

Supplementary Material for the Manuscript “Residual-Guided Randomized Neural Networks”

S.I. COMPUTATIONAL COMPLEXITY

At each stage, generating a pool of M candidate hidden features requires $O(npM)$ operations, corresponding to the evaluation of random affine mappings and activation functions. Scoring the candidates incurs an additional cost of $O(nMq)$ to compute the inner products $\mathbf{G}_t^{\text{pool}\top} \mathbf{R}_t$, along with $O(nM)$ operations to evaluate the associated ℓ_2 norms. Refitting the linear readout after stage t using a naive approach costs $O(n(p+h_t)^2)$ when using the primal formulation, or $O(n^2(p+h_t))$ when using the dual formulation. However, since only a small block of k hidden features is added at each stage, the readout update can be performed incrementally by exploiting the resulting low-rank modification of the augmented matrix. This reduces the refitting cost to $O(nk(p+h_t)) + O(k^2(p+h_t))$. Let T denote the total number of stages. Since $T \approx \lceil h/k \rceil$, the overall computational cost of the proposed method grows approximately linearly with the hidden-unit budget h for fixed pool size M and block size k .

pool size M specifies the number of candidate random hidden nodes generated at that stage. The choice of k and M is adapted based on the number of training samples n and the input dimensionality p . When $n \leq 2000$ or $p \leq 50$, we consider $k \in \{1, 2\}$ and $M \in \{50, 100\}$. For intermediate-scale settings where $2000 < n \leq 20000$ or $50 < p \leq 300$, the search space is expanded to $k \in \{1, 2, 4\}$ and $M \in \{100, 200\}$. For larger-scale problems, we use $k \in \{2, 4\}$ and $M \in \{100, 200\}$. In addition, the total number of hidden features is constrained by a predefined budget, which is set as $\max(50, \min(1000, \lfloor 0.2n \rfloor, 5p))$. This constraint ensures a balance between model expressiveness and computational efficiency while remaining consistent with the stagewise feature expansion procedure.

S.II. EXPERIMENTAL SETUP AND HYPERPARAMETER CONFIGURATION

All experiments are conducted using MATLAB R2023a on a system equipped with an 11th-generation Intel Core i7-11700 processor running at 2.50 GHz, 16 GB of RAM, and a Windows 11 operating system. To ensure a fair and statistically reliable evaluation, all models are assessed using a 5-fold cross-validation protocol combined with grid-based hyperparameter search. For each dataset, the samples are partitioned into five mutually exclusive folds. For a given hyperparameter configuration, the model is trained on four folds and evaluated on the remaining fold. This process is repeated until each fold has served once as the test set. The classification accuracy obtained across the five folds is averaged, and the configuration achieving the highest mean accuracy is reported as the final performance. In addition to the mean accuracy, the standard deviation across the five folds is also reported to reflect performance stability.

For RVFL, ELM, and their residual-guided counterparts, the regularization parameter λ is selected from the set $\{10^{-5}, 10^{-4}, \dots, 10^5\}$, and the number of hidden nodes is tuned within the range 5:10:205. For BLS and its residual-guided variant, the regularization parameter λ is chosen from $\{10^{-6}, 10^{-4}, \dots, 10^6\}$. The number of feature node windows is selected from 1:2:21, the number of feature nodes per window from 5:5:50, and the number of enhancement nodes from 5:10:105. For the proposed residual-guided framework, additional hyperparameters control the stagewise feature selection process. In particular, the block size k denotes the number of hidden features added at each stage, while the

TABLE I: Dataset-wise results on 32 binary datasets.

Dataset	RVFL	RG-RVFL [†]	ELM	RG-ELM [†]	BLS	RG-BLS [†]
acute_inflammation	100	100	100	100	100	100
acute_nephritis	100	100	100	100	100	100
molec_biol_promoter	71.8182	75.5411	68.9610	77.3593	83.9827	85.8874
parkinsons	81.0256	82.0513	80.5128	81.0256	81.0256	82.0256
pittsburg_bridges_T_OR_D	87.2381	89.2381	87.1429	88.1429	89.2381	90.1905
bank	89.6925	90.0022	89.5378	89.8032	89.7368	89.7589
blood	76.6380	76.9047	76.6389	77.0398	77.3047	78.1047
breast_cancer	70.1754	70.5263	70.1754	70.1754	70.9074	71.5910
breast_cancer_wisc	88.4173	90.1357	88.2785	89.5642	87.9908	88.9928
breast_cancer_wisc_diag	93.8457	95.2554	94.5552	95.0784	94.2028	95.3240
chess_krvkp	81.1655	88.8291	79.4141	87.9228	84.3870	83.7923
congressional_voting	63.2184	63.6782	63.2184	63.4483	63.4483	63.9080
cylinder_bands	65.6349	68.7626	68.1915	69.1357	69.5393	70.1275
echocardiogram	84.6724	85.4416	84.6724	86.2108	83.1624	85.1624
heart_hungarian	72.4547	76.1777	76.8615	76.1835	78.5973	77.9018
hepatitis	85.1613	85.8065	84.5161	85.8065	87.0968	88.2258
horse_colic	85.5942	86.6864	85.6016	87.2195	85.8793	86.0648
ionosphere	89.1911	92.0362	90.3380	91.4728	88.3461	89.1952
mammographic	79.9196	80.0248	79.6098	79.5056	79.0895	79.1899
monks_1	84.3292	93.1532	83.4299	91.8951	76.0505	81.9932
monks_2	82.3457	89.5014	82.5193	90.8375	73.1915	74.1942
monks_3	91.3382	92.7846	91.5152	93.1466	86.8272	88.9894
musk_1	67.2763	73.1206	67.2456	71.2368	76.2654	78.8969
oocytes_merluccius_nucleus_4d	82.2898	83.9517	82.1908	84.1502	82.7800	84.2688
oocytes_trisopterus_nucleus_2f	78.8314	79.8181	77.5206	80.0390	79.0554	80.2728
pima	73.5736	74.4877	72.6594	74.4843	72.5236	74.0049
spect	68.3019	68.6792	67.5472	67.9245	69.0566	71.9434
spectf	79.3431	80.4612	79.3431	79.7135	79.7135	79.7205
statlog_australian_credit	68.2609	68.5507	68.1159	68.9855	68.4058	68.7159
statlog_german_credit	77.2000	77.7000	76.4000	77.9000	76.9000	77.9000
statlog_heart	81.4815	81.8519	80.7407	80.7407	82.2222	84.2222
tic_tac_toe	89.0303	92.3653	88.7178	92.0561	96.0143	98.3273
Average Accuracy	80.92	82.92	80.82	82.76	81.65	82.78
Average Std. Dev.	8.91	7.88	8.36	7.76	6.24	5.75
Average Rank	1.97	1.03	1.88	1.13	1.91	1.09

[†] denotes the proposed counterpart.

TABLE II: Dataset-wise result on 39 multi-class datasets.

Dataset	RVFL	RG-RVFL [†]	ELM	RG-ELM [†]	BLS	RG-BLS [†]
abalone	63.4179	63.8732	63.3465	63.8729	63.4657	63.9856
annealing	89.1924	91.1962	89.6356	91.0838	89.6344	90.6400
arrhythmia	65.4823	71.0208	65.7192	68.3663	64.1587	65.2576
audiology_std	69.2949	69.8718	67.7821	69.8333	69.8333	70.8718
cardiotocography_10clases	69.6156	71.3099	69.2395	70.7451	65.5708	66.4182
cardiotocography_3clases	85.2331	86.2683	85.3743	86.2683	85.9390	86.8921
contrac	40.5239	41.6098	40.8666	41.2729	45.0847	45.3691
energy_y1	89.1902	91.5338	89.3116	90.8777	88.4135	89.5392
energy_y2	90.3599	91.9277	89.9728	91.5338	90.1070	91.3667
flags	52.1188	54.1430	52.1053	53.1309	53.1309	53.6302
glass	38.1506	43.2780	39.0808	42.8128	40.0111	40.9524
hayes_roth	61.2500	62.5000	60.0000	63.1250	65.6250	67.7500
heart_cleveland	59.6995	60.0437	58.6721	59.0601	59.6885	59.7104
heart_switzerland	45.6000	47.3000	47.3000	48.9000	47.2667	45.6667
heart_va	39.5000	41.0000	39.0000	41.0000	41.0000	42.0000
image_segmentation	87.8355	90.2597	86.9697	90.3030	88.7446	90.8596
iris	75.3333	76.0000	76.0000	78.0000	77.3333	79.3333
letter	80.3300	85.4300	80.0900	84.7800	84.7350	87.9345
low_res_spect	87.7588	89.2647	87.7605	89.0760	86.2511	88.3560
lung_cancer	50.9524	66.1905	53.8095	53.3333	71.9048	72.3810
lymphography	86.4828	88.4598	85.8161	88.4828	85.7701	86.0575
molec_biol_splice	51.8809	58.0251	51.8809	57.0219	68.0564	69.4679
nursery	70.5324	75.2546	70.2623	73.7809	70.7022	73.8426
optical	96.2100	98.1139	96.4769	97.9181	96.6370	97.1174
page_blocks	95.2491	95.7974	95.2490	95.6696	95.3771	96.7607
pendigits	98.4443	99.0448	98.4807	98.9902	98.9811	99.1630
pittsburg_bridges_MATERIAL	75.8442	81.5152	77.8788	82.4675	73.9827	75.1602
pittsburg_bridges_TYPE	42.8571	49.5238	42.8571	50.4762	42.8571	49.5238
post_operative	72.2222	73.3333	72.2222	72.2222	70.0000	70.3333
seeds	87.6190	89.5238	87.1429	89.0476	89.5238	91.9048
semeion	84.4321	91.0227	84.5565	89.9552	87.1925	92.1602
soybean	89.4450	90.6172	88.8622	89.5942	89.0103	88.8643
statlog_landsat	81.5385	84.6775	81.7249	84.5532	82.3621	84.8562
statlog_vehicle	81.0846	83.6881	81.3227	82.8625	81.3241	80.8514
teaching	70.7097	72.0215	70.7097	71.3548	73.3763	72.7097
vertebral_column_3clases	64.8387	65.4839	65.1613	65.1613	67.4194	69.6774
wall_following	77.2369	79.8034	77.1454	80.4447	78.1901	80.0443
wine	97.2222	96.6349	95.5238	96.0952	97.7778	97.2222
zoo	95.0000	95.0000	95.0000	95.0000	97.0000	97.0000
Average Accuracy	73.33	75.94	73.34	75.35	74.96	76.20
Average Std. Dev.	10.43	9.11	10.12	8.99	7.98	7.17
Average Rank	1.96	1.04	1.94	1.06	1.86	1.14

[†] denotes the proposed counterpart.