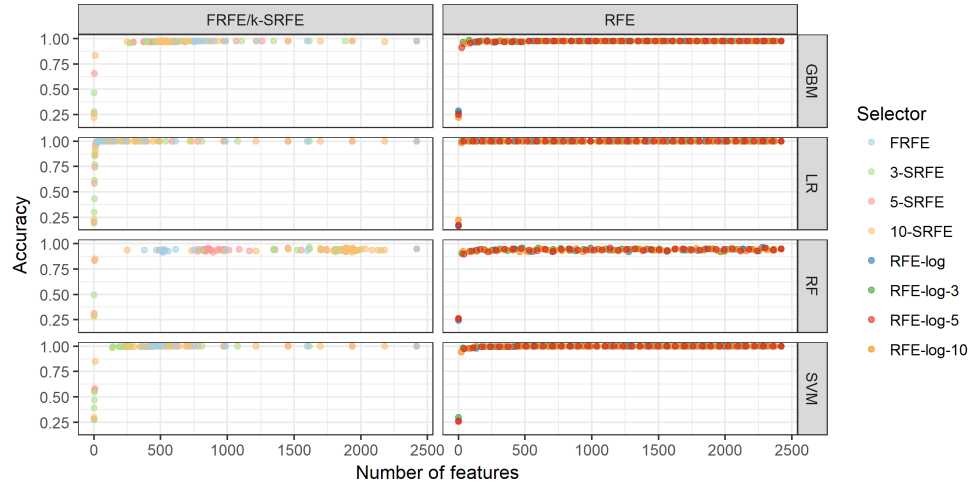


Figure S26. Mean validation scores for a single experiment fold during feature elimination on the warpPIE10P dataset; plot best viewed online in color.

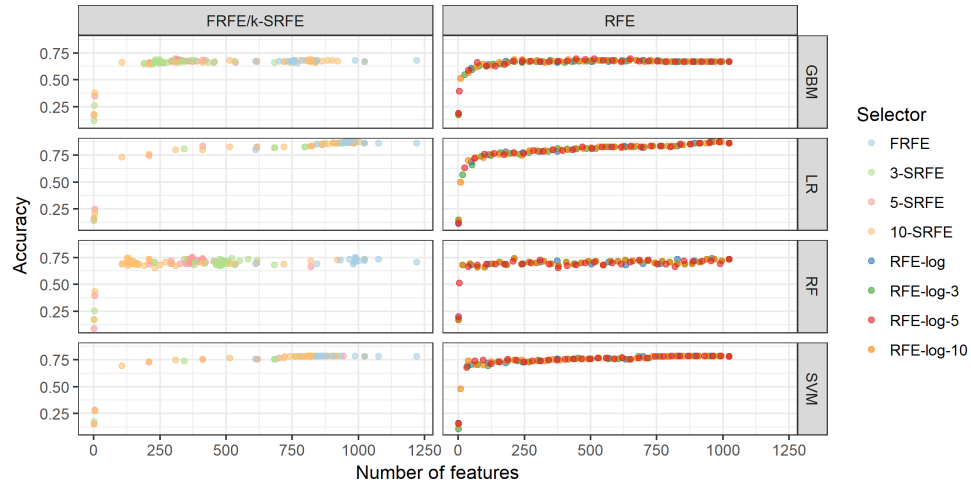


Figure S27. Mean validation scores for a single experiment fold during feature elimination on the Yale dataset; plot best viewed online in color.