

# TorchMD-NET Integration Report

## Machine Learning Forcefield Benchmarks

*Author: Sundar Jubilant*

Date: 2025-11-17

### System Information:

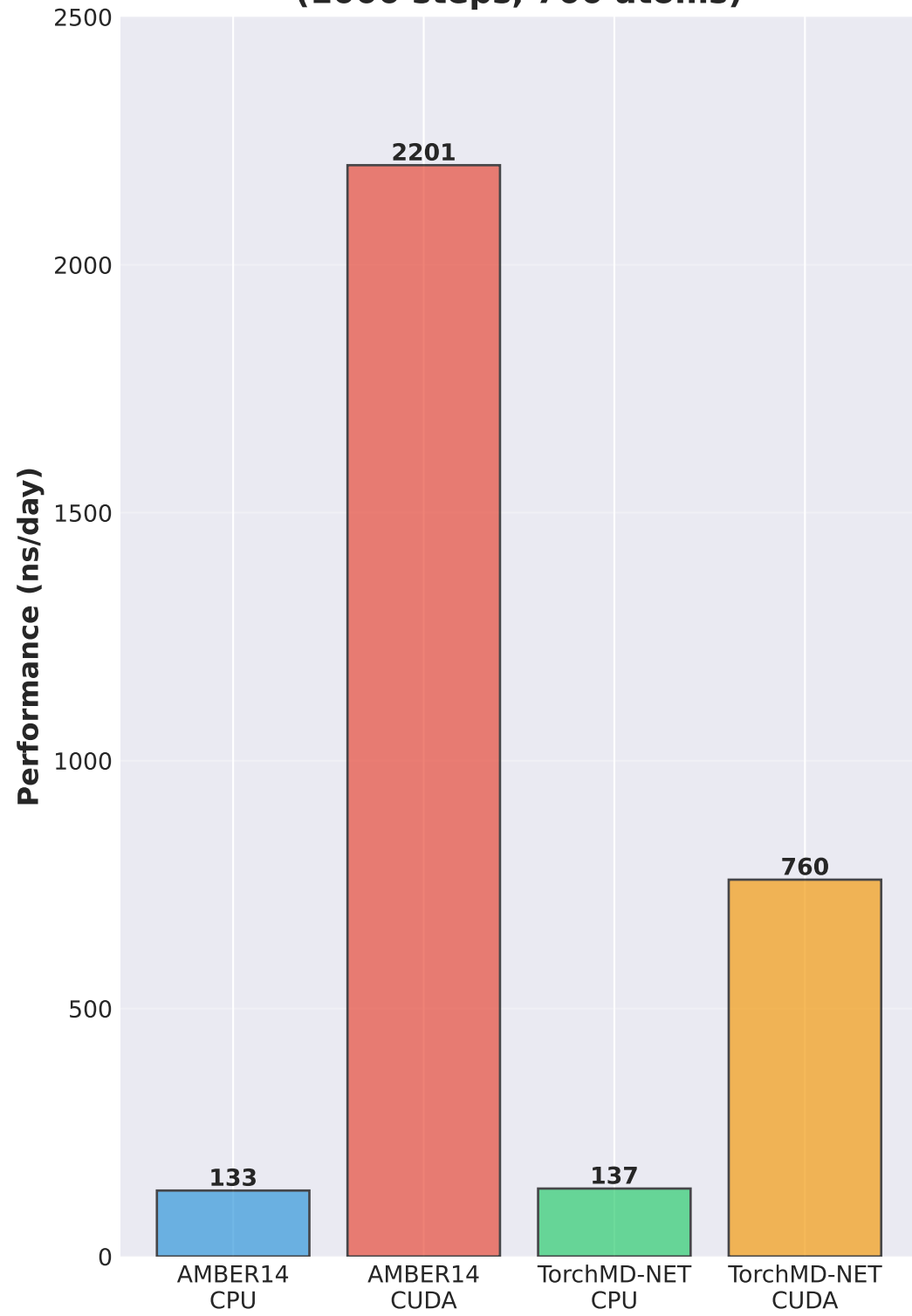
- GPU: Tesla T4 (CUDA 12.6)
  - PyTorch: 2.7.1
  - TorchMD-NET: 2.4.12
- OpenMM: Latest with OpenMM-Torch

### Test System:

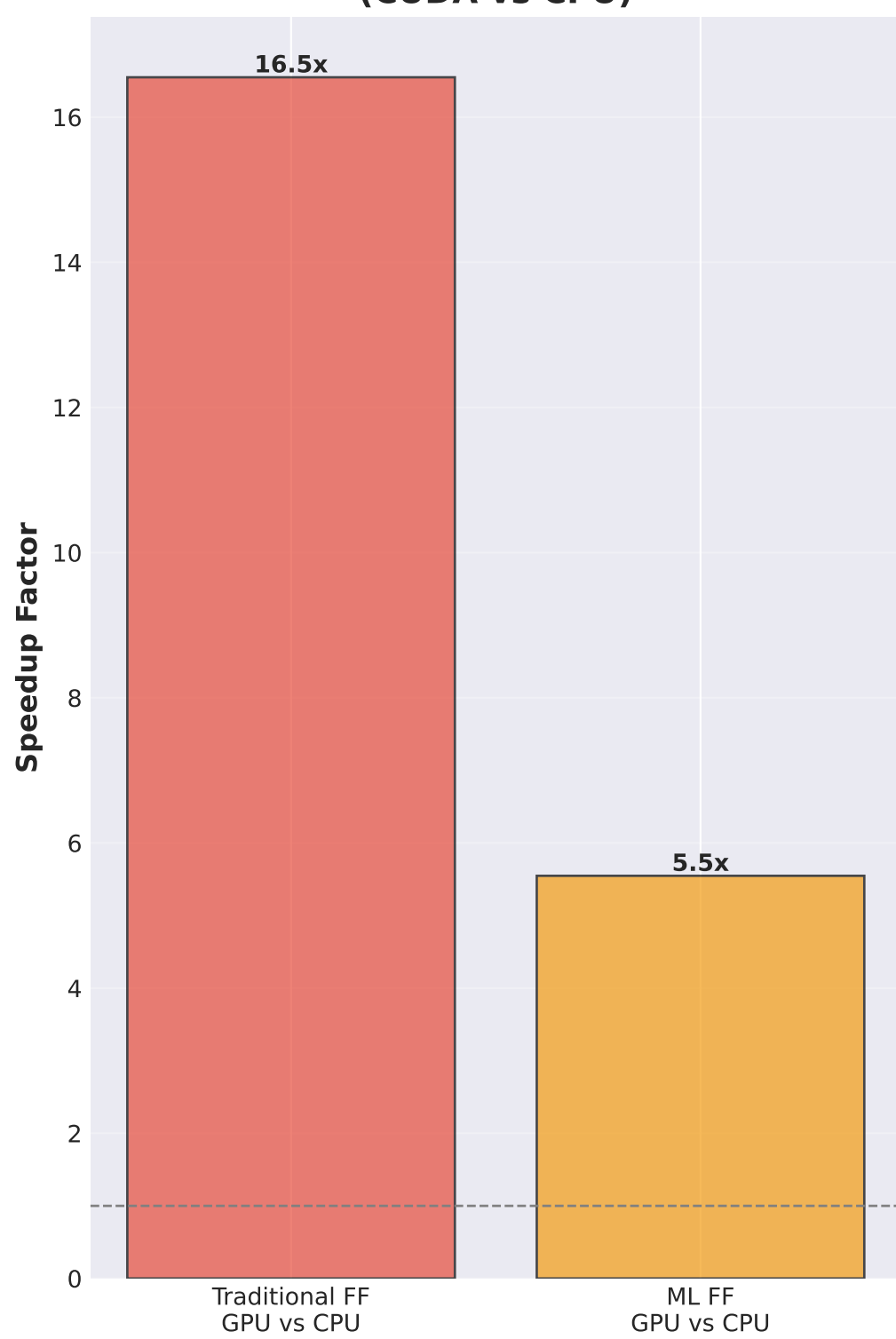
- Protein Segment Structure
  - 700 atoms, 43 residues
  - Benchmark: 1000 MD steps

*Complete Installation & Integration Test*

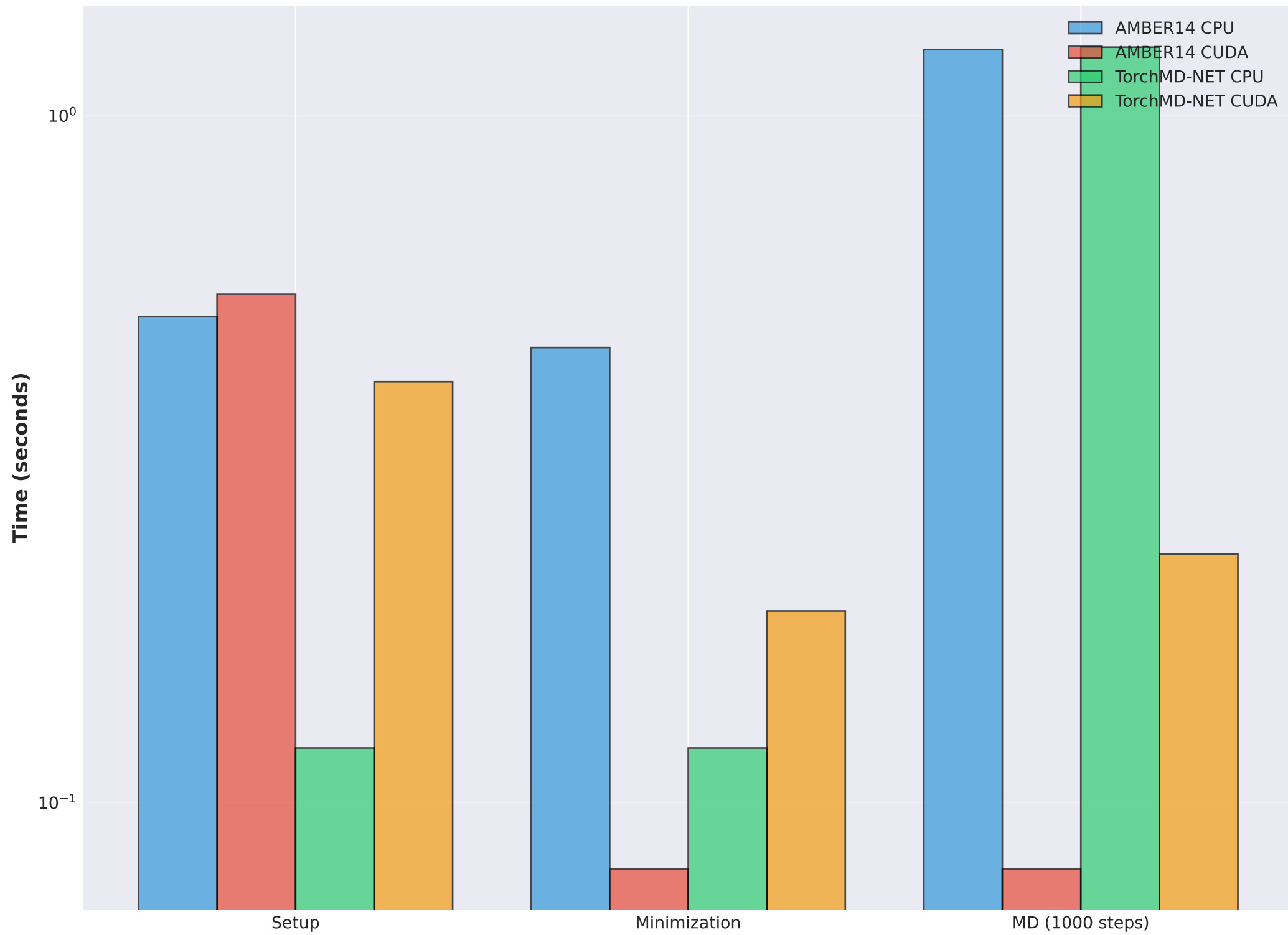
**MD Performance Comparison  
(1000 steps, 700 atoms)**



**GPU Acceleration  
(CUDA vs CPU)**



**Timing Breakdown by Phase  
(700 atoms)**



# TorchMD-NET Model Configuration

## Model Architecture: TensorNet

---

### Parameters:

- Total Parameters: 756,865
- Embedding Dimension: 128
  - Number of Layers: 2
- Radial Basis Functions: 32
- RBF Type: expnorm (Exponential Normal)
  - Activation: SiLU (Swish)

### Cutoff & Neighbors:

- Cutoff Distance: 5.0 Å
  - Max Neighbors: 64
- Equivariance Group: 0(3)

### Architecture Features:

- Equivariant message passing
- Tensor field network layers
  - Scalar output for energy
- Forces computed via autograd

### Integration Details:

- Framework: OpenMM with TorchForce
- Unit Conversion: nm  $\leftrightarrow$  Å, kJ/mol  $\leftrightarrow$  eV
- TorchScript: JIT compiled for performance
  - Platform Support: CPU and CUDA

Note: Current benchmarks use UNTRAINED model for framework testing. Production use requires trained models on appropriate QM datasets (e.g., SPICE, ANI).

# Installation & Integration Summary

✓ Installation Completed Successfully

---

Components Installed:

- PyTorch 2.7.1 with CUDA 12.6
- TorchMD-NET 2.4.12 (compiled from source)
  - OpenMM with OpenMM-Torch plugin
  - All Python dependencies

Tests Passed:

- ✓ Model creation (CPU & GPU)
  - ✓ Energy computation
- ✓ Force evaluation via autograd
  - ✓ OpenMM integration
- ✓ MD simulation propagation
- ✓ TorchScript compilation

Key Technical Solutions:

- Import Order: PyTorch before OpenMM (library conflict)
- Generator Fix: List comprehension for OpenMM's `sum()`
  - Unit Conversion: Automatic nm $\leftrightarrow$ Å, kJ/mol $\leftrightarrow$ eV
- TorchScript: JIT compilation for deployment

Available Scripts:

- `test_torchmdnet.py` - Validation tests
- `torchmdnet_openmm_integration.py` - Integration demo
- `comprehensive_ff_benchmark.py` - Benchmark suite

Documentation:

- `TORCHMDNET_SETUP_COMPLETE.md` - Full setup guide
- `TORCHMDNET_BENCHMARK_ANALYSIS.md` - Detailed analysis
  - This PDF - Visual summary

# Next Steps & Recommendations

## Production Deployment Roadmap

---

### Phase 1: Model Training (Required for Production)

- Train TorchMD-NET on relevant QM dataset
  - SPICE: Diverse organic molecules & peptides
    - ANI: Small molecules, proteins
  - Custom: Your specific system type
    - Validation on test set
- Checkpoint saving for deployment

### Phase 2: Performance Optimization

- Benchmark trained model on target systems
- Tune hyperparameters (cutoff, neighbors, layers)
  - Profile GPU memory usage
- Optimize batch sizes for throughput

### Phase 3: Production Integration

- Load trained checkpoint in production scripts
  - Set up simulation protocols
  - Implement analysis pipelines
    - Run convergence tests

### Phase 4: Scaling & Deployment

- Test on production-scale systems
- Multi-GPU support (if needed)
  - Long-timescale simulations
- Integration with analysis tools

## Quick Start Commands:

---

```
# Test installation
python3 test_torchmdnet.py

# Run demo simulation
python3 torchmdnet_openmm_integration.py hairpin.pdb \
--platform CUDA --steps 100

# Benchmark comparison
python3 comprehensive_ff_benchmark.py your_system.pdb
```

## Resources:

- TorchMD-NET repo: /home/ubuntu/MD/torchmd-net
- Example configs: /home/ubuntu/MD/torchmd-net/examples/
  - Documentation: TORCHMDNET\_SETUP\_COMPLETE.md