

Jintao Meng

Personal Information

Occupation: PH.D candidate in Institute of Computing Technology (ICT), University of Chinese Academy of Sciences

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Address: No.1068 Xueyuan Road, Nanshan district, Shenzhen, 518055, P.R. China

Organization: Shenzhen Institutes of Advanced Technology (SIAT), Chinese Academy of Sciences

Profile

(9 years) Good in C/C++, STL, data structure, algorithm design, and mathematical modeling
(5 years) Parallel and distributed system design and programming with MPI/OpenMP/Pthread
(4 years) Familiar with Unix/Linux OS, performance tuning skills in supercomputers
(5 years) Numerical computing, graph theory, probability theory, convex optimization, intelligent algorithms

Education

PHD: University of Chinese Academy of Sciences Sep.2011-Current

Research interest: High Performance Computing, Graph Analysis, Bioinformatics

Advisor: Shengzhong Feng (SIAT), Xiaofang Zhao (ICT)

MS Central China Normal University, Wuhan, P.R.China June.2005-June.2008

Major: Computer Science and Technology GPA: 3.2

Thesis: Protocol design and optimization in wireless networks (Excellent dissertation)

BE Central China Normal University, Wuhan, P.R.China Sep.2001-June.2005

Major: Computer Science and Technology GPA: 3.2 (rank 3/206)

Thesis: Primality testing and integer factorization (Excellent dissertation)

Work and Intership Experience

2014.12-current, Huawei Noah's Ark Lab, Hongkong, Visiting student

Research direction: Distributed graph computing system, recommendation system.

2014.9-2014.11, Argonne National Lab, Visiting scholar in Pavan Balaji's Group

Research direction: Performance tuning, extending SWAP's scalability to millions of cores on Mira (IBM Blue Gene Q).

2012.8-2014.9, BGI Shenzhen, Research Intern in Bingqiang Wang's Group

Research direction: Large-scale graph analysis and computing, graph algorithms optimization on Pregel system

2012.2-2012.8, University of Hong Kong, Visiting student in Francis Y.L. Chin's group

Research direction: Genome Assembly, Genome Sequence Clustering and Binning

2008.7-current Shenzhen Institutes of Advance Technology CAS, Engineer

Research direction: High performance computing, Parallel algorithm, large-scale graph analysis and computing, Bioinformatics.

Projects

2015.12-current, Huawei Noah's Ark Lab, Hongkong

* Large-scale distributed graph processing system, recommendation system development

Detail:

- 1). Reduce the communication volume with message aggregation & compression,
- 2). Balance the degree of parallelism and latency with message buffering algorithm, which can smoothly slipping from bulk communication (BSP) and peer to peer communication (LogP),
- 3). Distributed Simrank algorithm optimization on huge graphs with Monte calo method.
- 4). Implement simrank algorithm on Spark GraphX for performance comparison.

2010.3-current, Center for High Performance Computing, SIAT, CAS Shenzhen

* Large-scale distributed graph processing system for De Bruijn Assembly

Detail:

- 1). Design Small world Asynchronous Parallel Model(SWAP) for Large scale Graph with Small world Property.
- 2). Implement a fully parallelized and highly scalable genome assembler on SWAP. The communication complexity of this work is proved to be the lowest compared with previous work.
- 3). Our Assembler (SWAP2) can scale to 131,072 cores with an efficiency of 40% on Mira when processing a graph with 200 billion nodes constructed from 1000 Human Genome dataset.
- 4). This work was developed and test on Tianhe 2A, IBM Blue Gene Q-Mira, Tianhe 1A. All of them are world's top supercomputers with a rank of 1st, 5th, 26th in Top 500, respectively.

2009.2-2011.3 Center for High Performance Computing, SIAT, CAS Shenzhen

* Small World Asynchronous Parallel Model for Parallel Graph Processing

Detail:

- 1). Graph partition and load balancing algorithm design.
- 2). Small World Asynchronous Parallel Model design and development
- 3). SWAP can scales to 4096 cores on processing graphs with 20 billion nodes on TianHe 1A.
- 4). Software is available at <https://sourceforge.net/projects/swapassembler>. It has been downloaded for 370 times in the past one year. This software has been used in BGI research and Argonne National Lab for genome data analysis.

2008.12-2009.2 Institute of Computing Technology (ICT), CAS

Beijing

* Memory Trace Monitor and Analysis Based on HMTT

Detail:

- 1). Memory access trace data collecting, transport, and real-time visualization.
- 2). CPU, memory, and I/O usage analysis on main stream databases, office tools, Benchmarks (SPEC CPU/JBB,NPB).

Publications

1. Jintao Meng, Sangmin Seo, Pavan Balaji, Yanjie Wei, Bingqiang Wang, Shengzhong Feng, SWAP-Assembler 2: Optimization of De Novo Genome Assembler at Extreme Scale, in Proceeding of the 45th International Conference on Parallel Processing (ICPP 2016), Philadelphia, PA. (Accept rate: 18%)
2. Jintao Meng, Sangmin Seo, Pavan Balaji, Yanjie Wei, Bingqiang Wang, Shengzhong Feng, SWAP-Assembler 2: Scalable Genome Assembler towards Millions of Cores - Practice and Experience, in ATIP workshop in Supercomputing 2015 (Supercomputing 2015), Austin.
3. **Jintao Meng**, Sangmin Seo, Pavan Balaji, Yanjie Wei, Bingqiang Wang, Shengzhong Feng, SWAP-Assembler 2: Scalable Genome Assembler towards Millions of Cores - Practice and Experience, in 15th IEEE/ACM International Symposium on Cluster, Cloud and Grid Computing (CCGrid'15)-Doctoral Symposium, May, 2015.
4. **Jintao Meng**, Guixin Guo, Bingqiang Wang, Yanjie Wei, Jiefeng Cheng, Shengzhong Feng, An Ultra-fast Memory Efficient Parallel List Ranking Algorithm for BSP Based Graph Processing Systems, HPC-China 2014, Guangzhou.
5. **Jintao Meng**, Bingqiang Wang, Yanjie Wei, Shengzhong Feng, Pavan Balaji. SWAP-Assembler: Scalable and Efficient Genome Assembly towards Thousands of Cores, BMC Bioinformatics, Vol. 15 Supplement 9. (SCI, IF=2.8)
6. **Jintao Meng**, Bingqiang Wang, Yanjie Wei, Shengzhong Feng, Pavan Balaji. SWAP-Assembler: Scalable and Efficient Genome Assembly towards Thousands of Cores, in 4th annual RECOMB satellite workshop on massively parallel sequencing (RECOMB-seq 2014), April, 2014.
7. Li Zeng, Jiefeng Cheng, **Jintao Meng**, Bingqiang Wang, Shengzhong Feng. Improved Parallel Processing of Massive De Bruijn Graph for Genome Assembly, in 15th Asia-Pacific web conference (APWeb 2013), April, 2013, Sydney, Australia.
8. **Jintao Meng**, Jianrui Yuan, Shengzhong Feng, Yanjie Wei. An Energy Efficient Clustering Scheme for Data Aggregation in Wireless Sensor Networks, Journal of Computer Science and Technology, May 2013, V28(3): 564-573 (SCI, IF = 0.656)
9. **Jintao Meng**, Jianrui Yuan, Yanjie Wei, Jiefeng Cheng, Shengzhong Feng, Small World Asynchronous Parallel Model for Genome Assembly, in 9th IFIP International Conference on Network and Parallel Computing (NPC 2012), Sep.6, Gwangju, Korea (EI)
10. **Jintao Meng**, Jianrui Yuan, Yanjie Wei, Jiefeng Cheng, Shengzhong Feng, DGraph: Algorithms for Shotgun Reads Assembly Using De Bruijn Graph, in 9th IFIP International Conference on Network and Parallel Computing (NPC 2012), Sep.6, Gwangju, Korea (EI).
11. **Jintao Meng**, Jianrui Yuan, Shengzhong Feng, Liansheng Tan, Power Adjusting Algorithm: A New Cross-Layer Power Saving Mechanism for Mobile Ad-Hoc Networks. Journal of Computer Science and Technology, Jan 2013, V28(1): 42-53 (SCI, IF = 0.656)
12. Jianrui Yuan, **Jintao Meng**. A Power Adjusting Algorithm on Mobility Control in Mobile Ad Hoc Networks. In 8th IFIP International Conference on Network and Parallel Computing (NPC 2011), pp. 214-231, Changsha, China, Oct. 2011 (Best Paper candidate, EI)
13. Liansheng Tan, **Jintao Meng**, Jie Li and Han-Chieh Chao. PH-MAC: A Periodically Hybrid MAC Protocol for Wireless sensor networks, Journal of Internet Technology, Taiwan, Nov

2007. (SCI, IF = 0.508)

14. Jian Zhao, Danni Song, Qiang Zhang, **Jintao Meng**. A New Distributed Optimal Utility Max-Min Fair Resource Allocation. IEEE International Conference on Networking, Sensing and Control, 2008. ICNSC 2008 (EI)
15. **Jintao Meng**, Yanjie Wei, Gene and Disease Association Study with Metagenomics Assembling Tool: SWAP-Meta, e-Science Technology & Application, 2014, V5(3):30-37 (in chinese)
16. **Jintao Meng**, Jianrui Yuan, Yanjie Wei, Shengzhong Feng, The Analysis of De Novo Genome Assembly Software Based on De Bruijn Graph, e-Science Technology & Application, 2013, V4(5): 58-70.(in chinese)
17. **Jintao Meng**, Shuang Wang, Shengzhong Feng, An Introduction on Erroneous Kmers Filtering in Sequencing data, Bulletin of Advanced Technology Research, 2011, V1: 29-31. (in chinese)

Honors & Scholarships

- * Excellent employee in SIAT, CAS 2015 (20%)
- * Excellent employee in SIAT, CAS 2013 (20%)
- * Excellent employee in SIAT, CAS 2012 (20%)
- * Excellent employee in SIAT, CAS 2010 (20%)
- * Excellent Graduates, CCNU, 2008 (5%)
- * Direct Admission Students of CCNU 2005 (5%)
- * Excellent Graduates, CCNU, 2005 (5%)
- * The 2004 ACM/ICPC Asia Programming Contest-Shanghai, 2004 (Rank 27 in 400 Asia teams)
- * The 2004 ACM/ICPC Asia Programming Contest-Beijing, 2004 (Rank 38 in 360 Asia teams)
- * The 2003 ACM/ICPC Asia Programming Contest-GuangZhou, 2003 (Rank 36 in 72 Asia teams)
- * Excellent Student in Academic Research, CCNU, 2004
- * Excellent Student Third Prize, CCNU, 2003
- * Excellent Student First Prize, CCNU, 2002