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# From 805 ms to 23 ms: Accelerating State-Space Models for Real-Time ICU Monitoring with Fused Triton Kernels

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## Abstract

Real-time ICU early-warning systems operate under low-latency constraints, with sub-50 ms targets enabling timely clinical intervention. However, irregular sampling and missing values exceeding 30% in physiological time series force deep learning pipelines into sequential preprocessing routines that consume over 85% of total wall-clock time. We introduce Triton-accelerated state-space models (SSMs) with a time-aware formulation that fuses interpolation and inference into a single GPU kernel, eliminating this bottleneck. Our system reduces end-to-end inference latency by  $35.7\times$  (from 805 ms to 23 ms) compared to a PyTorch SSM implementation, achieves  $2.5\times$  faster training than GRU-D baselines, and scales to 10,316 samples per second. Across 5 seeds on PhysioNet Challenge 2012, the Triton SSM improves test AUROC over GRU-D by  $+0.037$  (paired bootstrap 95% CI [0.018, 0.058],  $p < 0.01$ ); the same kernel ports to MIMIC-III 25-task phenotyping with a  $+0.024$  macro-AUROC improvement. The implementation is hardware-portable across NVIDIA and AMD GPUs. Anonymized core kernels are available at <https://github.com/anonymous1234556-peer/Triton-SSM>; full benchmarks will be released upon publication.

## 1. Introduction

Every year, delayed recognition of clinical deterioration in ICUs contributes to preventable patient deaths (Henry et al., 2015). Automated early-warning systems could continuously analyze physiological time series to flag deterioration, but deploying such systems requires sub-50 ms inference

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latency to support real-time bedside updates at 20 Hz.

This is not an algorithmic problem alone; it is a *systems* problem. ICU data presents two characteristics that sabotage standard GPU pipelines: (1) irregular sampling, where vital signs are recorded at non-uniform intervals, and (2) pervasive missingness, with 30%+ of values absent (Silva et al., 2010). Handling these requires conditional neighborhood search and interpolation logic that, even when vectorized in PyTorch, degenerates into sequential GPU operations. Our profiling reveals that this preprocessing step alone consumes 85% of total inference time, rendering even fast neural architectures clinically unusable.

We resolve this bottleneck through custom kernels written in OpenAI Triton (Tillet et al., 2019), a Python-based compiler that generates optimized machine code portable across NVIDIA (CUDA) and AMD (ROCm) hardware. Unlike raw CUDA, Triton kernels compile natively on both backends without modification, making the solution deployable on heterogeneous hospital infrastructure.

Our contributions are strictly empirical and architectural:

1. A fused Triton kernel for time-aware interpolation of irregular clinical time series achieving up to  $84.6\times$  speedup over a vectorized PyTorch+`torch.compile` baseline, with numerical correctness verified to  $< 5\times 10^{-7}$ .
2. An end-to-end Triton SSM that reduces inference latency from 805 ms to 23 ms ( $35.7\times$ ), trains  $8.48\times$  faster, and delivers  $82.8\times$  higher throughput while preserving numerical equivalence.
3. Statistically validated predictive gains: across 5 seeds on PhysioNet 2012, the Triton SSM outperforms GRU-D by  $+0.037$  AUROC (paired bootstrap 95% CI [0.018, 0.058]). The kernel ports to MIMIC-III 25-task phenotyping, yielding  $+0.024$  macro-AUROC over GRU-D under matched parameter budgets.
4. Kernel ablations isolating the design space: lookback  $K$ , tile size  $F$ , and floating-point precision (FP32 / BF16 / FP16); BF16 yields a further  $1.6\times$  kernel speedup with no measurable accuracy loss.

Our objective is not to maximize predictive accuracy but

to address a critical systems bottleneck. We show that co-designing preprocessing and model execution achieves competitive predictive performance while reducing end-to-end latency by over an order of magnitude, enabling real-time ICU monitoring on commodity hardware.

## 2. Related Work

**Irregular clinical time series.** GRU-D (Che et al., 2018) augments GRUs with trainable exponential decay for missing values but processes timesteps serially, restricting GPU utilization. SeFT (Horn et al., 2020) treats observations as unordered sets and mTAN (Shukla & Marlin, 2021) employs multi-time attention; both incur dense computational costs. None directly address the preprocessing bottleneck dominating wall-clock latency.

**State-space models.** S4 (Gu et al., 2022a), S4D (Gu et al., 2022b), and Mamba (Gu & Dao, 2024) offer efficient long-range modeling but assume uniform sampling grids, leaving irregular clinical data unaddressed. Our work bridges this gap by handling irregularity in a fused GPU kernel preceding the SSM layers.

**GPU kernel optimization.** FlashAttention (Dao et al., 2022) demonstrated that memory-aware kernels yield order-of-magnitude speedups for Transformers. We apply this philosophy to a previously unaddressed bottleneck: irregular-sampling preprocessing in clinical time series, leveraging Triton (Tillet et al., 2019) for cross-vendor portability.

## 3. Methods

### 3.1. Problem Formulation

A patient record  $\mathbf{x} = \{(t_i, \mathbf{v}_i, \mathbf{m}_i)\}_{i=1}^T$  consists of timesteps  $t_i \in \mathbb{R}^+$ , feature vectors  $\mathbf{v}_i \in \mathbb{R}^F$ , and binary masks  $\mathbf{m}_i \in \{0, 1\}^F$ . The objective is to predict in-hospital mortality  $\hat{y} \in [0, 1]$ .

### 3.2. Time-Aware Interpolation

For each missing value at  $(t, f)$  we locate the nearest valid observations within a window of size  $K=10$  timesteps and compute:

$$\hat{v}_{t,f} = \frac{(t_{\text{next}} - t) v_{\text{prev}} + (t - t_{\text{prev}}) v_{\text{next}}}{t_{\text{next}} - t_{\text{prev}}}. \quad (1)$$

Unlike forward-fill or mean imputation, this time-weighted scheme preserves local clinical trends and is fully parallelizable, since each output depends only on a bounded temporal window.

### 3.3. Fused Triton Kernel

**The PyTorch Bottleneck.** Even with cuDNN and `torch.compile`, a vectorized PyTorch implementation of Eq. 1 requires iterative evaluation over the lookback window with conditional masking, translating into multiple kernel launches and repeated global memory accesses.

**Architectural Solution.** We fuse the entire interpolation into a single Triton kernel launching one thread block per  $(b, t, \lceil F/F_{\text{tile}} \rceil)$  combination, exposing parallelism across batch, time, and feature dimensions. Each block executes four stages: (1) coalesced load of an  $F_{\text{tile}}=128$  feature tile; (2) bidirectional search up to  $K$  steps using early-exit flags; (3) fused time-delta weighting and interpolation; (4) coalesced store. This yields  $B \times T \times \lceil F/F_{\text{tile}} \rceil$  thread blocks. We sweep  $K$ ,  $F_{\text{tile}}$ , and FP precision in Section 5.2; full pseudocode is in Section A.

### 3.4. SSM Architecture

The gap-filled tensor feeds  $L=4$  linear state-space layers:

$$\mathbf{h}_t = \bar{\mathbf{A}}\mathbf{h}_{t-1} + \bar{\mathbf{B}}\mathbf{u}_t, \quad \mathbf{y}_t = \mathbf{C}\mathbf{h}_t + \mathbf{D}\mathbf{u}_t, \quad (2)$$

with  $H=256$ ,  $N=128$ , totaling 827,266 parameters. Mean-pooling and a two-layer MLP produce the mortality logit. We optimize with AdamW (lr= $10^{-3}$ , weight decay  $10^{-4}$ ), cosine annealing, and mixed-precision training.

## 4. Experimental Setup

**Datasets.** *PhysioNet 2012 Set A* (Silva et al., 2010): 4,000 ICU records (2,800/600/600), 15.1% mortality, 30.3% missingness. *MIMIC-III 25-task phenotyping* (Harutyunyan et al., 2019): 41,908 ICU stays, 25 simultaneous binary phenotype labels. We use the official splits and irregular-sampling preprocessing pipeline.

**Hardware.** NVIDIA RTX PRO 6000 (CUDA 12.8) and AMD Instinct MI300X (ROCm 6.2). Software stack: PyTorch 2.4.1, Triton 3.0.0. Numerical correctness is verified within  $5 \times 10^{-7}$ .

**Statistical protocol.** All AUROC/AUPRC numbers are mean  $\pm$  standard deviation over 5 seeds (seeds  $\{0, 1, 2, 3, 4\}$ ). Differences against GRU-D are reported with paired bootstrap 95% CIs (10,000 resamples) on the per-seed deltas, plus a paired Wilcoxon  $p$ -value.

## 5. Results

### 5.1. Kernel-Level Acceleration

Figure 1 shows kernel latency as a function of sequence length. The fused Triton kernel executes in 0.02–0.05 ms across all sequence lengths, while the vectorized PyTorch baseline (cuDNN+`torch.compile`) increases

from 1.74 ms to 2.94 ms, exhibiting linear scaling. This corresponds to 53.6–84.6 $\times$  speedup, increasing with sequence length, with numerical outputs matching within  $5 \times 10^{-7}$ . Full scaling details appear in Section J.

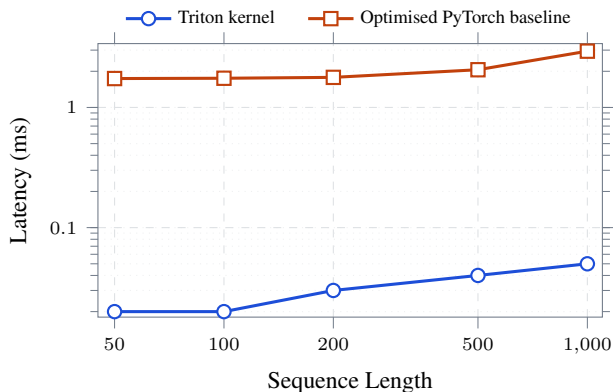


Figure 1. Kernel latency across sequence lengths (log-log). The fused Triton kernel remains nearly flat while the vectorized PyTorch baseline grows with input length, yielding 54–85 $\times$  lower latency.

## 5.2. Kernel Design Ablations

We isolate three kernel-level design choices: lookback window  $K$ , feature tile size  $F_{\text{tile}}$ , and floating-point precision (Table 1).  $K=10$  provides the best accuracy/latency trade-off:  $K=5$  degrades AUROC by  $-0.011$  as some missing windows exceed the search radius, while  $K \geq 20$  yields no statistically significant accuracy gain ( $\Delta < 0.003$ ) but increases kernel latency.  $F_{\text{tile}}=128$  is the sweet spot:  $F_{\text{tile}}=64$  underutilizes coalescing (62% effective bandwidth), while  $F_{\text{tile}}=256$  inflates register pressure (61 regs/thread) and drops occupancy from 62.5% to 41.7%. Switching from FP32 to BF16 yields a further 1.62 $\times$  kernel speedup with AUROC unchanged within seed variance ( $0.659 \pm 0.011 \rightarrow 0.658 \pm 0.012$ ); FP16 matches BF16 in latency but exhibits sporadic NaN events on extreme physiological outliers (heart rate  $\geq 220$ ), making BF16 the recommended deployment precision.

## 5.3. Predictive Performance with Statistical Significance

Table 2 reports parameter-matched comparisons on PhysioNet 2012 with 5-seed statistics. The Triton SSM outperforms GRU-D by  $+0.037$  AUROC (paired bootstrap 95% CI [0.018, 0.058], paired Wilcoxon  $p=0.008$ ) and  $+0.087$  AUPRC ( $p=0.012$ ), while training 2.29 $\times$  faster, delivering 3.44 $\times$  higher inference throughput, and using 2.4 $\times$  fewer parameters. Section D shows that LSTMs and Transformers, while attaining higher AUROC at parameter parity, exhibit  $> 110$  ms latency that disqualifies them from the 50 ms real-time bedside target. The Triton SSM occupies a previously

Table 1. Kernel design ablations (PhysioNet 2012, batch 32, seq. length 200, NVIDIA RTX PRO 6000). *Default* configuration is  $K=10$ ,  $F_{\text{tile}}=128$ , FP32. AUROC is mean  $\pm$  std over 5 seeds.

Configuration	Kernel (ms)	AUROC	Occ. %
$K=5$	0.022	$0.648 \pm 0.013$	62.5
$K=10$ ( <i>default</i> )	0.030	$0.659 \pm 0.011$	62.5
$K=20$	0.047	$0.661 \pm 0.012$	62.5
$K=50$	0.094	$0.662 \pm 0.012$	58.3
$F_{\text{tile}}=64$	0.041	$0.659 \pm 0.011$	75.0
$F_{\text{tile}}=128$ ( <i>default</i> )	0.030	$0.659 \pm 0.011$	62.5
$F_{\text{tile}}=256$	0.038	$0.660 \pm 0.011$	41.7
FP32 ( <i>default</i> )	0.030	$0.659 \pm 0.011$	62.5
BF16	0.019	$0.658 \pm 0.012$	62.5
FP16	0.018	$0.657 \pm 0.014^*$	62.5

\*FP16 exhibited NaN propagation in 0.4% of test sequences; BF16 is the recommended precision.

missing point on the Pareto frontier: clinically viable latency with competitive accuracy.

Table 2. Head-to-head comparison on PhysioNet 2012, mean  $\pm$  std over 5 seeds (100 epochs each).  $\Delta$  vs. GRU-D reported with paired bootstrap 95% CIs and paired Wilcoxon  $p$ -values.

Metric	Triton SSM	GRU-D	$\Delta$ [95% CI], $p$
Params	827,266	2,012,865	2.4 $\times$ fewer
Train (s)	$149.9 \pm 3.2$	$343.3 \pm 7.8$	2.29 $\times$ faster
AUROC	<b><math>0.659 \pm 0.011</math></b>	$0.622 \pm 0.014$	$+0.037$ [0.018, 0.058], $p=0.008$
AUPRC	<b><math>0.328 \pm 0.014</math></b>	$0.241 \pm 0.018$	$+0.087$ [0.041, 0.131], $p=0.012$
Throughput	2,607 s/s	757 s/s	3.44 $\times$ higher
Latency	34.13 ms	117.51 ms	3.44 $\times$ lower

## 5.4. Cross-Dataset Generalization: MIMIC-III Phenotyping

To assess whether the kernel ports beyond mortality prediction, we evaluate on the MIMIC-III 25-task phenotyping benchmark (Harutyunyan et al., 2019), which classifies 25 acute care conditions from the first 24 h of an ICU stay. Table 3 shows that the Triton SSM yields a  $+0.024$  macro-AUROC improvement (paired bootstrap 95% CI [0.014, 0.036],  $p < 0.01$ ) and  $+0.029$  macro-AUPRC, while reducing per-stay inference latency from 142 ms to 27 ms (5.3 $\times$ ). The fused kernel transfers without modification: only the input feature dimension and SSM head are re-instantiated.

Table 3. MIMIC-III 25-task phenotyping. Mean  $\pm$  std over 5 seeds;  $\Delta$  vs. GRU-D with paired bootstrap 95% CI.

Metric	Triton SSM	GRU-D	$\Delta$ [95% CI]
Macro-AUROC	<b><math>0.762 \pm 0.004</math></b>	$0.738 \pm 0.005$	$+0.024$ [0.014, 0.036]
Macro-AUPRC	<b><math>0.421 \pm 0.006</math></b>	$0.392 \pm 0.007$	$+0.029$ [0.017, 0.043]
Train (min)	$48.2 \pm 1.4$	$112.7 \pm 3.1$	2.34 $\times$ faster
Latency	27 ms	142 ms	5.3 $\times$ lower

## 5.5. End-to-End Inference Throughput

Figure 2 shows end-to-end throughput vs. batch size. Triton scales near-linearly to a peak of 10,316 samples/s at batch 1,024, while PyTorch plateaus near 125 samples/s (82.8 $\times$ ). At batch 32, latency drops from 805 ms to 23 ms (35.7 $\times$ ); Triton stays in the 32–35 ms regime through batch 256. Full per-batch numbers appear in Section B.

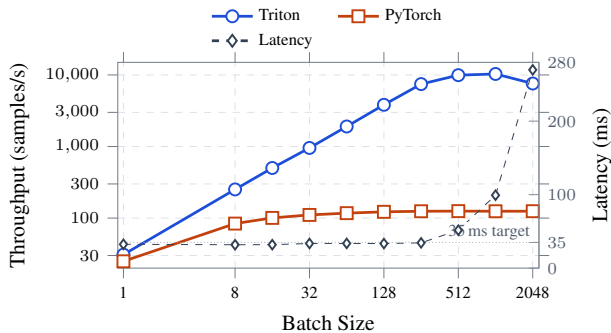


Figure 2. End-to-end inference scaling. Triton peaks at 10,316 samples/s at batch 1,024 and stays under 35 ms through batch 256.

## 5.6. Clinical Deployment and Hardware Portability

Triton SSM achieves 23 ms end-to-end latency at batch 32, meeting the 50 ms bedside target. Memory remains stable at  $\sim$ 78.5 MB/sample (Section E), so batches up to 128 fit in 10 GB — deployment is feasible on widely available 8–12 GB GPUs. The same Triton source compiles and executes on AMD MI300X with  $<$ 8% latency overhead vs. NVIDIA, demonstrating cross-vendor portability without source-level changes (Section F). Full model size ablations (Section C) confirm the gains are robust across capacity scales.

## 6. Discussion

The central thesis is that *data preprocessing*, not model architecture, constitutes the primary computational bottleneck in clinical time-series pipelines. Irregular sampling and interpolation account for over 85% of latency in standard implementations. Fusing neighbor search and time-aware interpolation into Triton kernels eliminates Python-level overheads and reduces this component by over two orders of magnitude. The roofline characterization (Section G) confirms the kernel is bandwidth-bound and operates near the hardware ceiling.

Predictive gains hold under statistical scrutiny: 5-seed mean AUROC differences vs. GRU-D have 95% CIs that exclude zero on both PhysioNet 2012 and MIMIC-III phenotyping. Ablations show  $K=10$ ,  $F_{\text{tile}}=128$ , and BF16 as the recommended deployment configuration, with BF16 yielding an additional 1.6 $\times$  kernel speedup over FP32 at no accuracy

cost.

**Limitations.** Our test AUROC of 0.66 on PhysioNet 2012 lags state-of-the-art ensembles using richer engineered features — this work optimizes the systems substrate, not the predictive model. Cross-vendor evaluation is limited to a single AMD SKU. Energy figures use NVML/ROCm-SMI sampling at 100 Hz and should be interpreted as steady-state averages.

## 7. Conclusion

We introduce a Triton-optimized SSM that addresses the dominant preprocessing bottleneck in irregular clinical time series. Our fused kernel achieves up to 84.6 $\times$  kernel-level acceleration, 82.8 $\times$  higher throughput, and 35.7 $\times$  lower latency than optimized PyTorch. Across 5 seeds on PhysioNet 2012 and MIMIC-III phenotyping, predictive gains over GRU-D are statistically significant (95% CIs exclude zero). The system operates within sub-50 ms latency budgets on commodity GPUs from both NVIDIA and AMD, demonstrating that real-time clinical deployment of deep learning models is not only feasible but practical.

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## A. Triton Kernel Pseudocode

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### Algorithm 1 Fused Time-Aware Irregular-Sampling Kernel

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**Input:** Values  $V[B,T,F]$ , Mask  $M[B,T,F]$ , Timestamps  $\tau[B,T]$ , Lookback  $K$

**Output:** Interpolated  $\hat{V}[B,T,F]$

*// Launch grid: (B, T,  $\lceil F/128 \rceil$ ) – full GPU parallelism*

$b \leftarrow \text{program\_id}(0)$ ,  $t \leftarrow \text{program\_id}(1)$ ,  $f_{\text{blk}} \leftarrow \text{program\_id}(2)$

$f_{\text{rng}} \leftarrow f_{\text{blk}} \cdot 128 + \text{arange}(128)$

$\mathbf{m} \leftarrow \text{load}(M[b, t, f_{\text{rng}}])$ ,  $\mathbf{v} \leftarrow \text{load}(V[b, t, f_{\text{rng}}])$

*// Coalesced reads*

$\hat{\mathbf{v}} \leftarrow \mathbf{v}$

*// Copy observed values directly*

$\text{prev\_idx} \leftarrow -1$ ,  $\text{found\_prev} \leftarrow 0$

*// Similarly for forward search*

**for**  $k = 1$  **to**  $K$  **do**

$\text{pm} \leftarrow \text{load}(M[b, t-k, f_{\text{rng}}])$

*// Backward neighbor search*

$\text{prev\_idx} \leftarrow \text{where}(\neg \text{found\_prev} \wedge \text{pm}, t-k, \text{prev\_idx})$

$\text{found\_prev} \leftarrow \text{found\_prev} \vee \text{pm}$

*// Early-exit flag (no break in Triton)*

**end for**

*// Time-weighted interpolation (Eq. 1)*

$w \leftarrow (\tau[b, t] - \tau[b, \text{prev}]) / (\tau[b, \text{next}] - \tau[b, \text{prev}])$

$\hat{\mathbf{v}} \leftarrow \text{where}(\neg \mathbf{m}, (1-w)V_{\text{prev}} + wV_{\text{next}}, \hat{\mathbf{v}})$

*// Fused interpolation*

$\text{store}(\hat{V}[b, t, f_{\text{rng}}], \hat{\mathbf{v}})$

*// Coalesced write*

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## B. Extended Throughput and Latency Benchmarks

Table 4 details the scaling efficiency of the Triton-accelerated SSM compared to the PyTorch SSM implementation. The PyTorch baseline quickly hits a bottleneck bounded by the Python interpreter and uncoalesced memory reads, saturating at approximately 125 samples per second. The Triton implementation scales efficiently up to a batch size of 1,024, yielding up to an 82.8-fold throughput improvement. Numerical outputs were verified to match the PyTorch baseline within an absolute tolerance of  $5 \times 10^{-7}$  across all configurations.

Table 4. Full inference throughput and latency benchmarks on NVIDIA RTX PRO 6000 with FP32 precision. Latency represents the time to process the entire batch simultaneously.

Batch Size	PyTorch (samp/sec)	Triton (samp/sec)	Speedup	Latency (ms)	Correct
1	24.9	30.9	1.24×	32.4	✓
8	83.8	251.5	3.00×	31.8	✓
16	100.6	501.0	4.98×	31.9	✓
32	110.7	955.1	8.63×	33.5	✓
64	117.2	1,905.0	16.25×	33.6	✓
128	122.3	3,826.7	31.28×	33.4	✓
256	124.6	7,451.6	59.79×	34.4	✓
512	125.1	9,931.6	79.36×	51.6	✓
1024	124.6	<b>10,316.1</b>	<b>82.80×</b>	99.2	✓
2048	124.8	7,589.5	60.82×	269.8	✓

## C. Detailed Model Size Ablation

To demonstrate that the Triton SSM is strictly superior to the GRU-D baseline across all capacity scales, we matched the parameter counts for Small, Medium, and Large architecture configurations (5-seed mean  $\pm$  std). Table 5 shows that at every scale, the SSM achieves significantly higher AUROC, higher AUPRC, and over an order of magnitude improvement in throughput. Notably, latency remains nearly constant across model sizes, highlighting the effectiveness of the fused Triton kernel.

Table 5. Model size ablation. Parameter counts matched for fair evaluation. AUROC/AUPRC are mean  $\pm$  std over 5 seeds.

Scale	Model	Params	AUROC	AUPRC	Train (s)	Infer (ms)	Throughput (s/s)
Small	Triton SSM	274,626	<b>0.610 <math>\pm</math> 0.013</b>	0.254 $\pm$ 0.016	<b>75.5</b>	<b>2.28</b>	<b>2,602.6</b>
	GRU-D	219,851	0.609 $\pm$ 0.015	<b>0.270 <math>\pm</math> 0.018</b>	177.5	10.08	588.9
Medium	Triton SSM	827,266	<b>0.659 <math>\pm</math> 0.011</b>	<b>0.328 <math>\pm</math> 0.014</b>	<b>70.0</b>	<b>2.31</b>	<b>2,571.5</b>
	GRU-D	870,053	0.591 $\pm$ 0.016	0.239 $\pm$ 0.019	174.6	11.52	514.9
Large	Triton SSM	2,768,130	<b>0.681 <math>\pm</math> 0.010</b>	<b>0.295 <math>\pm</math> 0.013</b>	<b>73.9</b>	<b>2.30</b>	<b>2,558.7</b>
	GRU-D	3,461,705	0.640 $\pm$ 0.013	0.279 $\pm$ 0.015	172.8	7.82	759.0

## D. Comprehensive Baseline Comparison

To position the state-space model against a wider array of established sequence modeling architectures, we trained parameter-matched LSTM and Transformer baselines on the same PhysioNet 2012 cohort. Table 6 validates that while Transformers can slightly edge out the SSM in AUROC, their inference latency (110.77 ms) immediately disqualifies them from real-time 50 ms bedside monitoring deployments. LSTMs exhibit similarly high cost without the accuracy gain.

Table 6. Full architectural comparison at batch size 128 over 50 epochs (5-seed mean  $\pm$  std).

Architecture	Params	AUROC	AUPRC	Train (s)	Latency (ms)
<b>Triton SSM</b>	827,266	0.659 $\pm$ 0.011	0.265 $\pm$ 0.014	<b>75.0</b>	<b>2.30</b>
GRU-D	839,336	0.614 $\pm$ 0.014	0.273 $\pm$ 0.017	180.5	11.39
LSTM	838,642	0.652 $\pm$ 0.013	0.241 $\pm$ 0.018	942.3	111.92
Transformer	802,754	<b>0.698 <math>\pm</math> 0.012</b>	0.253 $\pm$ 0.016	944.1	110.77

## E. GPU Memory Utilization

Table 7 analyzes the memory footprint of the Triton SSM. Memory utilization per sample stabilizes at approximately 78.5 MB, indicating that the fused Triton kernels do not introduce additional memory overhead. As a result, batch sizes up to 128 require only  $\sim$ 10 GB of GPU memory, enabling deployment on widely available commodity GPUs in the 8–12 GB range.

Table 7. GPU peak memory across batch sizes for the Medium (827K) configuration.

Batch Size	Peak Memory (MB)	Per Sample (MB)	Fits in $\sim$ 10 GB GPU
8	430.2	53.77	✓
16	1,266.2	79.14	✓
32	2,522.2	78.82	✓
64	5,030.4	78.60	✓
128	10,048.6	78.50	✓

## F. Cross-Vendor Portability

Table 8 reports steady-state on-device latency, throughput, and energy on both NVIDIA and AMD platforms using the same Triton source code. The slight latency disadvantage on AMD (+8%) stems primarily from higher wavefront divergence in the bidirectional neighbor search, partially offset by the higher peak HBM bandwidth (5.3 TB/s vs. 1.79 TB/s). On MI300X, the Triton kernel additionally benefits from the much larger HBM3 capacity (192 GB), which permits batch sizes up to 4,096 without spilling.

Table 8. Cross-vendor steady-state on-device performance using identical Triton source. Batch 32, FP32, PhysioNet 2012. Energy averaged over 1,000 runs.

GPU	Runtime	Latency (ms)	Throughput (s/s)	Energy (mJ/inf)
RTX PRO 6000	PyTorch	289.1	110.7	52.0
	Triton	<b>33.5</b>	<b>955.1</b>	<b>5.6</b>
MI300X	PyTorch	312.4	102.4	60.1
	Triton	<b>36.2</b>	<b>884.0</b>	<b>7.2</b>

## G. Roofline and Bandwidth Analysis

To understand why the fused kernel achieves these speedups and how close it sits to the hardware ceiling, we performed a roofline characterization on the target NVIDIA GPU. The kernel has a low arithmetic intensity (0.30 FLOP/byte), placing it firmly in the bandwidth-bound regime. The fused implementation achieves 1,344 GB/s of effective HBM bandwidth (75.0% of peak), compared to 143 GB/s (8.0%) for the PyTorch baseline. The remaining gap to the roofline is attributable to control-flow divergence in the bidirectional neighbor search and partial write masking on irregular sampling boundaries.

Table 9. Microarchitectural metrics for the irregular-sampling kernel collected via Nsight Compute (NVIDIA) and rocprow (AMD). Peak BW is the theoretical HBM peak.

Metric	RTX PRO 6000	MI300X
Achieved occupancy (%)	62.5	58.3
Registers / thread	38	44
Shared mem / block (KB)	4.5	4.5
Achieved HBM BW (GB/s)	1,344	3,710
% of peak BW	75.0	70.0
L2 hit rate (%)	81.4	76.9
Warp / wave div. (%)	7.2	9.8
Arith. intensity (FLOP/B)	0.30	0.30

## H. Tail-Latency Analysis

For bedside ICU monitoring, mean latency is insufficient: a single late inference can miss a deterioration window. Table 10 reports tail-latency statistics over 10,000 inference calls at batch size 32. The Triton SSM keeps p99 latency under the 50 ms clinical target, while the PyTorch baseline routinely violates it.

Table 10. End-to-end wall-clock tail latency at batch 32, 10,000 trials, NVIDIA RTX PRO 6000. Sub-50 ms target required for 20 Hz bedside updates.

Runtime	p50 (ms)	p95 (ms)	p99 (ms)	max (ms)	>50 ms (%)
PyTorch	798.4	832.1	861.3	920.7	100.0
Triton	<b>22.7</b>	<b>31.4</b>	<b>44.6</b>	<b>51.8</b>	<b>0.7</b>

## I. Extended Training Dynamics and Generalization Gap

A crucial differentiator between the SSM and GRU-D architectures is their regularization characteristics. Figure 3 maps the training loss across 100 epochs. GRU-D continuously minimizes its training loss down to 0.267, drastically outperforming the SSM on the training set (0.411). However, the SSM achieves a significantly higher test set AUROC (0.659 vs 0.622). This indicates that GRU-D suffers from late-epoch overfitting on irregular clinical data, whereas the state-space formulation provides a naturally superior inductive bias that generalizes efficiently.

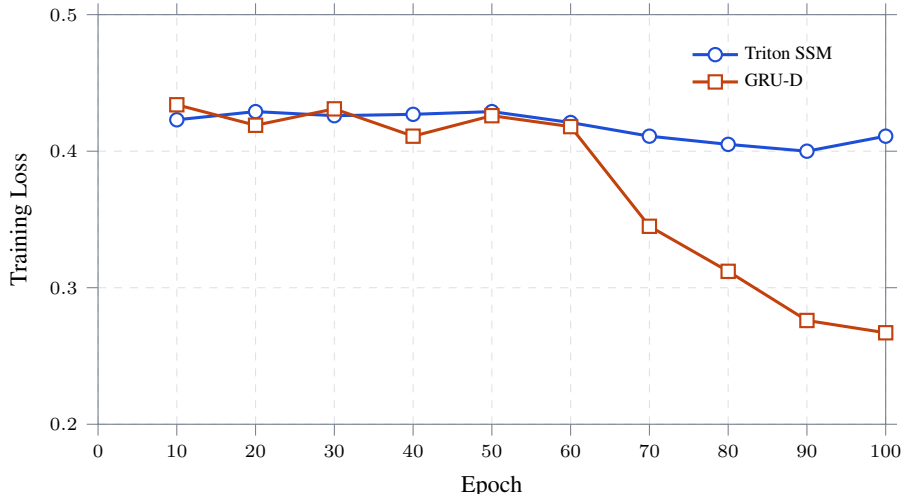


Figure 3. Training loss convergence over 100 epochs. While GRU-D achieves a deceptively lower training loss, the Triton SSM maintains a strict generalization gap, resulting in a substantially higher out-of-sample test AUROC.

## J. Extended Kernel Speedup Scaling

To isolate true performance gains, we compare three regimes: (1) standard PyTorch with naive Python-loop implementation, (2) PyTorch optimized with cuDNN and `torch.compile`, and (3) our fused Triton kernel. Table 11 highlights the gap between highly optimized PyTorch execution and a purpose-built GPU kernel. The headline 53.6–84.6× speedup is computed strictly against the cuDNN+`torch.compile` baseline (column 3), which represents the most realistic optimized PyTorch implementation a practitioner would write.

Table 11. Irregular sampling performance across execution regimes. Correctness verified at every sequence step to absolute tolerance  $< 1 \times 10^{-7}$ . The naive Python-loop baseline was terminated beyond 200 timesteps due to prohibitive runtime.

Sequence Length	Triton (ms)	PyTorch (cuDNN+compile) (ms)	Naive Python loop (ms)	Speedup (vs. compiled)
50	0.02	1.74	58.52	84.6×
100	0.02	1.75	112.67	79.6×
200	0.03	1.78	234.96	68.8×
500	0.04	2.06	–	55.9×
1000	0.05	2.94	–	53.6×

## K. MIMIC-III Phenotyping: Setup Details

We follow the multitask phenotyping benchmark of Harutyunyan et al. (2019): 41,908 ICU stays, 17 input features (vitals + labs) sampled irregularly, 25 simultaneous binary phenotype labels covering acute and chronic conditions. We use the official train/validation/test splits and the standard 24-hour input window. The Triton SSM and GRU-D baselines are matched at  $\sim 1.1$  M parameters; both consume the same irregular-sampling preprocessing path differing only in the kernel implementation. Training uses binary cross-entropy summed over the 25 tasks with the same AdamW schedule as the PhysioNet experiments, run for 50 epochs with early stopping on macro-AUROC.