

# Hyundoo Jeong

Work Address:  
College of IT Convergence, #6119  
309 Pilmoon-daero, Dong-gu  
61452, Gwangju, Republic of Korea

Contact:  
+82-62-230-7107  
hdjeong@chosun.ac.kr  
<https://jeonglab.github.io>

CURRENT POSITION	<b>Chosun University</b> , Gwangju, South Korea Assistant professor, Electronic Engineering	Sept. 2018 - Present
EDUCATION & TRAINING	<b>Baylor College of Medicine</b> , Houston, Texas Postdoctoral research associate Advisors: Dr. Zhandong Liu and Dr. Joshua M. Shulman	Aug. 2017 - Aug. 2018
	<b>Texas A&amp;M University</b> , College Station, Texas Ph.D., Electrical and Computer Engineering Advisors: Dr. Byung-Jun Yoon and Dr. Xiaoning Qian	Sept. 2012 - Aug. 2017
	<b>Seoul National University</b> , Seoul, South Korea M.S., Electrical Engineering and Computer Science Advisor: Dr. Jae Hong Lee	Mar. 2007 - Feb. 2009
	<b>Inha University</b> , Incheon, South Korea B.S., Electronic Engineering Magna Cum Laude (Ranked in 2 out of 199 students)	Mar. 1999 - Feb. 2007
RESEARCH INTERESTS	Signal processing, machine learning, probabilistic graphical models, bioinformatics, single cell genomics, computational network biology, statistical network analysis, image processing, and large-scale data analysis.	
HONORS AND AWARDS	Young Scholar Research Award, Korean Institute of Intelligent Systems    Fall 2018 Travel Grants <ul style="list-style-type: none"> <li>• 14th annual MCBIOS conference, Little Rock, AR    Mar. 2017</li> <li>• NSF supported grant for 3rd CNB-MAC workshop, Seattle, WA    Oct. 2016</li> <li>• 13th annual MCBIOS conference, Memphis, TN    Mar. 2016</li> <li>• NSF supported grant for 2nd CNB-MAC workshop, Atlanta, GA    Sept. 2015</li> <li>• NSF supported grant for XSEDE15 conference, St. Louis, MO    July 2015</li> <li>• 12th annual MCBIOS conference, Little Rock, AR    Mar. 2015</li> </ul> Scholarship <ul style="list-style-type: none"> <li>• Graduate research assistantship, Texas A&amp;M University    Sept. 2013 - Aug. 2017</li> <li>• \$1,000 scholarship with an in-state tuition waive, Texas A&amp;M University    2012</li> <li>• Samsung education scholarship    2008</li> <li>• BK21 (Brain Korea) research scholarships, National Research Foundation of Korea    2007, 2008</li> <li>• Honor scholarships (six semesters), Inha University    2001, 2005, and 2006</li> <li>• English scholarship, Inha University    2005</li> </ul> Magna Cum Laude, Inha University    2007	
RESEARCH GRANT	<b>Network alignment and clustering algorithms for comparative analysis of dynamic biological networks</b> Mar. 2019 - Feb. 2022 Research grant from National Research Foundation of Korea : 90,000,000 KRW (30,000,000 KRW / year) Developing comparative network analysis algorithms for dynamic biological networks	

RESEARCH EXPERIENCE	<b>Jan and Dan Duncan Neurological Research Institute</b> Houston, TX <i>Postdoctoral Research Associate</i> Aug. 2017 - Aug. 2018 Developed effective algorithms to analyze single cell RNA sequencing
	<b>Genomic Signal Processing Lab.</b> , Texas A&M University College Station, TX <i>Research Assistant</i> Sept. 2013 - Aug. 2017 Developed global network alignment and querying algorithms
	<b>AgriLife Research</b> , Texas A&M University College Station, TX <i>Research Assistant</i> Sept. 2013 - Aug. 2014 Developed a quality assessment pipeline for de novo transcriptome assembly
	<b>Institute of New Media &amp; Communications</b> Seoul, South Korea <i>Research Assistant</i> Mar. 2007 - Jan. 2009 Performed research on wireless communications (PHY layer)
INDUSTRIAL EXPERIENCE	<b>Patent Information Promotion Center</b> Seoul, South Korea <i>Patent Search Professional</i> Feb. 2012 - June 2012 Searched and reviewed technical documents, and made review reports
	<b>Samsung Electronics</b> Suwon, South Korea <i>Software Engineer at Mobile Communication Division</i> Feb. 2009 - Mar. 2011 Developed smart phone device drivers (Windows platform)
JOURNAL IN PREPARATION	<ol style="list-style-type: none"> <li>1. <b>H. Jeong</b> and Z. Liu, "PRIME: Probabilistic imputation and smoothing for single cell RNA sequencing," under revision after first review (Bioinformatics).</li> <li>2. H.-M. Woo<sup>†</sup>, <b>H. Jeong</b><sup>†</sup>, and B.-J. Yoon "Comprehensive updates in network synthesis models to benchmark comparative network analysis," will be submitted. (manuscript is available) <sup>†</sup>Equally contributed</li> <li>3. Y. Wang<sup>†</sup>, <b>H. Jeong</b><sup>†</sup>, X. Qian, and B.-J Yoon, "ClusterM: a scalable algorithm for computational prediction of conserved protein complexes across multiple protein interaction networks," will be submitted. (manuscript is available) <sup>†</sup>Equally contributed</li> </ol>
JOURNAL PUBLICATIONS	<ol style="list-style-type: none"> <li>1. C.-C Chen, <b>H. Jeong</b>, X. Qian, and B.-J Yoon, "TOPAS: network-based structural alignment of RNA sequences," Accepted to Bioinformatics.</li> <li>2. N. Ghaffari<sup>†</sup>, O. A. Arshad<sup>†</sup>, <b>H. Jeong</b><sup>†</sup>, J. Thiltges, M.F. Criscitiello, B.-J. Yoon, A. Datta, and C. D. Johnson, "Examining de novo transcriptome assemblies via a quality assessment pipeline," IEEE/ACM Transaction on Computational Biology and Bioinformatics, vol.15, no.2, pp. 494 - 505, Mar. 2018. <sup>†</sup>Equally contributed</li> <li>3. <b>H. Jeong</b>, X. Qian, and B.-J Yoon, "CUFID-query: random walk based network querying through network flow estimation," BMC Bioinformatics, 18(Suppl. 14):12, 2017.</li> <li>4. <b>H. Jeong</b> and B.-J Yoon, "SEQUOIA: significance enhanced network querying through context-sensitive random walk and minimization of network conductance," BMC Systems Biology, 11(Suppl. 3):20, 2017.</li> <li>5. <b>H. Jeong</b>, X. Qian, and B.-J Yoon, "Effective comparative analysis of protein-protein interaction networks by measuring the steady state network flow using a Markov model," BMC Bioinformatics, 17(Suppl. 13):395, 2016.</li> <li>6. <b>H. Jeong</b> and B.-J Yoon, "Effective estimation of node-to-node correspondence between different graphs," IEEE Signal Processing Letters, vol. 22, no. 6, pp. 661-665, June 2015.</li> <li>7. <b>H. Jeong</b> and B.-J Yoon, "Accurate multiple network alignment through context-sensitive random walk," BMC Systems Biology, 9(Suppl. 1):S7, 2015.</li> </ol>

CONFERENCE  
PUBLICATIONS

1. H.-M. Woo<sup>†</sup>, **H. Jeong**<sup>†</sup>, and B.-J Yoon, "Comprehensive updates in network synthesis models to create an improved benchmark for network alignment algorithms," 9th ACM-BCB, Washington, DC, USA, Aug. 2018. <sup>†</sup>Equally contributed
2. **H. Jeong** and B.-J Yoon, "SEQUOIA: Significance enhanced network querying through context-sensitive random walk and minimization of network conductance," 7th ACM-BCB, Seattle, WA, Oct. 2016.
3. **H. Jeong** and B.-J Yoon, "Identifying molecular complexes in biological networks through context sensitive network querying," 6th ACM-BCB, Atlanta, GA, Sept. 2015.
4. **H. Jeong** and B.-J Yoon, "Accurate multiple network alignment through context-sensitive random walk," Asian Pacific Bioinformatics Conference (APBC) 2015, Hsinchu, Taiwan, Jan. 2015.
5. N. Ghaffari<sup>†</sup>, O. A. Arshad<sup>†</sup>, **H. Jeong**<sup>†</sup>, et al., "De novo transcriptome assemblies and annotation for pacific whiteleg shrimp," IEEE Global Conference on Signal and Information Processing (GlobalSIP) 2014, Atlanta, GA, USA, Dec. 2014. <sup>†</sup>Equally contributed
6. **H. Jeong** and B.-J Yoon, "A novel context-sensitive random walk model for estimating node correspondence between two biological networks," 5th ACM-BCB, Newport Beach, CA, USA, Sept. 2014.
7. **H. Jeong**, J. H. Lee, and H. Seo, "Resource allocation for uplink multiuser OFDM relay networks with fairness constraints," IEEE Vehicular Technology Conference (VTC) 2009 Spring, Barcelona, Spain, Apr. 2009.

INVITED TALKS

1. **H. Jeong**, "Network-based signal processing in bioinformatics," Korean Institute of Intelligent Systems Fall Conference, Wonju, S. Korea 2018.

ORAL & POSTER  
PRESENTATIONS

1. **H. Jeong**, X. Qian, and B.-J Yoon, "CUFID-query: Accurate network querying through estimation of network flow between query and target networks based on random walk," 14th Annual Conference of the MidSouth Computational Biology and Bioinformatics Society (MCBIOS), Little Rock, AR, USA, Mar. 2017.
2. **H. Jeong**, X. Qian, and B.-J Yoon, "CUFID-multialign: Enhanced multiple alignment of biological networks through estimation of steady-state flow using a random walk model," 14th Annual Conference of the MidSouth Computational Biology and Bioinformatics Society (MCBIOS), Little Rock, AR, USA, Mar. 2017.
3. **H. Jeong** and B.-J Yoon, "SEQUOIA: Significance enhanced network querying through context-sensitive random walk and minimization of network conductance," 3rd Int'l Workshop on Computational Network Biology: Modeling, Analysis, and Control (CNB-MAC), Seattle, WA, USA, Oct. 2016.
4. B.-J Yoon, and **H. Jeong**, "Predicting potential functional module in biological networks through context-sensitive random walk based network querying," Qatar Foundation-Annual Research Conference (QF-ARC), Doha, Qatar, Mar. 2016.
5. **H. Jeong** and B.-J Yoon, "Effective comparative analysis of protein-protein interaction networks by measuring the steady state network flow using a Markov model," 13th Annual Conference of the MidSouth Computational Biology and Bioinformatics Society (MCBIOS), Memphis, TN, USA, Mar. 2016.
6. C.-C Chen, **H. Jeong**, X. Qian, and B.-J Yoon, "Pairwise global structural alignment for RNA sequences through topological networks," 13th Annual Conference of the MidSouth Computational Biology and Bioinformatics Society (MCBIOS), Memphis, TN, USA, Mar. 2016.

7. **H. Jeong** and B.-J. Yoon, "Identifying molecular complexes in biological networks through context sensitive network querying," 2nd Int'l Workshop on Computational Network Biology: Modeling, Analysis, and Control (CNB-MAC), Atlanta, GA, USA, Sep. 2015.
8. **H. Jeong**, O. A. Arshad, N. Ghaffari, J. Thiltges, P. Blood, M. F. Criscitiello, B.-J. Yoon, A. Datta, and C. D. Johnson, "Comparative de novo transcriptome assemblies for Pacific whiteleg shrimp empowered by XSEDE resources," Extreme Science Engineering Discovery Environment (XSEDE), Saint Louis, MO, USA, July 2015.
9. **H. Jeong** and B.-J. Yoon, "Querying networks using context-sensitive random walk," 12th Annual Conference of the MidSouth Computational Biology and Bioinformatics Society (MCBIOS), Little Rock, AR, USA, Mar. 2015.
10. **H. Jeong** and B.-J. Yoon, "A novel context-sensitive random walk model for estimating node correspondence between two biological networks," Int'l Workshop on Computational Network Biology: Modeling, Analysis, and Control (CNB-MAC), Newport Beach, CA, USA, Sep. 2014.
11. **H. Jeong** and B.-J. Yoon, "A novel random walk model for comparing protein interactions networks," IEEE Int'l. Workshop on Genomic Signal Processing and Statistics (GENSIPS) 2013, Houston, TX, USA, Nov. 2013.

#### PATENTS

1. J. H. Lee and **H. Jeong** et. al "Method of allocating resources for cooperative diversity," 10-1523098, South Korea.

#### PROFESSIONAL ACTIVITY

Board member, KIIS (Korea Institute of Intelligent Systems) 2019 - Present  
 Board member, KICS (Korea Information and Communications Society) 2019-Present  
 Member, IEEE (Institute of Electrical and Electronics Engineers)  
 Member, ACM (Association for Computing Machinery)

#### SERVICE

##### Reviewer

IEEE/ACM Transactions on Computational Biology and Bioinformatics, PLOS ONE, BMC Bioinformatics, Pattern Recognition Letters, ACM-BCB (2017), EURASIP Journal on Bioinformatics and Systems Biology, Journal of Biological Systems, and Communications for Statistical Applications and Methods.

##### Other

Korean Student Association at Texas A&M University 2014 - 2017  
 Student volunteer, XSEDE 2015 2015

#### TEACHING EXPERIENCE

**Chosun University**, Gwangju, South Korea Sept. 2018 - Present  
 Spring 2019

- Electric Circuit 1
- Signals and Systems
- Object Oriented Programming (C++)
- Introduction to Programming (Programming language: C)

Fall 2018

- Electric Circuit 2
- Introduction to Programming (Programming language: Python)
- Advanced Programming (Programming language: C)
- Digital Logic Lab.

*Last updated: March 28, 2019*