

437 **A Training details**

438 We use ten memory items for our MEMTO model, corresponding to the number of clusters in our
 439 K -means clustering. We elaborate on our process for deciding the number of clusters in Appendix C.2
 440 To determine anomalies, we set the threshold as the top- $p\%$ of the combined results of the anomaly
 441 scores from both the training and validation data, with specified values of p for each dataset outlined
 442 in Table 5, following [40]. We set λ in the objective function to 0.01, use Adam optimizer [15] with a
 443 learning rate of $5e-5$, and employ early stopping with the patience of 10 epochs against the validation
 444 loss during training. Our experiments are conducted using the Pytorch framework on four NVIDIA
 445 GTX 1080 Ti 12GB GPUs. Furthermore, during the execution of our experiment, we make partial
 446 references to the code of [40].

447 **A.1 Hyperparameter settings**

448 Important hyperparameters of MEMTO were determined through grid search, while others were set
 449 to commonly used default values based on empirical observations. We performed a grid search to
 450 determine the values of each hyperparameter within the following range:

- 451 • $\lambda \in \{1e+0, 5e-1, 1e-1, 5e-2, 1e-2, 5e-3, 1e-3\}$
- 452 • $lr \in \{1e-4, 3e-4, 5e-4, 1e-5, 3e-5, 5e-5\}$
- 453 • $\tau \in \{0.1, 0.3, 0.5, 0.7, 0.9\}$
- 454 • $M \in \{5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100\}$

455 , where lr , τ , and M denote the learning rate, the temperature in the softmax function, and the
 456 number of clusters, respectively. Since we set the centroids of clusters as memory items, the number
 457 of memory items and that of clusters are the same. We set the optimal hyperparameters as follows:
 458 λ as $1e-2$, lr as $5e-5$, τ as 0.1, and M as 10. All experiments in this paper are conducted using the
 459 same hyperparameters regardless of the dataset.

460 **A.2 Dataset**

Table 5: Details in five benchmarks. The number of samples in the training, validation, and test sets is represented in the columns labeled ‘Train,’ ‘Valid,’ and ‘Test,’ respectively. The ‘ $p\%$ ’ column indicates the anomaly ratio used in the experiment. The ‘Dim’ column shows the dimension size of the data for each dataset.

	Train	Valid	Test	$p(\%)$	Dim
SMD	566,724	141,681	708,420	0.5	38
MSL	46,653	11,664	73,729	1.0	55
PSM	105,984	26,497	87,841	1.0	26
SMAP	108,146	27,037	427,617	1.0	25
SWaT	396,000	99,000	449,919	0.1	53

461 Table 5 shows the statistical details of datasets used in experiments. We obtained SWaT by submitting
 462 a request through https://itrust.sutd.edu.sg/itrust-labs_datasets/.

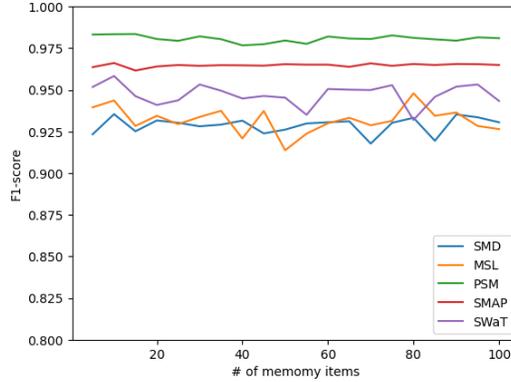


Figure 4: Number of memory items

480 the performance variance across datasets is small. Nevertheless, increasing the number of memory
 481 items raises the number of clusters needed for K -means clustering, thereby increasing computational
 482 complexity. Hence, we designate ten memory items as the default value after weighing performance
 483 and computational complexity.

484 Our study highlights the effectiveness of employing a restricted number of memory items to extract
 485 prototypical features of normal patterns in time series data. Unlike computer vision, which may
 486 require thousands of memory items [8], we demonstrate that only ten memory items were necessary
 487 for this task in the time series domain.

488 C.3 Number of decoder layers

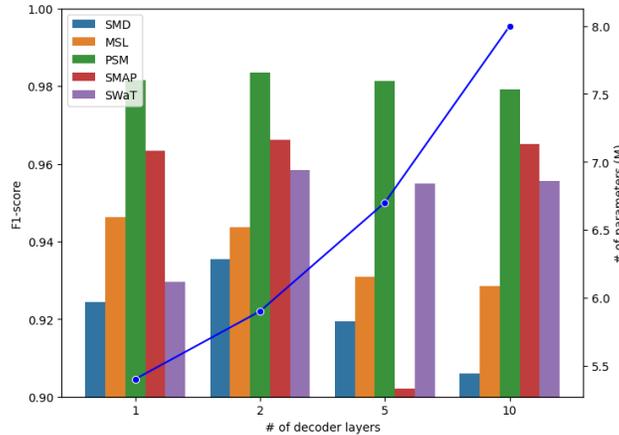


Figure 5: F1-score and number of parameters, according to the number of decoder layers. The right y-axis represents the values of the blue line graph in million units, while the left y-axis represents the values of the bar graph.

489 Figure 5 provides the performance of MEMTO under different numbers of decoder layers. As
 490 shown in Figure 5, a decoder that is too shallow (e.g., a decoder with a single layer) performs
 491 worse because it lacks sufficient capacity to reconstruct the input data accurately. On the other
 492 hand, if the decoder is too large (e.g., decoder with ten layers), it can become overly expressive
 493 and reconstruct even anomalies regardless of the encoding ability of the encoder. Therefore, it can
 494 lead to an over-generalization problem, which can ultimately decrease the performance of anomaly
 495 detection by reconstructing anomalies too accurately. Furthermore, a larger decoder layer with more
 496 parameters can increase computational and memory costs. We empirically find that considering
 497 the balance between performance and resource cost, a decoder with two layers is most suitable for
 498 anomaly detection tasks presented in our paper.

499 **D Additional details for discussion**

500 **D.1 LSD values**

Table 7: The mean LSD values corresponding to test data.

	SMD		MSL		PSM		SMAP		SWaT	
	Normal	Abnormal								
MemAE	814.7836	842.2023	622.5195	640.4954	766.2473	782.1895	710.4929	706.3115	795.7227	770.9069
MNAD	259.3633	258.0175	791.6371	788.2654	292.3340	293.4836	301.3480	301.2153	303.1933	310.9818
Ours	297.5692	330.1162	249.8632	263.4532	340.7552	363.7520	237.0070	234.7110	450.0926	721.3093

501 Table 7 shows mean LSD values of normal and abnormal samples across various domains of datasets
 502 while using different memory module mechanisms. In most datasets, our proposed Gated memory
 503 module consistently exhibits a lower mean LSD value for normal samples than for abnormal samples.
 504 Furthermore, the relative difference between these values is more significant than other memory
 505 module mechanisms. These results demonstrate the efficacy of our memory module mechanism in
 506 capturing prototypical features of normal patterns in data.

507 **D.2 Anomaly score**

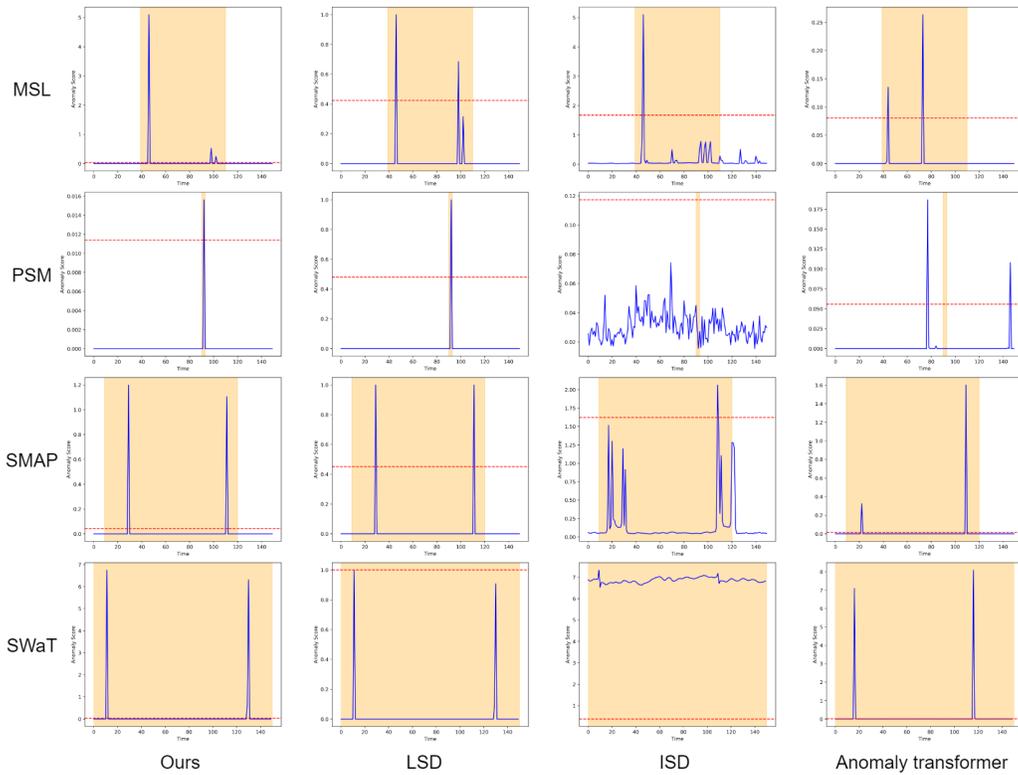


Figure 6: Visualization of anomaly scores for MSL, PSM, SMAP, and SWaT datasets.

508 Figure 6 visually represents the anomaly scores for benchmark datasets not discussed in Section 4.4
 509 We randomly sampled data of length 150 from MSL, PSM, SMAP, and SWaT test datasets and
 510 plotted the anomaly scores for each segment. Compared to other baselines, our proposed method
 511 consistently detects anomalies precisely with a low false positive rate from the perspective of the
 512 point adjustment method.