

RESEARCH MOTIVATION

Graph analysis is key for the study of biological, chemical, social, and other networks.

- Real-world graphs are big, irregular, complex
 - Graph analytics is one of DARPA's 23 toughest mathematical challenges
 - Web graph: 50B sites, 1T+ links; Brain graph: 100B neurons, 1,000T synaptic connections
- Modern computational systems are also big and complex
 - Multiple levels of parallelism, memory hierarchy, configurations
 - Heterogenous host, GPU, coprocessors (Xeon Phi MIC)
 - Optimization account for socket-level, node-level, and system-level

How can we design graph algorithms to be performant on large modern systems?

SUMMARY OF CONTRIBUTIONS

- Multistep connectivity algorithms; on average $2 \times$ faster than state-of-the-art
- **FASCIA** subgraph counting program; ordersof-magnitude execution time improvement over prior art
- **PuLP** multi-objective multi-constraint partitioner; order of magnitude faster, order of magnitude less memory, comparable or better partition quality than state-of-the-art utilities
- Methodology for in-memory **distributed** graph layout; $1.5 - 5 \times$ performance improvements over naive methods
- Using techniques derived from above accomplishments, provided **first-ever complex** analysis of largest publicly available web crawl (3.5B vertices and 129B edges)

ACKNOWLEDGEMENTS

This research is part of the Blue Waters sustained-petascale computing project, which is supported by the National Science Foundation (awards OCI-0725070, ACI-1238993, and ACI-1444747) and the state of Illinois. Blue Waters is a joint effort of the University of Illinois at Urbana-Champaign and its National Center for Supercomputing Applications. This work is also supported by NSF grants ACI-1253881, CCF-1439057, and the DOE Office of Science through the FASTMath SciDAC Institute. Sandia National Laboratories is a multi-program laboratory managed and operated by Sandia Corporation, a wholly owned subsidiary of Lockheed Martin Corporation, for the U.S. Department of Energy's National Nuclear Security Administration under contract DE-AC04-94AL85000.

PARALLEL GRAPH ALGORITHMS ON MODERN SYSTEMS

George M. Slota (gms50160psu.edu, www.gmslota.com), Penn State University Kamesh Madduri, Penn State (advisor), Siva Rajamanickam, Sandia National Labs (mentor)

Algorithm Design for Graph Analytics

Graph Connectivity, Strong Connectivity, and Weak Connectivity

- Multistep approach to graph connectivity (Slota et al. 2014)
- On average $2 \times$ faster than prior state-of-the-art for SCC
- Key optimizations: threadlocal queues, minimize global atomics and synchronization, direction optimizing BFS





Multistep performance scaling relative to the state-of-the-art Hong et al. 2013 SCC code.

- Optimized SCC code for high performance on manycore processors such as GPUS (Slota et al. 2015)
- $3.25 \times$ performance improvement over optimized CPU code on most irregular test graphs
- Key optimizations: loop manipulation for higher parallelism, shared-memory and other locality considerations, warp and teambased atomics and operations (team scan)

PARTITIONING AND IN-MEMORY LAYOUT FOR LARGE IRREGULAR GRAPHS

- Developed the **PuLP** partitioner for real-world irregular graphs (Slota et al. 2014)
- Exploits the label propagation community detection algorithm
- Order-of-magnitude faster execution times and memory consumption than state-of-the-art with comparable partition quality
- Allows for concurrent multiple constrain and multiple objective partitioning • Minimize edge cut and max per-part edge cut (communication) while balancing vertices and edges per-part (computation and memory)



of graph analytics.

Fast Approximate Subgraph Counting using Color-coding

- Implemented the Alon et al. 1995 color-coding approach for counting tree-structured subgraphs
- Shared and distributed memory implementations (FASCIA) give real-time count estimates of up to 7 vertex subgraphs on billion edge networks (order-of-magnitude improvement over prior art) (Slota and Madduri 2013, 2014, 2015)



Graphlet frequency distance between various biological and other networks. Red indicates high inter-network similarity while yellow and white indicate lower similarity.



Execution times for PuLP relative to METIS and ParMETIS (top) and partition quality in terms of edge cut for PuLP and METIS (bottom).

- intra-part vertex ordering
- $1.5 \times$ speedup against naive methods

Nationa



Time to count subgraphs of varying sizes on several networks in shared (top) and distributed (bottom) memory.

- Fast counts allow similarity comparison between large networks
- Subgraph frequency analysis allows for detection of recurring motifs on large networks
- **Key optimizations**: restructure algorithm to exploit simpler indexing methods, use of efficient communication and computation avoidance strategies

• Analyzed distributed graph layout in terms of partitioning objectives and

• Partition quality and objectives can have up to a $5 \times$ speedup on execution times; vertex orderings on larger networks is also considerable, with up to