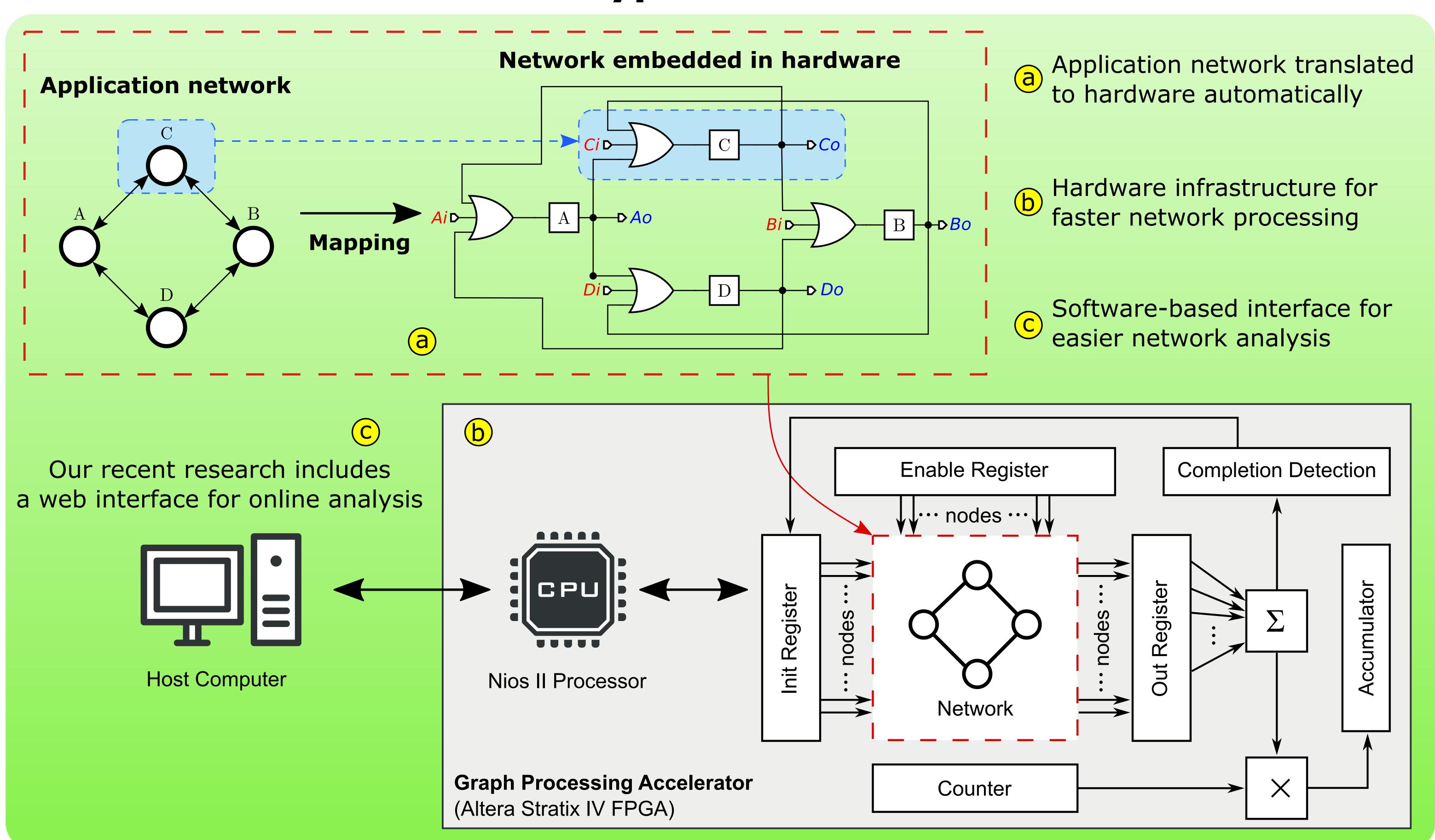
Fast Network Analysis in Silicon

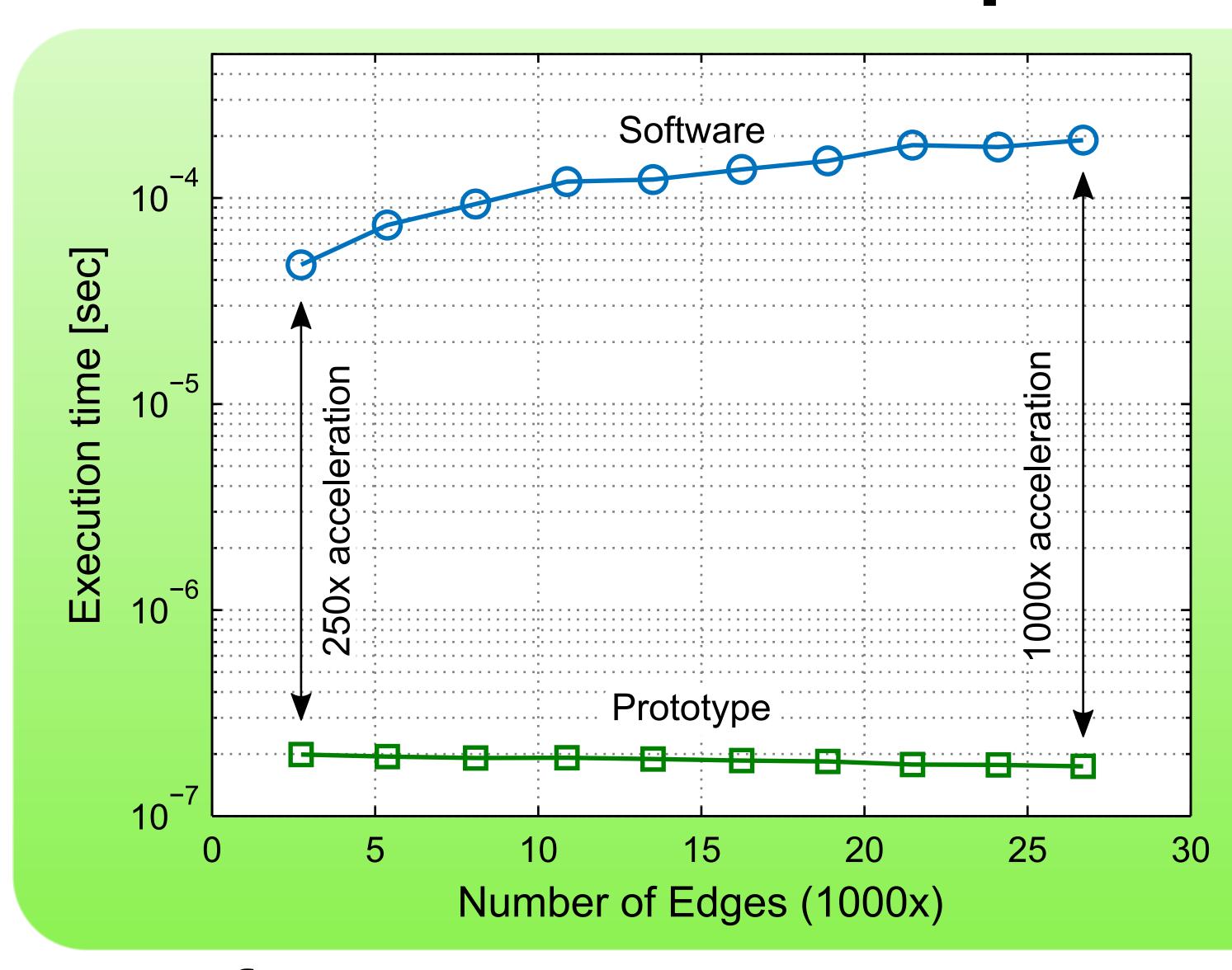
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- Many applications use networks as efficient data structures. Their analysis help characterise system properties.
- In drug discovery, for example, networks model biological systems. These go through computationally intensive analyses that help characterise their "resilience" in order to support the discovery of suitable drugs.
- It is inefficient to process such networks on commodity computers, as the algorithms used for characterising their properties (e.g. graph traversal) make poor use of the memory hierarchy, slowing down the analysis.
- We present a methodology, supported by a hardware prototype, for easier and faster network analysis.

Prototype architecture



Experimental results



- **Analysis is hundreds times faster than software** Prototype working frequency is 100-150 Mhz
- Reconfigurability of the network for multiple simulations without reprogramming the FPGA

Nodes	Edges	Logic utilization	Avg. (peak) interconn.	Acceleration
87	402	<1%	<1(2)%	173x
349	3k	2%	<1(16)%	592x
1628	27k	11%	8(75)%	1829x
3487	58k	25%	25(91)%	2505x
Board: Altera DE4 FPGA: Stratix IV EP4SGX230				

Reference: A. Mokhov et al: "Language and hardware acceleration backend for graph processing". FDL 2017.





