

Haifeng Chen

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Objective

- To apply for a PhD program in Bioinformatics and Algorithm Design

Highlights of Qualification

- Submitted one paper on *de novo* peptide sequencing to **RECOMB 2012**
- Three Silver Medals of ACM-ICPC Asia Regional Contest
- Solid background in algorithm design, especially in computational geometry, dynamic programming and graph theory
- Two-year research experience in bioinformatics, especially in computational mass spectrometry-based proteomics
- **Computer Skills:** Six years C/C++ programming experience; Proficient in Matlab, Java;
Tools: Visual Studio 2010, Eclipse C++

Education

M.S. in Computer Application Technology (July 2012), Institute of Computing Technology, Chinese Academy of Sciences, Beijing

Thesis: *De novo* Peptide Sequencing using Complementary HCD and ETD Tandem Mass Spectra (Advisor: Prof. Si-Min He)

B.E. in Computer Science and Technology (June 2009), China University of Geosciences, Wuhan

GPA: 87.2/100 (**top 3**), Major GPA: 89.9/100

Publication

Haifeng Chen, Hao Chi, Si-Min He, Meng-Qiu Dong, et al. "pNovo+: *De novo* Peptide Sequencing using Complementary HCD and ETD Tandem Mass Spectra", submitted to *16th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2012)*

Awards and Honors

- **Silver Medal** of the 33th ACM-ICPC Asia Hefei Regional Contest, 2008
- **Silver Medal** of the 33th ACM-ICPC Asia Chengdu Regional Contest, 2008
- **Silver Medal** of the 32th ACM-ICPC Asia Beijing Regional Contest, 2007
- **Bronze Medal** of the 32th ACM-ICPC Asia Changchun Regional Contest, 2007
- **1st Prize**, Contemporary Undergraduate Mathematical Contest in Modeling, Hubei province, 2007
- **Inspirational National Scholarship**, China, 2008 (top 1%)
- **Excellent Graduate Scholarship**, China University of Geosciences (Wuhan), 2009 (top 2%)
- **Excellent Student Scholarships**, China University of Geosciences (Wuhan), 2006, 2007, 2008 (top 2%)
- **Innovation Talent Award**, China University of Geosciences (Wuhan), 2008 (top 1%)

Research Experience

11/2010–present Graduate Research Assistant, Institute of Computing Technology, Chinese Academy of Sciences, Beijing

Project: pNovo+: *De novo* Peptide Sequencing via Tandem Mass Spectrometry (Advisor: Prof. Si-Min He and Prof. Meng-Qiu Dong)

- Principally developed the new algorithm, pNovo+, which took advantage of the complementary HCD and ETD tandem mass spectra to improve fragmentation

information and determine the fragment ion types

- Fully considered ion types in ETD spectra, including hydrogen-rearranged fragment ions such as $z + H$ and $c - H$
- Verified the anti-symmetry restriction is not necessary in high-resolution spectra, which is much different from the previous algorithms
- Developed an efficient k longest paths algorithm to find all candidate peptides, which enables pNovo+ taking average 0.07 second per spectrum, 10 to 100 times faster than the previously reported running times
- Defined a variable GAP , the distance between peptide length and number of edges in the corresponding path, for each peptide, which is simple but effective to rank all candidate peptides

03/2009–present Graduate Research Assistant, Institute of Computing Technology, Chinese Academy of Sciences, Beijing

Project: pBuild: Post-Processing Results From Multiple Protein Identification Search Engines (Advisor: Prof. Si-Min He)

- Independently developed the algorithm and software, pBuild, whose internal algorithm was implemented in C++ programming language and interface was designed in Java programming language
- Implemented following functions in pBuild: (1) Filter spectra/peptide using Target-Decoy Approach to get more reliable results from multiple protein identification search engines, such as Mascot, SEQUEST or pFind; (2) Plot the mass deviation distribution diagram for observing the precursor deviation of the mass spectrometry data and setting the proper precursor tolerance to filter reliable peptides; (3) Plot false discovery rate curve for comparing the performance of different search engines; (4) Highlight the sequences of proteins which are identified; (5) Plot the Venn Diagram for obviously learning the union and intersection of spectra, peptides and proteins from different search engines
- Applied a greedy set cover algorithm to derive a minimal protein list according to parsimony principle
- Introduced indexing technique which enables pBuild to process big data
- pBuild has been used by over 200 researchers for routine mass spectrometry data analysis, which is an honorable accomplishment for me

10/2007–05/2009 Undergraduate Research Assistant, National University Student Innovation Program, China

Project: Vehicle Recognition System Based on the Real-Time Videos (Advisor: Prof. Guang-Ming Dai)

- Applied with a team of three students for the National University Student Innovation Program in China and received 30,000 Yuan support funding
- Designed background dynamic update mechanism for adapting to dynamically changing environments
- Developed a flexible relaxation method for extracting the notable features of vehicles

04/2008–04/2009 Undergraduate Research Assistant, Outstanding and Innovative Talents Cultivation Program, China University of Geosciences (Wuhan)

Project: Genetic Algorithm for Scheduling Optimization of Multi-resources (Advisor: Associate Prof. Xiang Li)

- Independently applied for the Outstanding and Innovative Talents Cultivation Program at China University of Geosciences (Wuhan) and received 1,000 Yuan support funding
- Used self-adaptive genetic algorithm to resolve multi-resource balanced scheduling optimization

Extracurricular Experience

03/2007–06/2009 Undergraduate Assistant Coach, instructed students in Computational Geometry Algorithm for two years at China University of Geosciences (Wuhan)