

On-Chip Network-Enabled Multi-Core Platforms Targeting Maximum Likelihood Phylogeny Reconstruction

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Objective

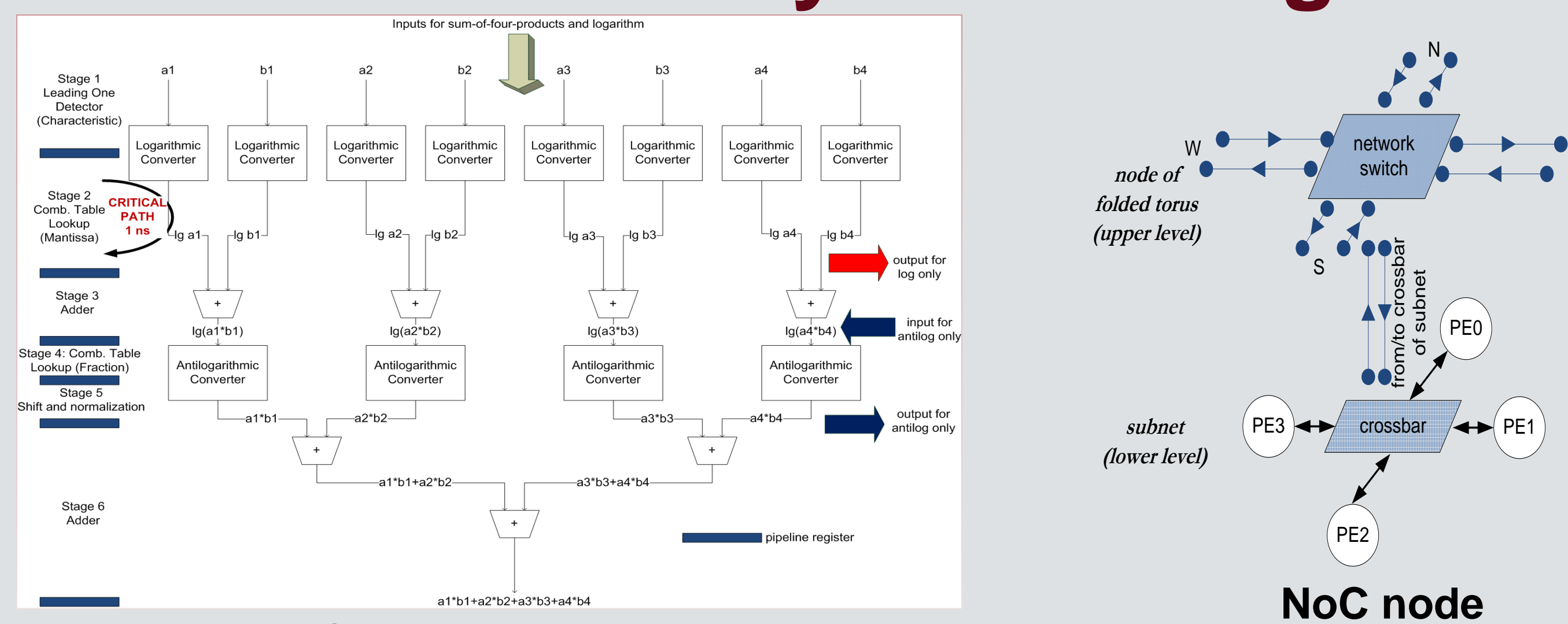
- Finding a **phylogenetic tree** that best explains the evolutionary relationship among a given set of species is **computationally complex** because of the **greater than exponential search-space** (real, multi-dimensional) and **floating point arithmetic** computation.

Why Network-on-Chip?

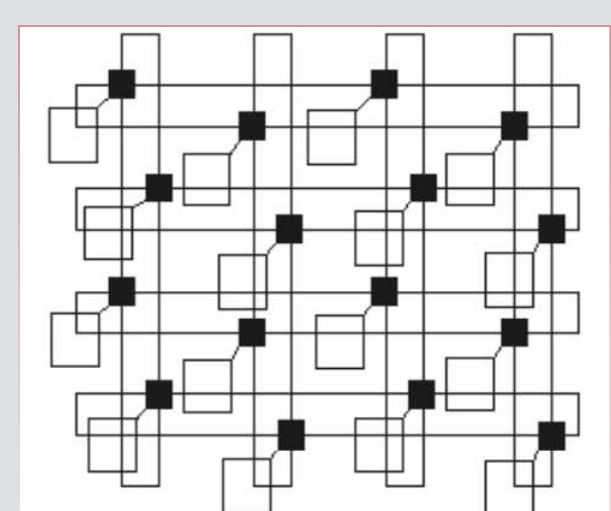
- Phylogenetic tree reconstruction is **data/computation intensive**.
- Use parallelism**: Divide into a large number of smaller **semi-independent** sub-problems that can be computed **concurrently**.

- NoC** {
- A large number of cores to deal with sub-problems
 - Low-latency inter-core communication

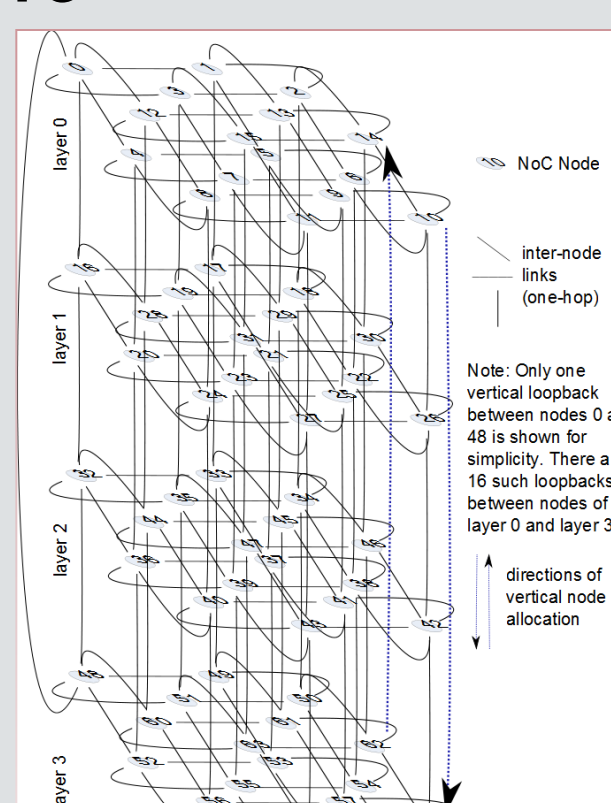
Multi-core System Design



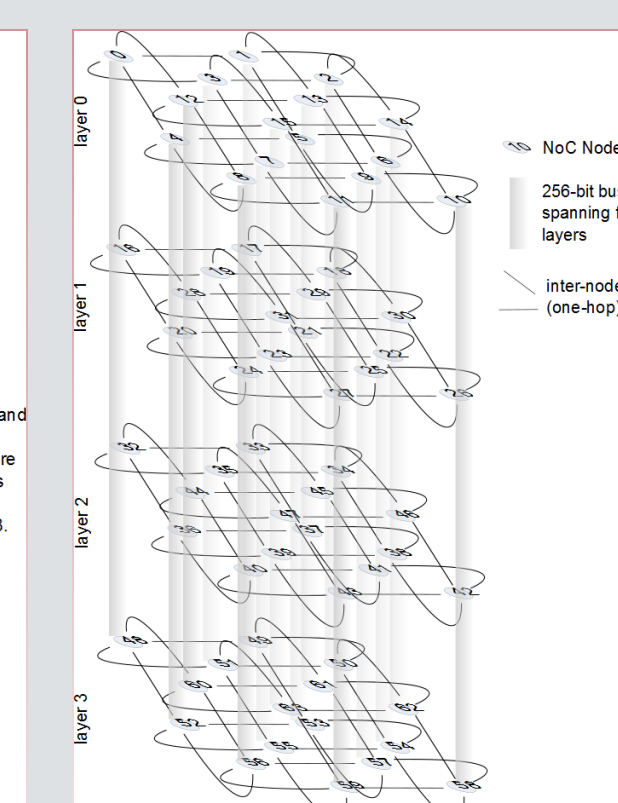
Network architectures:
2-D folded torus (2D_serial, 2D_parallel)



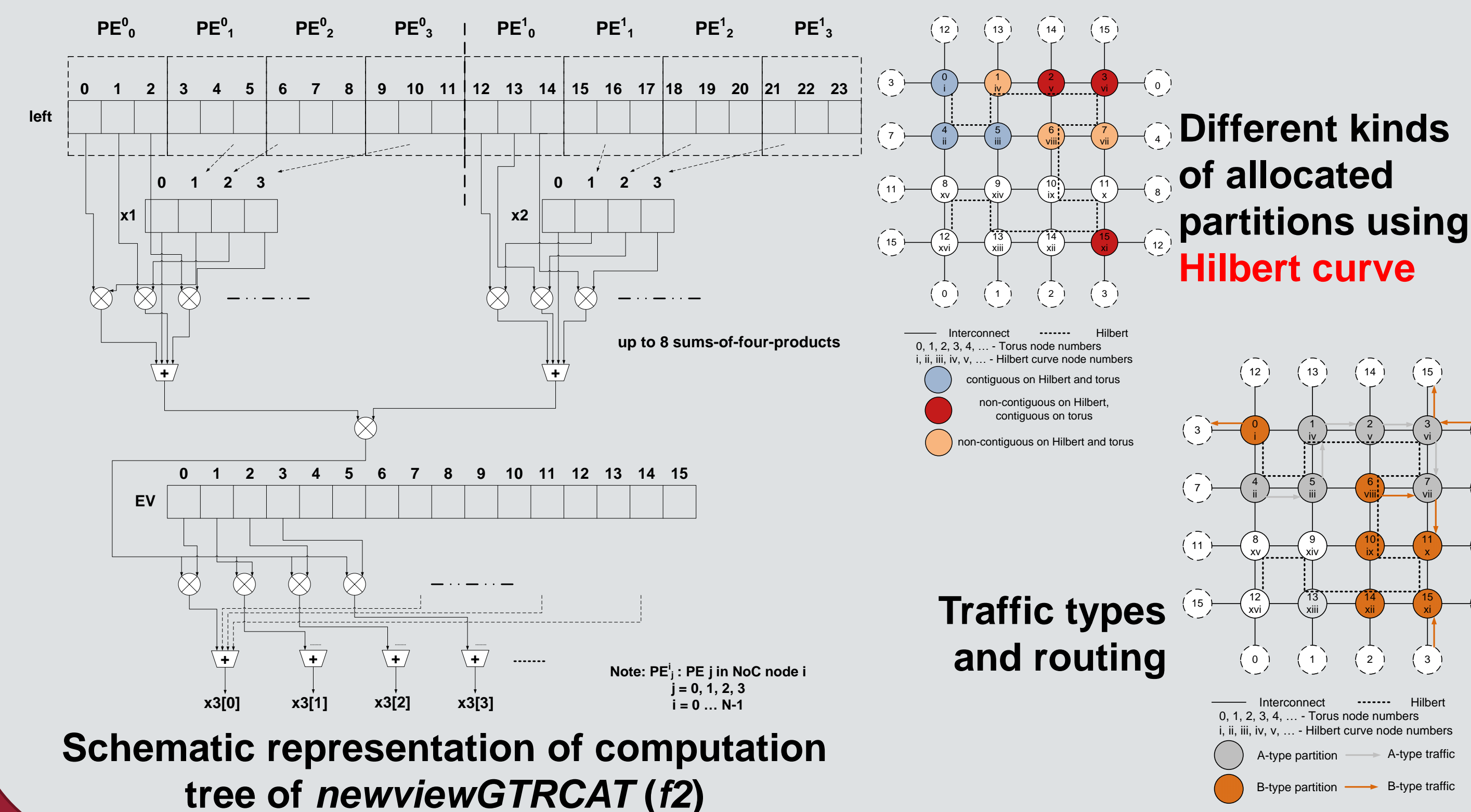
3-D folded torus (3D_torus)



3-D stacked torus (3D_sttorus)



Dynamic Node Allocation



Experimental Setup

Computation core

- Datapath: 64 bit
- Number representation accuracy of 2^{-52} using Fixed-Point Hybrid Number System
- All components designed with Verilog HDL and synthesized with 65 nm standard libraries

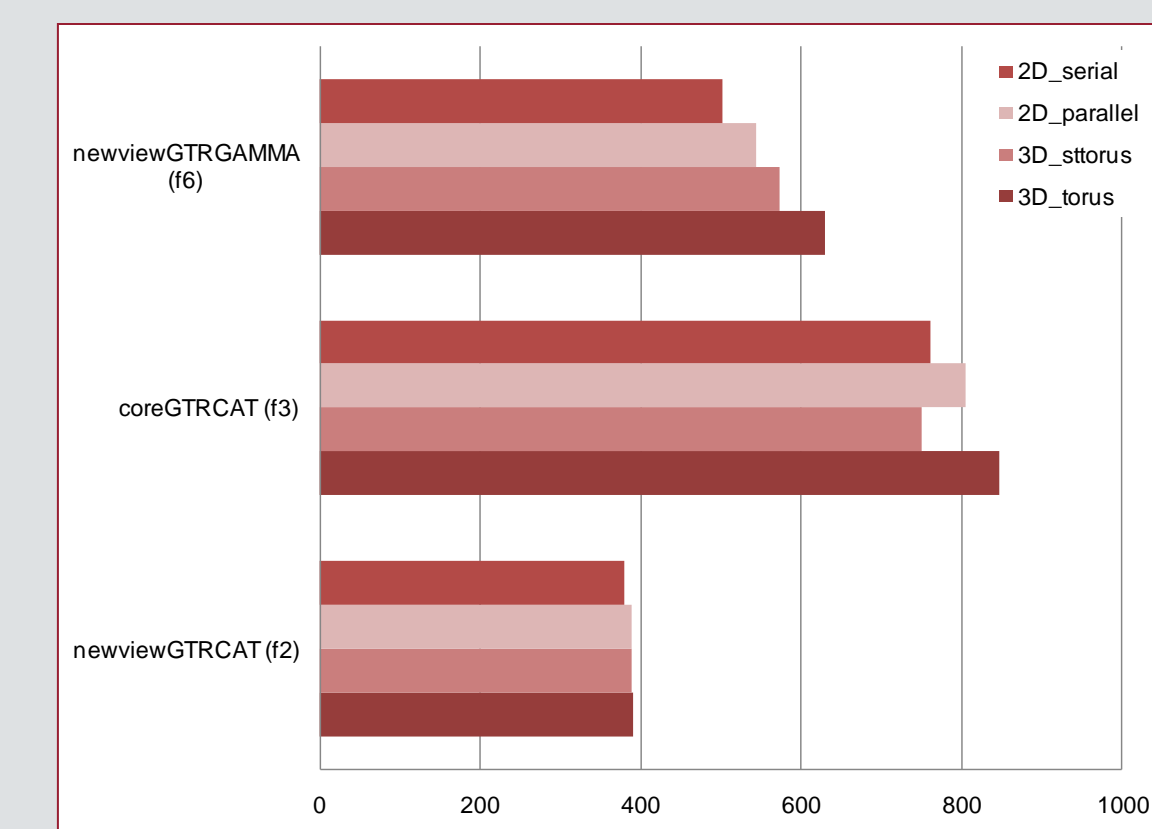
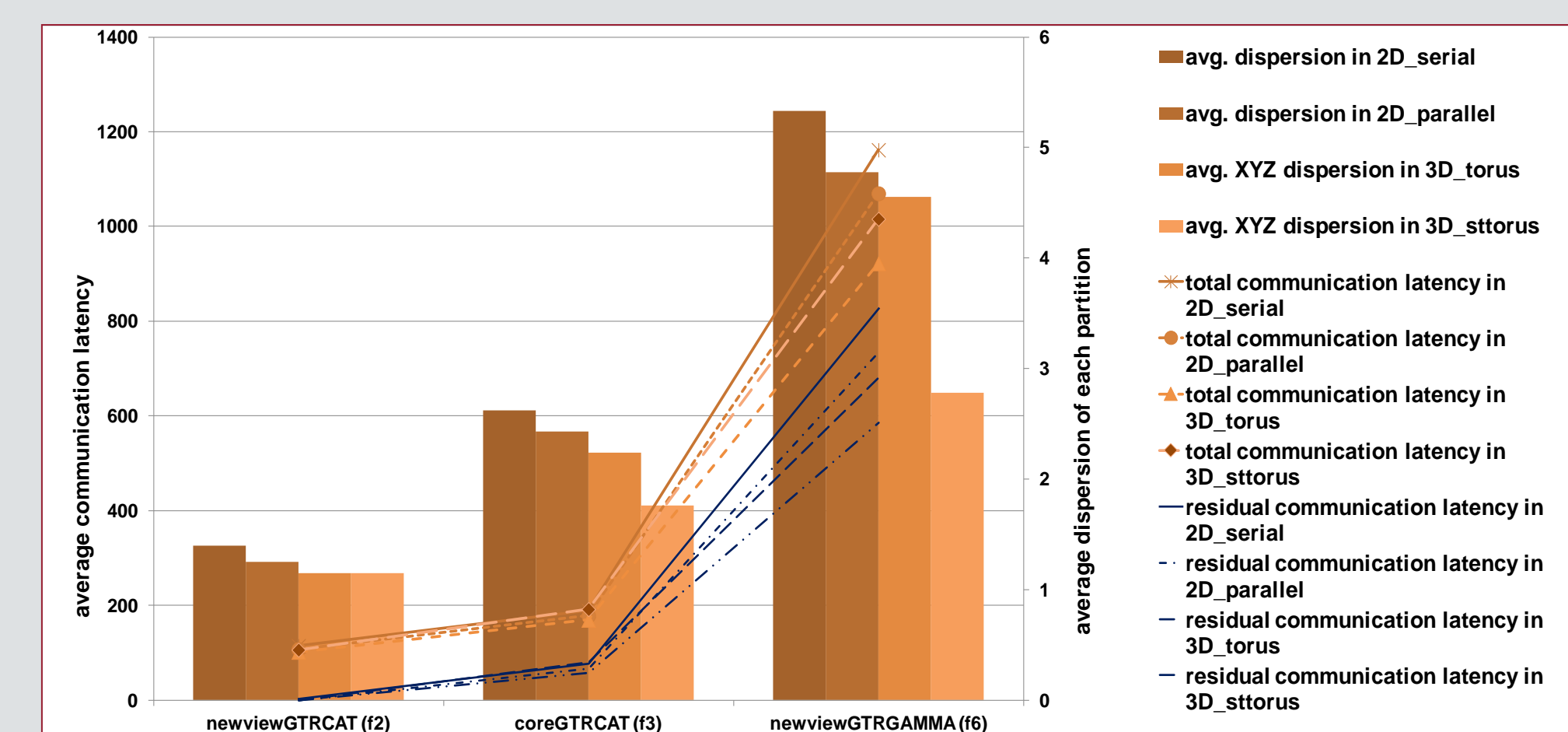
Multi-core System

- Interconnects laid out, parasitics (resistance, capacitance) extracted to determine physical parameters (power dissipation, delay)
- $N=16$ and $N=64$ system sizes simulated using TreeSim
- 32-lane PCIe 2.0 interface (5 Gbps)

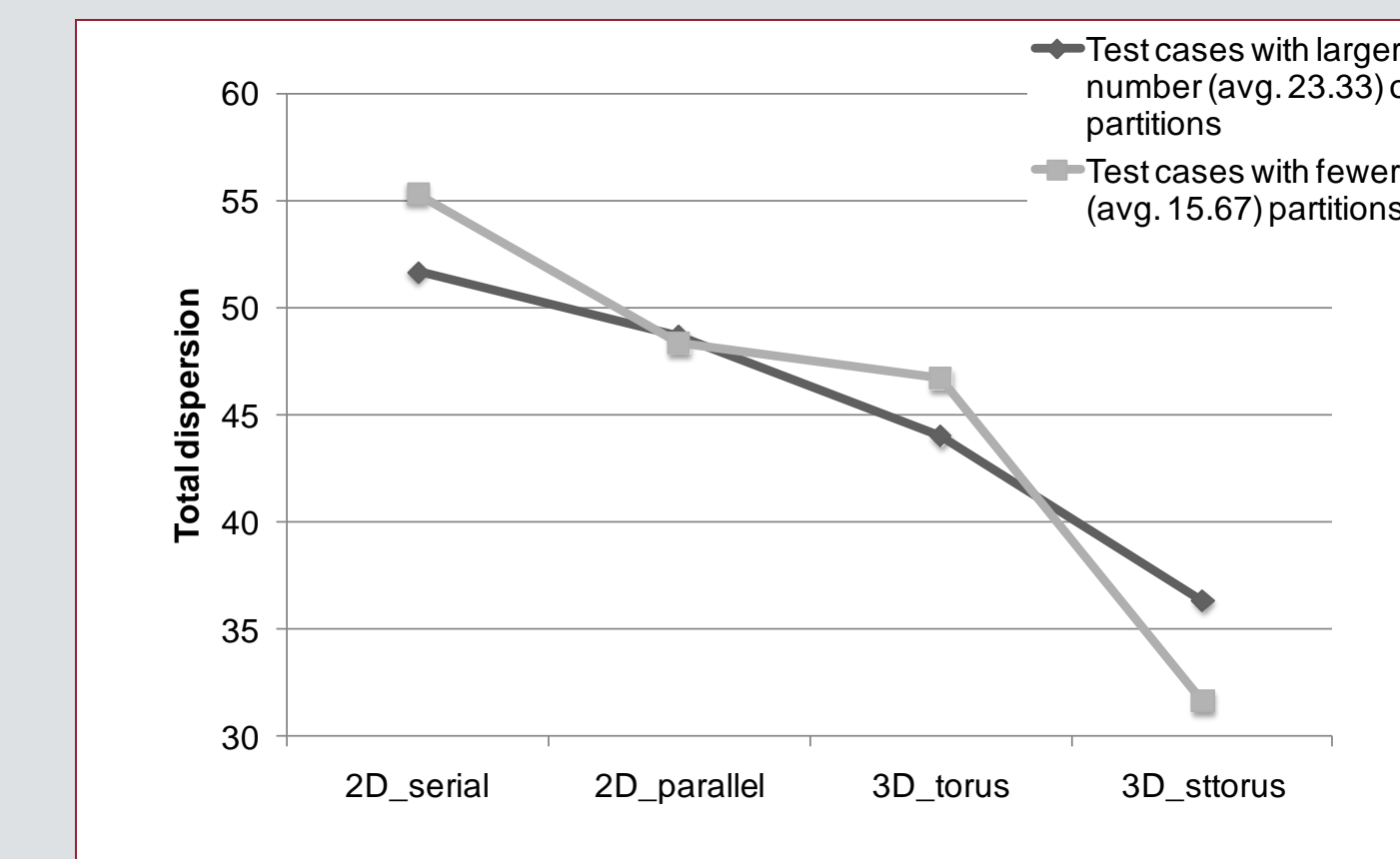
Software

- RAXML-VI-HPC (version 7.0.4) on three inputs sourced from 2,177-taxon 68-gene mammalian dataset
- Pentium IV 3.2 GHz dual-core CPU; GNU *gprof* utility for profiling
- Best software runtime used as the baseline
- Functions *coreGTRCAT (f3)* (48%), *newviewGTRGAMMA (f6)* (21%) and *newviewGTRCAT (f2)* (17%) collectively account for more than 85% of the total runtime

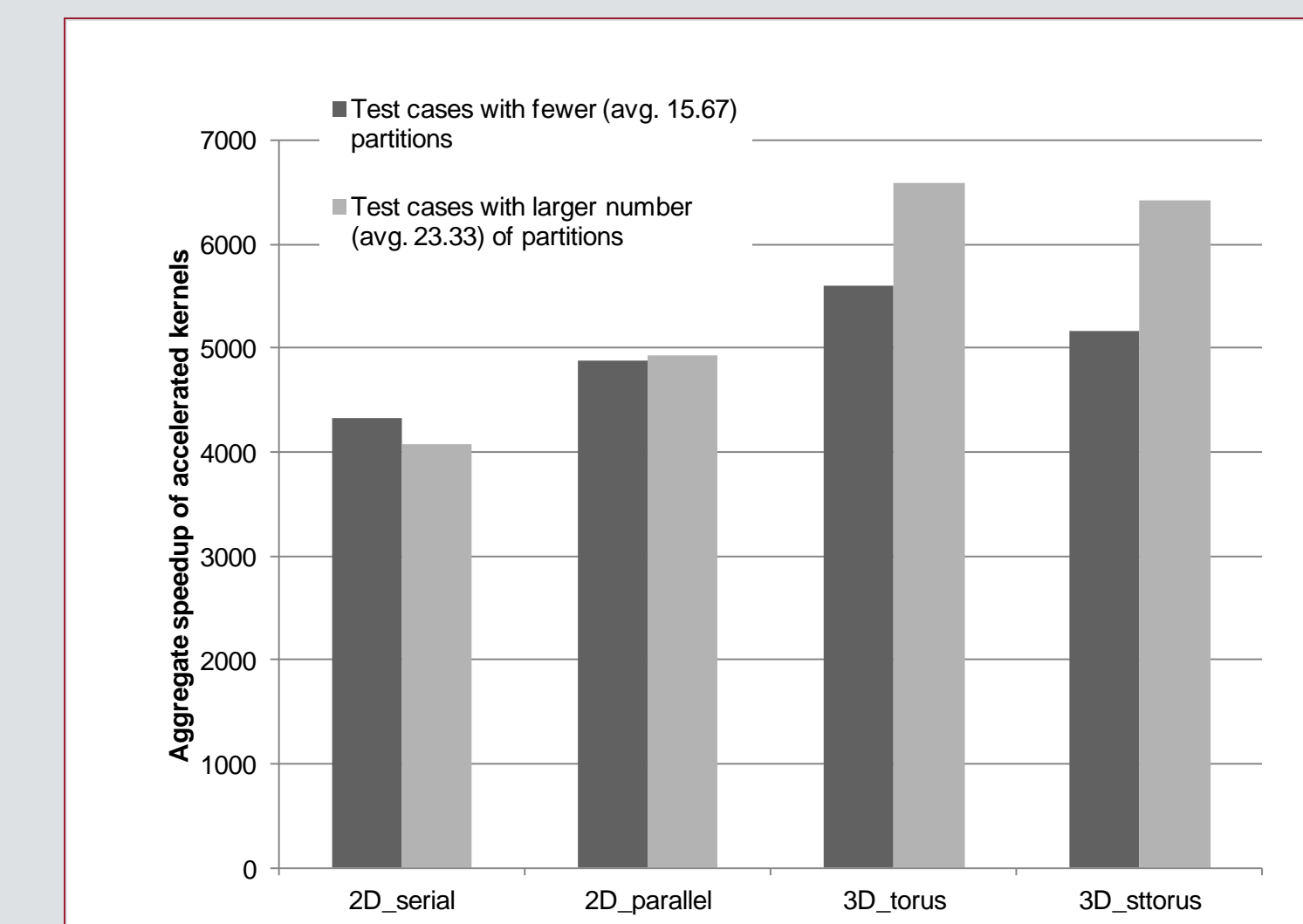
Results



Results (cont'd.)



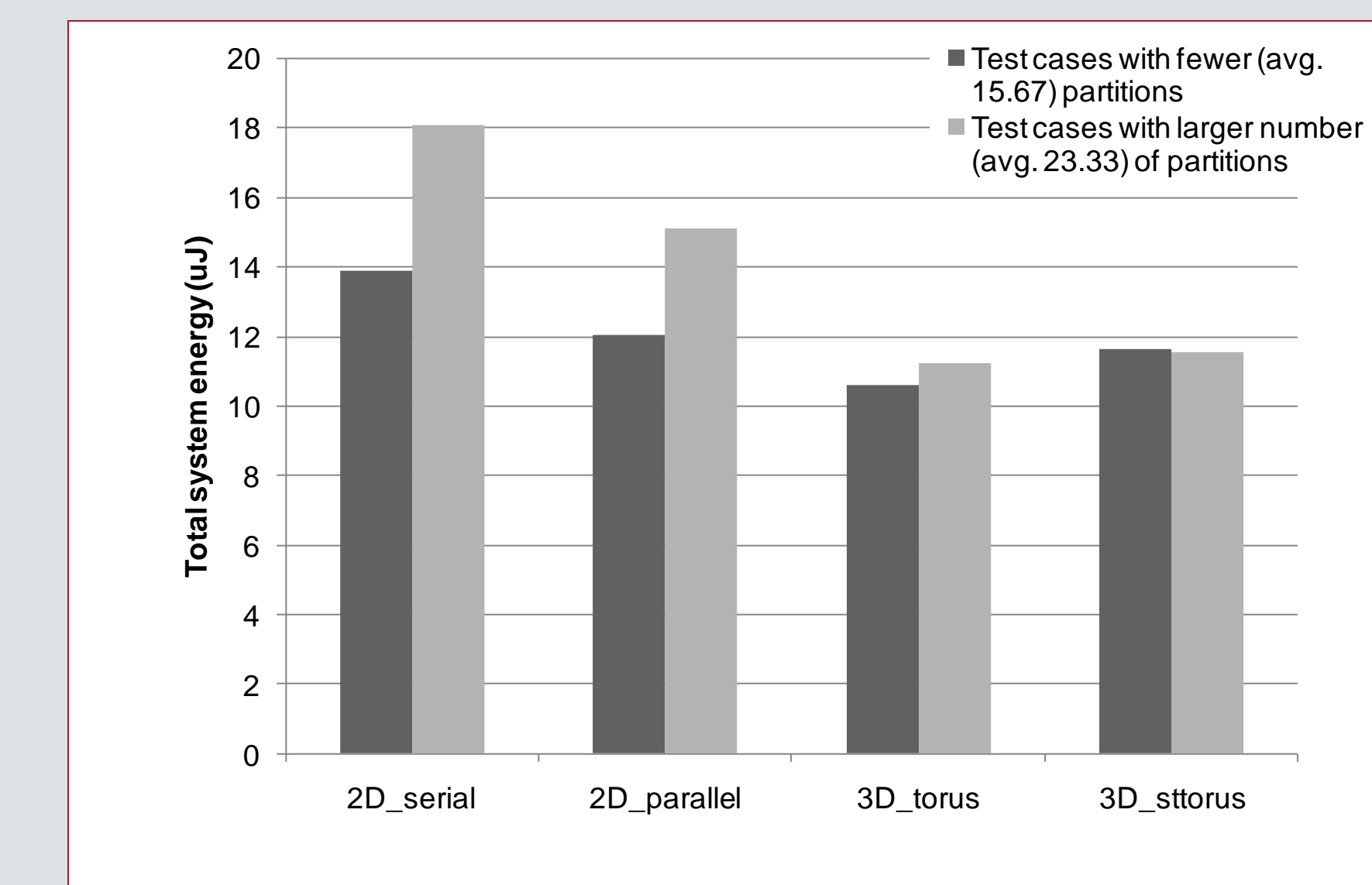
Total dispersion across different NoC architectures



Average aggregate speedup of the accelerated kernels across different NoC architectures

Total run-times for different inputs using different NoC-based platforms vis-à-vis only software

Input data (DNA)		Unaccelerated software run-time (s)	Time spent in accelerated kernels (s)	Allocation time (s)	PCIe interface time (s)	Total run-time using NoC platform as hardware accelerator (s)	Total 4T software run-time (s)
50_5000	2D_serial	292.000444	0.515478	0.130387	0.145065	292.791374	924.052039
	2D_parallel	292.000444	0.481303	0.104805	0.145065	292.731617	924.052039
	3D_torus	292.000444	0.433625	0.050889	0.145065	292.630024	924.052039
	3D_sttorus	292.000444	0.474657	0.050889	0.145065	292.671056	924.052039
500_5000	2D_serial	7038.847538	19.1142	8.467062	8.273363	7074.702162	37124.7233
	2D_parallel	7038.847538	18.04733	6.805803	8.273363	7071.974034	37124.7233
	3D_torus	7038.847538	16.766102	3.304655	8.273363	7067.191658	37124.7233
	3D_sttorus	7038.847538	18.102936	3.304655	8.273363	7068.528491	37124.7233



Total system energy consumption across different NoC architectures

Summary

- Network-on-Chip (NoC) based multi-core platform for accelerating Maximum Likelihood (ML) based phylogeny reconstruction
- Chief contributions
 - design of a fine-grained parallel PE architecture
 - novel algorithm to dynamically allocate nodes to tasks based on Hilbert space-filling curves
 - design and extensive evaluation of different 2-D and 3-D NoC architectures
- Function-level speedup of ~847x, aggregate speedup of the accelerated portion up to ~6,500x, and overall run-time reduction of more than 5x over multithreaded software; exceeds the performance of all state-of-the-art hardware accelerators for this application class.