# Sayed Mohammad Ebrahim Sahraeian

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## Education / Training

**UC Berkeley**                                                                          Berkeley, CA
Postdoctoral Researcher in Computational Genomics Research Group          Jan. 2013 - Present
*Research Topic*: Automated Protein Function Prediction
*Advisor*: Prof. Steven Brenner

**Texas A&M University**                                                         College Station, TX
Ph.D. in Electrical Engineering                                               Sep. 2008 - May 2013
*Research Topic*: Biological Sequence and Network Analysis
*Advisor*: Prof. Byung-Jun Yoon
*GPA*: 4.0/4.0

**Sharif University of Technology**                                                   Tehran, Iran
Master of Science in Electrical Engineering                                   Sep. 2005 - Jan. 2008
*Thesis title*: Wavelet based Image Denoising
*Advisor*: Prof. Farokh Marvasti
*GPA*: 18.57/20

**Sharif University of Technology**                                                   Tehran, Iran
Bachelor of Science in Electrical Engineering                                 Sep. 2001 - Sep. 2005
*Thesis title*: Free Format Assembly Language
*Advisor*: Dr. Bijan Vosoughi Vahdat
*GPA*: 17.33/20

## Research Interest

Computational Biology, Bioinformatics, Big Data, Comparative Genomics, Network Biology, Automated Protein Function Prediction, Biological Network Alignment, Biological Network Querying, Biological Sequence Alignment, Genomic Signal Processing

## Honors and Awards

Best poster award at the International Conference on Intelligent Systems for Molecular Biology (ISMB), Automated Protein Function Prediction (AFP) SIG, 2014

NSF travel award for RECOMB2012

Best paper award in 9th Asia Pacific Bioinformatics Conference (APBC2011)

Rank $4^{th}$ among M.Sc. students in Communication Systems, Dept. of Electrical Engineering, Sharif university of Technology, 2008.

Rank $4^{th}$/10,000 in Iran's National University Entrance Exam for M.S. degree in Electrical Engineering, 2005.

Rank $39^{th}$/400,000 Iran's National University Entrance Exam for B.S. degree, 2001.

# Publications

## *Journal Publications*

1. **S.M.E. Sahraeian**, K.R. Luo, and S.E. Brenner, "SIFTER Search: A web server for accurate phylogeny-based protein function prediction", *Nucleic Acids Research*, Web Server Issue 2015, accepted.

2. Pablo Meyer, et al., "Inferring gene expression from ribosomal promoter sequences, a crowdsourcing approach", *Genome Research*, 23:1928-1937, 2013.

3. D.T. Morishige, P.E. Klein, J.L. Hilley, **S.M.E. Sahraeian**, A. Sharma, and J.E. Mullet, "Digital genotyping of sorghum–a diverse plant species with a large repeat-rich genome", *BMC Genomics*, 14:448, Jul. 2013.

4. **S.M.E. Sahraeian** and B.J. Yoon, "SMETANA: Accurate and Scalable Algorithm for Probabilistic Alignment of Large-Scale Biological Networks", *PLOS ONE*, 8(7): e67995, Jul. 2013.

5. Y.H. Wang, H.D. Upadhyaya, A.M. Burrell, **S.M.E. Sahraeian**, R.R. Klein, and P.E. Klein, "Genetic structure and linkage disequilibrium in a diverse, representative collection of the C4 model plant, *Sorghum bicolor*", *G3: Genes Genomes Genetics*, 3(5): 783-793, May 2013.

6. **S.M.E. Sahraeian** and B.J. Yoon, "RESQUE: Network reduction using semi-Markov random walk scores for efficient querying of biological networks", *Bioinformatics*, 28(16): 2129-2136, 2012. (**Presented in RECOMB 2012**)

7. **S.M.E. Sahraeian** and B.J. Yoon, "A Network Synthesis Model for Generating Protein Interaction Network Families", *PLOS ONE*, 7(8): e41474, 2012.

8. B.J. Yoon, X. Qian, and **S.M.E. Sahraeian**, "Comparative Analysis of Biological Networks Using Markov Chains and Hidden Markov Models", *IEEE Signal Processing Magazine*, 29(1): 22-34, Jan. 2012.

9. X. Qian, **S.M.E. Sahraeian**, and B.J. Yoon, "Enhancing the accuracy of HMM-based conserved pathway prediction using global correspondence scores", *BMC Bioinformatics*, 12(Suppl 10):S6, 2011.

10. **S.M.E. Sahraeian** and B.J. Yoon, "PicXAA-Web: a web-based platform for non-progressive maximum expected accuracy alignment of multiple biological sequences", *Nucleic Acids Research*, Web Server Issue, doi:10.1093/nar/gkr244, Apr. 2011.

11. **S.M.E. Sahraeian** and B.J. Yoon, "A Novel Low-Complexity HMM Similarity Measure", *IEEE Signal Processing Letters, 18(2): 87-90, Feb. 2011.*

12. **S.M.E. Sahraeian** and B.J. Yoon, "PicXAA-R: Efficient structural alignment of multiple RNA sequences using a greedy approach ", *BMC Bioinformatics*, 12(Suppl 1):S38, 2011. (**Best Paper Award APBC 2011**)

13. **S.M.E. Sahraeian** and B.J. Yoon, "PicXAA: Greedy probabilistic construction of maximum expected accuracy alignment of multiple sequences", *Nucleic Acids Research*, 38(15): 4917-4928, 2010.

14. **S.M.E. Sahraeian**, M.A. Akhaee, B. Sankur, and F. Marvasti, "Information hiding with maximum likelihood detector for correlated signals", *Digital Signal Processing*, 36: 144-155, 2015.

15. M.A. Akhaee and **S.M.E. Sahraeian**, "Scaling-based watermarking with universally optimum decoder", *Multimedia Tools and Applications* , 1-24, 2014.

16. M.A. Akhaee, **S.M.E. Sahraeian**, and C. Jin, "Blind Image Watermarking Using a Sample Projection Approach", *IEEE Transactions on Information Forensics and Security*, 6(3): 883-893, Sept. 2011.

17. M.A. Akhaee, **S.M.E. Sahraeian**, and F. Marvasti, "Contourlet Based Image Watermarking Using Optimum Detector in a Noisy Environment", *IEEE Transactions on Image Processing, 15(4): 967-980, Apr. 2010.*

18. M.A. Akhaee, **S.M.E. Sahraeian**, F. Marvasti, and B. Sankur, "Robust Scaling-Based Image Watermarking Using Maximum-Likelihood Decoder With Optimum Strength Factor", *IEEE Transactions on Multimedia*, 11(5): 822-833, Aug. 2009.

## Book Chapters

1. **S.M.E. Sahraeian** and B.J. Yoon, "PicXAA: A Probabilistic Scheme for Finding the Maximum Expected Accuracy Alignment of Multiple Biological Sequences", *Multiple Sequence Alignment Methods, Methods in Molecular Biology*, Edited by D. Russell, Springer, 1079: 203-210, 2014.

## Conference Publications

1. **S.M.E. Sahraeian** and B.J. Yoon, "Probabilistic Consistency Transformation for Multiple alignment of Biological Networks", *Proc. 9th IEEE International Workshop on Genomic Signal Processing and Statistics (GENSIPS)*, pp. 52-53 San Antonio, TX, Dec. 2011.

2. **S.M.E. Sahraeian** and B.J. Yoon, "Fast Network Querying Algorithm for Searching Large-scale Biological Networks ", *Proc. 36th IEEE Inter. Conf. on Acoustics, Speech, and Signal Processing (ICASSP)*, pp. 6008-6011, Prague, Czech Republic., May 2011.

3. **S.M.E. Sahraeian**, M.A. Akhaee, F. Marvasti, "Distribution Independent Blind Watermarking," *Proc. 16th IEEE International Conference on Image Processing (ICIP)*, pp. 125-128, Cairo, Egypt, Nov. 2009.

4. **S.M.E. Sahraeian**, M.A. Akhaee, F. Marvasti, "Information Hiding with Optimal Detector for Highly Correlated Signals, *Proc. 9th IEEE International Conference on Communications (ICC)*, Dresden, Germany, Jun. 2009.

5. **S.M.E. Sahraeian**, M.A. Akhaee, F. Marvasti, "Blind Image Watermarking Based on Sample Rotation with Optimal Detector", *Proc. 17th European Signal Processing conference (EUSIPCO)*, pp. 278-282, Glasgow, Scotland, Aug. 2009.

6. **S.M.E. Sahraeian**, M.A. Akhaee, S. A. Hejazi, F. Marvasti, "Contourlet Based Image Watermarkin Using Optimum Detector in the Noisy Environment", *Proc. 15th IEEE International Conference on Image Processing (ICIP)*, pp. 429-432, San Diego, CA, Oct. 2008.

7. **S.M.E. Sahraeian**, M.A. Akhaee, B. Sankur, and F. Marvasti, "Robust Multiplicative Watermarking Technique with Maximum Likelihood Detector", *Proc. 16th European Signal Processing conference (EUSIPCO)*, Lausanne, Switzerland, Aug. 2008.

8. **S.M.E. Sahraeian**, B. Vosoughi Vahdat, "A new approach to assembly level programming", *Proc. IEEE International Conference on Computer as a tool (Eurocon)*, pp. 439-445, Warsaw, Poland, Sep. 2007.

9. **S.M.E. Sahraeian**, E. Fatemizadeh, "Wavelet-based 2-D ECG Data Compression method using SPIHT and VQ coding", *Proc. IEEE International Conference on Computer as a tool (Eurocon)*, pp. 133-137, Warsaw, Poland, Sep. 2007.

10. **S.M.E. Sahraeian**, F. Marvasti, "An Improved Image Denoising Technique Using Cycle Spinning", *Proc. 14th IEEE International Conf. on Telecommunications (ICT)*, Malaysia, May 2007.

11. **S.M.E. Sahraeian**, F. Marvasti and N. Sadati, "Wavelet image denoising based on improved thresholding neural network and cycle spinning", *Proc. 32nd IEEE Inter. Conf. on Acoustics, Speech, and Signal Processing (ICASSP)*, vol. 1, pp. 585–588, Honolulu, HI, April 2007.

12. N. Mohammadiha, **S.M.E. Sahraeian**, B. Vosoughi Vahdat, A. Azizi, A. Shah Ahmadi, "Measuring the Geometrical Parameters of Steel Billets during Molding Process Using Image Processing", *Proc. 6th IEEE Symposium on Signal Processing and Information Technology (ISSPIT)*, pp. 59-63, Vancouver, Canada, Aug. 2006.

## Talks/Posters

1. **S.M.E. Sahraeian**, A.L. Lin, and S.E. Brenner, "Predicting Protein Function for the CAFA 2014 Experiment using Phylogenetic Function Prediction Embedded in SIFTER.", *22th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), Automated Protein Function Prediction(AFP) SIG*, Boston, MA, July 2014. (Invited Talk as a top-performing group in CAFA 2014)(**Best Poster Award ISMB AFP-SIG 2014**)

2. **S.M.E. Sahraeian** and S.E. Brenner, "Automated function prediction using SIFTER: an application and validation on Desulfovibrio vulgaris Hildenborough genome", *22th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2014)*, Boston, MA, July 2014.

3. **S.M.E. Sahraeian**, M.L. Souza, B.E. Engelhardt, M.I. Jordan, and S.E. Brenner, "Automated function prediction using SIFTER: an application and validation on Desulfovibrio vulgaris Hildenborough genome", *Ecosystems and Networks Integrated with Genes and Molecular Assemblies retreat*, Berkeley, CA, Aug 2013.

4. **S.M.E. Sahraeian** and B.J. Yoon, "Efficient Maximum Expected Accuracy Alignment of Multiple Biological Networks", *20th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2012)*, Long Beach, CA, July 2012.

5. **S.M.E. Sahraeian** "Probabilistic Approaches in Comparative Studies of Biological Interaction Networks", *Invited Talk*, Shiraz University, Dept. Electrical Eng., Shiraz, Iran, May 2012.

6. X. Qian, **S.M.E. Sahraeian**, and B.J. Yoon, "Enhancing the accuracy of HMM-based conserved pathway prediction using global correspondence scores", *8th Annual Conference of the MidSouth Computational Biology and Bioinformatics Society (MCBIOS 2011)*, College Station, TX, April 2011.

7. **S.M.E. Sahraeian** and B.J. Yoon, "Accurate and Scalable Network Querying Algorithm Using Semi-Markov Random Walk And Network Reduction Approach", *8th Annual Conference of the MidSouth Computational Biology and Bioinformatics Society (MCBIOS 2011)*, College Station, TX, April 2011.

8. **S.M.E. Sahraeian** and B.J. Yoon, "Efficient querying of protein interaction networks using semi-Markov random walk and network reduction approach", *6th Annual RECOMB Satellite on Systems Biology*, New York, NY, Nov. 2010.

9. **S.M.E. Sahraeian** and B.J. Yoon, "PicXAA-R: Probabilistic Structural Alignment of Multiple RNA Sequences Using a Greedy Approach", *8th IEEE International Workshop on Genomic Signal Processing and Statistics (GENSIPS)*, Cold Spring Harbor, NY, Nov. 2010.

# Software

PicXAA: Probabilistic maximum accuracy alignment of multiple biological sequences

PicXAA-R: Extension of PicXAA for RNA structural alignment

RESQUE: Efficient querying of biological networks based on network reduction scheme using semi-Markov random walk scores

NAPAbench: Network alignment performance assessment benchmark

SMETANA: Accurate and scalable algorithm for probabilistic alignment of large-scale biological networks

SIFTER Search: A web server for accurate phylogeny-based protein function prediction

# Research Experience

**Computational Genomics Research Group, UC Berkeley**      Berkeley, CA
*Postdoctoral Researcher*      Jan. 2013 - Present
• Automated protein function prediction
• Under supervision of Prof. Steven Brenner.

**Genomic Signal Processing (GSP) Laboratory, Texas A&M University**      College Station, TX
*Research Assistant*      Sep. 2008 - Dec. 2012
• Studying biological sequence and network analysis problems. Developing PicXAA, a greedy probabilistic sequence alignment algorithm. Developing RESQUE and SMETANA, biological network querying and alignment algorithms.

- Under supervision of Prof. Byung-Jun Yoon.

**Sorghum genomics Laboratory, Agrilife Research Center, Texas A&M University**      College Station, TX
*Research Assistant*      Mar. 2011 - Aug. 2012
- Digital genotyping and population structure inference of sorghum genome, a diverse plant species, using next generation sequencing data.
- Under supervision of Prof. Patricia Klein.

**Advanced Communication Research Institute (ACRI), Sharif University of Technology**      Tehran, Iran
*Research Assistant*      Mar. 2006 - Sep. 2008
- Researcher in Multimedia Laboratory working on Image denoising and Watermarking Projects.
- Under supervision of Prof. Farokh Marvasti.

**Bina Industrial Automation and Machine Vision Company**      Tehran, Iran
*Research Engineer*      Oct. 2005 - April 2006
- Developed an Image Processing based system for Measuring the Geometrical Parameters of Steel Billets during Molding Process.

**Iran Telecommunication Institute (ITI)**      Shiraz, Iran
*Internship*      May 2004 - Sep. 2004
- Developed a new SMD component counter device using 8051 Microcontroller

## Teaching Experience

**BioE24:Aspects of Bioengineering, UC Berkeley**      Berkeley, CA
*Guest lecturer on protein function prediction*      Fall 2014

**ECEN447:Digital Image Processing, Texas A&M University**      College Station, TX
*Teaching Assistant*      Fall 2010

**ECEN215: Principals of Electrical Engineering, Texas A&M University**      College Station, TX
*Teaching Assistant*      Spring 2010

**Digital Signal Processing (DSP) II, Sharif Univ. of Technology**      Tehran, Iran
*Teaching Assistant*      Fall 2006

## Computer Skills

Programming : Python, C++, Matlab, MathCad, Visual Basic, Pascal, Assembly, R, Django, SQL

Electrical Engineering software: Orcad, Pspice, Keil

## Graduate Level Coursework

*Texas A&M University*

Graph Theory, Applied Probability, Probability Models, Probabilistic Graphical Models, Advanced Probabilistic Graphical Models, Pattern Recognition, Computational Biology, Statistical Computation in Genomic Signal Processing, Linear Network Analysis.

*Sharif University of Technology*

Time-Frequency Signal Processing, Artificial Neural Networks, Digital Image Processing, Digital Signal Processing II, Speech Processing, Advanced Programming with VC++, Digital Signal Processing, Practical electronics, Microprocessors II.

## Professional Activities

Reviewer: Nucleic Acids Research, Bioinformatics, PlOS ONE, IEEE Transactions on Signal Processing, IEEE Signal Processing Letters, IEEE Transactions on Image Processing, IEEE Transactions on Information Forensics and Security, IEEE Transactions on Multimedia, IEEE Transactions on Computational Biology and Bioinformatics, IEEE Transactions on Systems, Man and Cybernetics-Part B, EURASIP Journal on Bioinformatics and Systems Biology, EURASIP Journal on Advances in Signal Processing, International Journal of Computer Assisted Radiology and Surgery, International Journal of Image and Graphics, Information Sciences, International Journal of Electronics and Communications.

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