

Shaun Mahony

The Pennsylvania State University,
404 South Frear Bldg,
University Park, PA 16802
☎ (814) 865-3008
✉ mahony@psu.edu
<http://mahonylab.org>

EDUCATION

- 2002–2006 **Ph.D., Information Technology (Computational Biology)**, *National University of Ireland, Galway*
Thesis: “Self-organizing neural networks for biological sequence analysis”
- 1998–2002 **B.E., Electronic & Computer Engineering**, *National University of Ireland, Galway*
First class honors.

RESEARCH EXPERIENCE

- 2016 – 2016 **Assistant Professor (tenure track)**, *The Pennsylvania State University*
2012 – 2016 **Assistant Professor (fixed term)**
Center for Eukaryotic Gene Regulation
Center for Comparative Genomics and Bioinformatics
Department of Biochemistry & Molecular Biology
- 2011–2012 **Visiting Scientist**, *Harvard University*
Department of Stem Cell and Regenerative Biology.
- 2010–2012 **Research Scientist**, *Massachusetts Institute of Technology*
Computer Science and Artificial Intelligence Laboratory.
- 2007–2010 **Postdoctoral Research Associate**, *Massachusetts Institute of Technology*
Research group of David Gifford, Computer Science and Artificial Intelligence Laboratory.
- 2005–2007 **Postdoctoral Research Associate**, *University of Pittsburgh*
Research group of Takis Benos, Department of Computational & Systems Biology.
- Fall 2004 **Visiting Researcher**, *University of Pittsburgh*
Research group of Takis Benos, Department of Human Genetics.
- Fall 2003 **Visiting Researcher**, *University of California, Berkeley*
Research group of Daniel Rokhsar,
Department of Molecular Cell Biology and Joint Genome Institute.
- 2002–2005 **Research Assistant**, *National University of Ireland, Galway*
Research groups of Terry Smith and Aaron Golden,
National Center for Biomedical Engineering Science.

PUBLICATIONS

45. *Alignment and quantification of ChIP-exo crosslinking patterns reveal the spatial organization of protein-DNA complexes*
N Yamada, MJ Rossi, N Farrell, BF Pugh, S Mahony
Nucleic Acids Research (2020) gkaa618 (doi: 10.1093/nar/gkaa618) [NAR Breakthrough Article]
44. *Assessing relationships between chromatin interactions and regulatory genomic activities using the self-organizing map*
T Kunz, L Rieber, S Mahony
Methods (2020) S1046-2023(19)30277-4
43. *An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis*
G Xiang, CA Keller, E Heuston, BM Giardine, L An, AQ Wixom, A Miller, A Cockburn, J Lichtenberg, B Göttgens, Q Li, D Bodine, S Mahony, J Taylor, GA Blobel, MJ Weiss, Y Cheng, F Yue, J Hughes, DR Higgs, Y Zhang, RC Hardison
Genome Research (2020) 30:472-484

42. *ChExMix: a method for identifying and classifying protein-DNA interaction subtypes*
N Yamada, PK Kuntala, BF Pugh, [S Mahony](#)
Journal of Computational Biology (2020) 27(3):429-435
41. *Systematic integration of GATA transcription factors and epigenomes via IDEAS paints the regulatory landscape of hematopoietic cells*
RC Hardison, Y Zhang, CA Keller, G Xiang, EF Heuston, L An, J Lichtenberg, BM Giardine, D Bodine, [S Mahony](#), Q Li, F Yue, MJ Weiss, GA Blobel, J Taylor, J Hughes, DR Higgs, B Göttgens.
IUBMB Life (2020) 72(1):27-38 [review article]
40. *Sequence and chromatin determinants of transcription factor binding and the establishment of cell type-specific binding patterns*
D Srivastava & [S Mahony](#)
BBA - Gene Regulatory Mechanisms (2020) 1863(6):194443 [review article]
39. *Direct prediction of regulatory elements from partial data without imputation*
Y Zhang & [S Mahony](#)
PLoS Computational Biology (2019) 15(11):e1007399
38. *Joint inference and alignment of genome structures enables characterization of compartment-independent 3D relocalization across cell types*
L Rieber & [S Mahony](#)
Epigenetics & Chromatin (2019) 12(1):61
37. *Proneural factors *Ascl1* and *Neurog2* contribute to neuronal subtype identities by establishing distinct chromatin landscapes*
B Aydin, A Kakumanu, M Rossillo, M Moreno-Estelles, G Garipler, N Ringstad, N Flames, [S Mahony](#)*, EO Mazzoni*
Nature Neuroscience (2019) 22(6):897-908 (*corresponding authors)
36. *Characterizing protein-DNA binding event subtypes in ChIP-exo data*
N Yamada, WKM Lai, N Farrell, BF Pugh, [S Mahony](#)
Bioinformatics (2019) 35(6):903-913
35. *Widespread and precise reprogramming of yeast protein-genome interactions in response to heat shock*
V Vinayachandran, R Reja, MJ Rossi, B Park, L Rieber, C Mittal, [S Mahony](#), BF Pugh
Genome Research (2018) 28: 357-366
34. *Deconvolving sequence features that discriminate between overlapping regulatory annotations*
A Kakumanu, S Velasco, EO Mazzoni, [S Mahony](#)
PLoS Computational Biology (2017) 13(10):e1005795
33. *miniMDS: 3D structural inference from high-resolution Hi-C data*
L Rieber, [S Mahony](#)
Bioinformatics (2017) 33 (14): i261-i266
32. *A multi-step transcriptional and chromatin state cascade underlies motor neuron programming*
S Velasco&, MM Ibrahim&, A Kakumanu&, G Garipler, B Aydin, MA Al-Sayegh, A Hirsekorn, F Abdul-Rahman, R Satija, U Ohler*, [S Mahony](#)*, EO Mazzoni*
Cell Stem Cell (2017) 20(2):205-217 (& equal contribution, *corresponding authors)
31. *The pioneer transcription factor *FoxA* maintains an accessible nucleosome configuration at enhancers for tissue-specific gene activation*
M Iwafuchi-Doi, G Donahue, A Kakumanu, JA Watts, [S Mahony](#), BF Pugh, D Lee, KH Kaestner, KS Zaret
Molecular Cell (2016) 62(1): 72-91
30. *Engineered stomach tissues as a renewable source of functional beta-cells for blood glucose regulation*
C Ariyachet, A Tovaglieri, G Xiang, J Lu, MS Shah, CA Richmond, C Verbeke, DA Melton, BZ Stanger, D Mooney, RA Shivdasani, [S Mahony](#), Q Xia, DT Breault, Q Zhou
Cell Stem Cell (2016) 18(3):410-421
29. *Phenome-wide interaction study (PheWIS) in AIDS clinical trials group data (ACTG)*
SS Verma, AT Frase, A Verma, SA Pendergrass, [S Mahony](#), DW Haas, MD Ritchie
Pacific Symposium on Biocomputing (2016) 21:57-68
28. *Genome-wide organization of *GATA1* and *TAL1* determined at high resolution*
GC Han, V Vinayachandran, A Bataille, B Park, KY Chan-Salis, CA Keller, M Long, [S Mahony](#), RC

- Hardison, BF Pugh
Molecular & Cell Biology (2015) 36(1):157-172
27. *Protein-DNA binding in high resolution*
S Mahony, BF Pugh
Critical Reviews in Biochemistry and Molecular Biology (2015) 50(4):269-283 [review article]
 26. *Gene co-regulation by Fezf2 selects neurotransmitter identity and connectivity of corticospinal neurons*
S Lodato, BJ Molyneax, E Zuccaro, LA Goff, H-H Chen, W Yuan, A Meleski, E Takahashi, S Mahony, JL Rinn, DK Gifford, P Arlotta
Nature Neuroscience (2014) 17(8):1046-54
 25. *An integrated model of multiple-condition ChIP-seq data reveals predeterminants of Cdx2 binding*
S Mahony* & MD Edwards & EO Mazzoni, RI Sherwood, A Kakumanu, CA Morrison, H Wichterle, DK Gifford*
PLoS Computational Biology (2014) 10(3):e1003501 (*& equal contribution, *corresponding authors*)
 24. *A Cdx4-Sall4 regulatory module controls the transition from mesoderm formation to embryonic hematopoiesis*
EJ Paik, S Mahony, RM White, EN Price, A DiBiase, B Dorjsuren, C Mosimann, AJ Davidson, DK Gifford, LI Zon
Stem Cell Reports (2013) 1(5):425-436
 23. *Synergistic binding of transcription factors to cell-specific enhancers programs motor neuron identity*
EO Mazzoni*, S Mahony*, M Closser, CA Morrison, S Nedelec, DJ Williams, D An, DK Gifford, H Wichterle
Nature Neuroscience (2013) 16(9):1219-1227 (** equal contribution*)
 22. *Saltatory remodeling of Hox chromatin in response to rostrocaudal patterning signals*
EO Mazzoni*, S Mahony*, M Peljto*, T Patel, SR Thornton, S McCuine, C Reeder, LA Boyer, RA Young, DK Gifford, H Wichterle
Nature Neuroscience (2013) 16(9):1191-1198 (** equal contribution*)
 21. *A multi-parametric flow cytometric assay to analyze DNA-protein interactions*
M Arbab, S Mahony, H Cho, J Chick, PA Rolfe, J Van Hoff, V Morris, S Gygi, RL Maas, DK Gifford, R Sherwood
Nucleic Acids Research (2013) 41(2):e38
 20. *High resolution genome wide binding event finding and motif discovery reveals transcription factor spatial binding constraints*
Y Guo, S Mahony*, DK Gifford*
PLoS Computational Biology (2012) 8(8):e1002638 (** corresponding authors*)
 19. *Embryonic stem cell based system for the discovery and mapping of developmental transcriptional programs*
EO Mazzoni, S Mahony, M Iacovino, CA Morrison, G Mountoufaris, M Closser, WA Whyte, RA Young, M Kyba, DK Gifford, H Wichterle
Nature Methods (2011) 8(12):1056-1058
 18. *Large scale comparison of innate responses to viral and bacterial pathogens in mouse and macaque*
GE Zinman, R Brower-Sinning, CH Emeche, J Ernst, GT Huang, S Mahony, AJ Myers, DM O'Dee, JL Flynn, GJ Nau, TM Ross, RD Salter, PV Benos, Z Bar-Joseph, PA Morel
PLoS ONE (2011) 6(7):e22401
 17. *Ligand-dependent dynamics of retinoic acid receptor binding during early neurogenesis*
S Mahony*, EO Mazzoni*, S McCuine, RA Young, H Wichterle, DK Gifford
Genome Biology (2011) 12(1):R2 (** equal contribution*)
 16. *Discovering homotypic binding events at high spatial resolution*
Y Guo, G Papachristoudis, RC Altshuler, GK Gerber, TS Jaakkola, DK Gifford, S Mahony*
Bioinformatics (2010) 26(24):3028-3034 (** corresponding author*)
 15. *Global control of motor neuron topography mediated by the repressive actions of a single Hox gene*
H Jung, J Lacombe, EO Mazzoni, KF Leim, J Grinstein, S Mahony, D Mukopadhyay, DK Gifford, RA Young, KV Anderson, H Wichterle, JS Dasen
Neuron (2010) 67(5):781-796
 14. *Feed-forward regulation of a cell fate determinant by an RNA-binding protein generates asymmetry in yeast*
JJ Wolf, RD Dowell, S Mahony, M Rabani, DK Gifford, GR Fink
Genetics (2010) 185:513-522

13. *ORegAnno: an open-access community-driven resource for regulatory annotation*
OL Griffith, SB Montgomery..., S Mahony (7th of 29 authors)..., CM Bergman, SJM Jones
Nucleic Acids Research (2008) 36:D107-D113
12. *Combined analysis reveals a core set of cycling genes*
Y Lu, S Mahony, PV Benos, R Rosenfeld, I Simon, LL Breeden, Z Bar-Joseph
Genome Biology (2007) 8(7):R146
11. *Inferring protein-DNA dependencies using motif alignments and mutual information*
S Mahony, PE Auron, PV Benos
Bioinformatics (2007) 23(13): i297-i304
10. *Regulatory conservation of protein coding and miRNA genes in vertebrates: lessons from the opossum genome*
S Mahony, DL Corcoran, E Feingold, PV Benos
Genome Biology (2007) 8(5):R84
9. *Genome of the marsupial *Monodelphis domestica* reveals innovation in non-coding sequences*
TS Mikkelsen, MJ Wakefield..., S Mahony (37th of 64 authors)..., ES Lander, K Lindblad-Toh
Nature (2007) 447:167-177
8. *STAMP: a web tool for exploring DNA-binding motif similarities*
S Mahony, PV Benos
Nucleic Acids Research (2007) 35:W253-W258
7. *DNA familial binding profiles made easy: comparison of various motif alignment and clustering strategies*
S Mahony, PE Auron, PV Benos
PLoS Computational Biology (2007) 3(3):e61
6. *Gene prediction in metagenomic libraries using the self-organising map and high performance computing techniques*
N McCoy, S Mahony, A Golden
Springer Lecture Notes in Bioinformatics (2007) 4360: 99-109
5. *Self-organizing neural networks to support the discovery of DNA-binding motifs*
S Mahony, PV Benos, TJ Smith, A Golden
Neural Networks (2006) 19 (6-7): 950-962
4. *Reconstructing an ancestral mammalian immune supercomplex from a marsupial Major Histocompatibility Complex*
K Belov, JE Deakin, AT Papenfuss, ML Baker, SD Melman, HV Siddle, N Gouin, DL Goode, TJ Sargeant, MD Robinson, MJ Wakefield, S Mahony, JG Cross, PV Benos, PB Samollow, TP Speed, JA Graves, RD Miller
PLoS Biology (2006) 4 (3): e46
3. *Improved detection of DNA motifs using a self-organized clustering of familial binding profiles*
S Mahony, A Golden, TJ Smith, PV Benos
Bioinformatics (2005) 21 (Suppl 1): i283-i291
2. *Transcription factor binding site identification using the Self-Organizing Map*
S Mahony, D Hendrix, A Golden, TJ Smith, DS Rokhsar
Bioinformatics (2005) 21(9): 1807-14
1. *Gene prediction using the Self-Organizing Map: automatic generation of multiple gene models*
S Mahony, JO McNerney, TJ Smith, A Golden
BMC Bioinformatics (2004) 5:23

Preprints & Submitted Manuscripts

3. *High resolution protein architecture of a eukaryotic genome*
MJ Rossi, PK Kuntala, WKM Lai, N Yamada, N Badjatia, C Mittal, G Kuzu, K Bocklund, NP Farrell, TR Blanda, JD Mairose, AV Basting, KS Mistretta, DJ Rocco, ES Perkinson, GD Kellogg, S Mahony, BF Pugh
Under review
2. *Hox binding specificity is directed by DNA sequence preferences and differential abilities to engage inaccessible chromatin*

M Bulajić*, D Srivastava*, JS Dasen, H Wichterle, S Mahony, EO Mazzoni
bioRxiv 890335 (* equal contribution, doi: <https://doi.org/10.1101/2019.12.29.890335>)

1. *An interpretable bimodal neural network characterizes the sequence and preexisting chromatin predictors of induced TF binding*
D Srivastava, B Aydin, EO Mazzoni, S Mahony
bioRxiv 672790 (doi: <https://doi.org/10.1101/672790>)

RESEARCH FUNDING

Active Funding

Grant	Title	Grant Period	Funding	
			Direct	Total
NIH NIGMS R01 (R01-GM121613) PI: S Mahony Co-I: RC Hardison	A 2D segmentation method for jointly characterizing epigenetic dynamics in multiple cell lines	08/2018 – 07/2021 (NCE)	\$450,000	\$685,035
NIH NIGMS R01 (R01-GM125722) PI: S Mahony PI: BF Pugh	Genome-wide structural organization of proteins within human gene regulatory complexes	01/2018 – 12/2021	\$840,000	\$1,280,459
	(Equipment supplement)	09/2018	\$61,750	\$61,750

Completed Funding

Grant	Title	Grant Period	Funding	
			Direct	Total
NSF ABI Innovation (1564466) PI: S Mahony	Characterizing protein-DNA interactions from high-resolution assays	06/2016 – 05/2020	\$437,120	\$657,054
NIH NICHD R01 (1R01 HD079682) PI: E Mazzoni Co-I: S Mahony	Molecular mechanisms of direct neuronal programming	09/2014 – 08/2019	\$1,037,500 (Mahony: \$155,369)	\$1,442,297 (Mahony: \$223,653)
American Cancer Society Institutional Research Grant PI: S Mahony	Characterizing the global epigenomic response to Ikaros tumor suppressor restoration in T-cell Acute Lymphoblastic Leukemia	06/2015 – 05/2016	\$29,775	\$29,775
PA Dept. of Health CURE Program Co-PIs: M Szpara S Mahony	Mapping transcriptional control sites in human herpes simplex virus	01/2015 – 12/2015	\$50,930	\$57,750

TEACHING

Full Courses (* denotes newly developed courses)

- **BMMB-541: Critical Analysis of Literature in Bioinformatics and Genomics**
Penn State University, Dept. of Biochemistry & Molecular Biology.
Lecturer: Fall 2020 (16 students)
Fall 2019 (21 students)
Fall 2018 (12 students)
- ***BMB-482: Introduction to Computational Biology**
Penn State University, Dept. of Biochemistry & Molecular Biology.
Lecturer: Fall 2020 (16 students)
Fall 2019 (22 students)
Fall 2018 (19 students)
Fall 2017 (22 students)
Fall 2015 (10 students)
Fall 2014 (21 students)
Fall 2013 (24 students)
- **BMMB-551: Genomics**
Penn State University (World Campus), Dept. of Biochemistry & Molecular Biology.
Lecturer: Spring 2018 (16 students)
- ***MCIBS-503 / BMMB-503: Critical Elements of Genetics and Molecular and Cellular Biology**
Penn State University, Dept. of Biochemistry & Molecular Biology.
Co-Lecturer: Fall 2017 (16 students)
Fall 2016 (17 students)
Fall 2015 (9 students)
- **6.874: Computational Systems Biology**
Massachusetts Institute of Technology, CSAIL.
Co-Lecturer: Spring 2011 (13 students)
- **CT523: Object Oriented Design**
NUI, Galway, Department of Information Technology.
Lecturer: Spring 2003 (17 students)
- **CT470: Object-Oriented Programming**
NUI, Galway, Department of Information Technology.
Teaching Assistant: 2002 – 2004
- **C, C++, Java, and Network Programming laboratory classes**
NUI, Galway, Department of Information Technology.
Laboratory Class Assistant: 2000 – 2004

Workshops

- **Software carpentry & data analysis reproducibility bootcamp**
Penn State University, CBIOS training program.
Instructor: Summer 2019
Summer 2018
Summer 2017

Guest Lectures

- **BIOE-509: Mechanobiology** (Guest lecture on functional genomics)
Penn State University, Dept. of Biological Engineering.
Guest lectures: Fall 2019
- **DS-200: Introduction to Data Sciences** (Guest lecture on computational biology)
Penn State University, Data Science degree program.
Guest lectures: Fall 2018
- **BMMB-554: Foundations in Data Driven Life Sciences** (Guest lectures on ChIP-seq analysis)
Penn State University, Dept. of Biochemistry & Molecular Biology.
Guest lectures: Spring 2017, Spring 2016, Spring 2015, Spring 2014

- **MICRB-416: Microbial Biotechnology** (Guest lecture on bioinformatics)
Penn State University, Dept. of Biochemistry & Molecular Biology.
Guest lectures: Fall 2019, Fall 2017
- **MICRB-450: Microbial & Molecular Genetics** (Guest lecture on genomics)
Penn State University, Dept. of Biochemistry & Molecular Biology.
Guest lectures: Fall 2017
- **MCIBS-596: Orientation and Teaching Assistant Training** (Guest lectures on research methods)
Penn State University, IBIOS Bioinformatics & Genomics program.
Guest lectures: Fall 2017, Fall 2016, Fall 2015, Fall 2014, Fall 2013, Spring 2013
- **CSE-598C/BMMB-598F: Algorithms and Data Structures in Bioinformatics** (Guest lectures on Expectation Maximization)
Penn State University, Dept. of Computer Science & Engineering.
Guest lectures: Spring 2013
- **BMMB-597D: Analyzing High Throughput Sequencing Data** (Guest lecture on motif-finding)
Penn State University, Dept. of Biochemistry & Molecular Biology.
Guest lecture: Fall 2012
- **BIN219: Bioinformatics** (Guest lecture on gene prediction methodologies)
St. Vincent College, Bioinformatics Program.
Guest lecture: Fall 2006

Outreach

- **Science-U summer camp**
Penn State University, Eberly College of Science
Volunteer Instructor: Summer 2017
- **Research Experience for Teachers program**
Hosted research experiences: Summer 2020 (Janet Magargal, Upper Darby High School, PA)

RESEARCH MENTORING

Ph.D. thesis direction

<u>Student</u>	<u>Advisor</u>	<u>Location / Graduate Program</u>	<u>Dates</u>
Alexis Morrissey	Mahony	Penn State (Bioinformatics & Genomics)	2019 – .
Divyanshi Srivastava	Mahony	Penn State (Bioinformatics & Genomics)	2016 – .
Naomi Yamada	Mahony	Penn State (Bioinformatics & Genomics)	2015 – 2020
Lila Rieber	Mahony	Penn State (Bioinformatics & Genomics)	2015 – 2020
Akshay Kakumanu	Mahony	Penn State (Bioinformatics & Genomics)	2013 – 2017

Research personnel

<u>Individual</u>	<u>Advisor(s)</u>	<u>Position</u>	<u>Dates</u>
Daniela James	Mahony	Research Project Manager	2020 – .
Sonny Arora	Mahony	Computational Scientist	2018 – .
Kelly Cochran	Mahony	Research Technologist	2018 – 2019
Guray Kuzu	Mahony	Postdoctoral Research Associate	2017 – 2019
Belinda Giardine	Hardison & Mahony	Programmer / Analyst	2016 – .

Masters thesis direction

<u>Student</u>	<u>Advisor</u>	<u>Location / Degree</u>	<u>Dates</u>
Natalie Zesati	Mahony	Penn State (M.S. Bioinf. & Genomics)	2019 – .
Rachel Cooper	Mahony	Penn State (M.S. Bioinf. & Genomics)	2019 – .
Siddarth Wekhande	Mahony	Penn State (M.S. Bioinf. & Genomics)	2018 – 2019
Guanjue Xiang	Mahony	Penn State (M. Biotechnology)	2014

Undergraduate honors thesis direction

<u>Student</u>	<u>Advisor</u>	<u>Location / Degree</u>	<u>Dates</u>
----------------	----------------	--------------------------	--------------

BMMB program:

Victoria Bonnell, Andrew Renda, Melanie Yap, Mackenzie Shipley

*MCIBS program:*Xueyuan Jiang, Jacob Heldenbrand, Kai Hu (*chair*), Mengyang Fang, Haining Chen**Awards & honors for mentored individuals**

<u>Individual</u>	<u>Award</u>	<u>Dates</u>
Divyanshi Srivastava	Robert T. Simpson Graduate Student Award for Innovative Research	2020
Divyanshi Srivastava	Academic Computing Fellowship	2018 – 2021
Tim Kunz	Fred Wedler Award for Outstanding Undergraduate Dissertation in BMB	2017
Lila Rieber	NSF Graduate Research Fellowship	2016 – 2019

PROFESSIONAL ACTIVITIES**Grant proposal peer reviewer**NIH GCAT Study Section, *ad hoc reviewer* (2019)National Science Foundation, *Panelist* (2018)Israeli Science Foundation, *ad hoc reviewer* (2016)**Journal editorial board member**

Biochimica et Biophysica Acta - Gene Regulatory Mechanisms (2019 –)

Ad-hoc journal reviewer. 140+ articles

Cell (2018), eLife (2018), Nature Methods (2014-2017), Nature Genetics (2019-2020), Bioinformatics (2008-2020), Nucleic Acids Research (2012-2020), Genome Research (2020), Genome Biology (2015-2020), PLoS Computational Biology (2013-2020), Molecular Systems Biology (2016), BMC Bioinformatics (2008, 2012-2014), PLoS Genetics (2017), Cell Reports (2014, 2017), PLoS ONE (2012-2013, 2016-2017), Nature Communications (2016), Methods (2020), BMC Genomics (2008-2009), BMC Molecular Biology (2009), RECOMB (2011-2012), ECCB (2012-2013), BioData Mining (2015), BBA Gene Regulatory Mechanisms (2015-2019), G3 (2018), Scientific Reports (2018), Quantitative Biology (2015), IEEE Transactions on Neural Networks (2006, 2010, 2014), IEEE Transactions on Computational Biology and Bioinformatics (2006), Expert Systems (2006, 2011), Artificial Intelligence in Medicine (2007-2008), Neural Processing Letters (2006), International Journal of Computational Intelligence Research (2005), Biosystems (2004).

Conference organizing committee memberGreat Lakes Bioinformatics Conference (Minneapolis, MN), 2021 – *Publications Chair*

Intelligent Systems in Molecular Biology (virtual conference), 2020

- *Program Area Chair – Comparative & Functional Genomics*

- *RegSys Program Co-Chair*

Intelligent Systems in Molecular Biology (Basel, Switzerland), 2019 – *RegSys Poster Chair*ACM Conference on Bioinformatics and Computational Biology (Niagra, NY), 2019 – *Tutorials Chair*Great Lakes Bioinformatics Conference (Madison, WI), 2019 – *Sponsorship Chair*

38th Summer Symposium in Molecular Biology at The Pennsylvania State University, 2019

Workshop on Emerging Methods for Sequence Analysis (Penn State University), 2018

34th Summer Symposium in Molecular Biology at The Pennsylvania State University, 2015

Conference program committee member

RECOMB/ISCB Conference on Regulatory and Systems Genomics, 2020

Machine Learning in Computational Biology, 2019

RECOMB/ISCB Conference on Regulatory and Systems Genomics, 2019

ISMB/ECCB 2019 (RegSys CoSI)

RECOMB/ISCB Conference on Regulatory and Systems Genomics, 2018

ISMB 2018 (RegSys CoSI & Poster Awards committee)

RECOMB/ISCB Conference on Regulatory and Systems Genomics, 2017

ISMB/ECCB 2017 (Regulatory Genomics CoSI & Poster Awards committee)

ACM Conference on Bioinformatics, Computational Biology and Health Informatics, 2017

RECOMB/ISCB Conference on Regulatory and Systems Genomics, 2016

Great Lakes Bioinformatics / Canadian Computational Biology Conference, 2016
 ISMB 2016 (Gene Regulation subject area)
 ACM Conference on Bioinformatics, Computational Biology and Health Informatics, 2016
 RECOMB/ISCB Conference on Regulatory and Systems Genomics, 2015
 ISMB/ECCB 2015 (Gene Regulation & Transcriptomics subject area)
 ACM Conference on Bioinformatics, Computational Biology and Health Informatics, 2014
 ISMB 2014 (Gene Regulation & Transcriptomics subject area)
 ISMB/ECCB 2013 (Gene Regulation & Transcriptomics subject area)
 ISMB 2012 (Gene Regulation & Transcriptomics subject area)

Conference session chair

RECOMB/ISCB Conference on Regulatory and Systems Genomics, 2019
 ISMB/ECCB 2019 (RegSys CoSI)
 CSHL Systems Biology Meeting 2015 (Regulatory Elements session)
 ISMB RegGenSIG 2014
 HHMI Janelia conference on Biological Sequence Analysis and Probabilistic Models 2013

University & Departmental Committees

Huck Institutes Bioinformatics & Genomics graduate program, Program Committee (2020 –)
 Huck Institutes Bioinformatics & Genomics graduate program, Admissions Committee (2018 – 2020)
 Institute for CyberScience Coordinating Committee (2018 –)
 Eberly College of Science IT Committee (2018 –)
 Biochemistry & Molecular Biology Dept., Undergraduate Program Steering Committee (2018 –)
 Biochemistry & Molecular Biology Dept., Curricular Affairs and Assessment Committee (2018 – 2019)
 Biochemistry & Molecular Biology Dept., Honors & Awards (2018 – 2019)
 Biochemistry & Molecular Biology Dept., Distinguished Lecture Committee (2015 – 2018)
 Biochemistry & Molecular Biology Dept., Graduate Student Recruitment Committee (2016 – 2018)
 Biochemistry & Molecular Biology Dept., Undergraduate Affairs Committee (2017 – 2018)
 Biochemistry & Molecular Biology Dept., Climate & Diversity Committee (2013 – 2014, 2016 – 2018)
 Biochemistry & Molecular Biology Dept., Undergraduate Professional Development (2015 – 2016)
 Huck Institutes Bioinformatics & Genomics graduate program, Admissions Committee (2013 – 2016)

International Society for Computational Biology

Chair, Junior PI Community of Special Interest (2019 –)
 Committee Member, Junior PI Community of Special Interest (2018 – 2019)
 Member, inaugural ISCB Student Council (2004)
 Society Member (2002 –)

INVITED & CONTRIBUTED PRESENTATIONS

Invited presentations at universities, research institutes, & international meetings:

25. Invited speaker, **Indiana University, Center for Bioinformatics Research** (Bloomington, IN), *Using neural networks to characterize the predeterminants of induced transcription factor binding sites*. [forthcoming: 17 Sept. 2020 – virtual]
24. Invited speaker, **Cincinnati Children's Hospital Medical Center** (Cincinnati, OH), *Characterizing sequence and chromatin predeterminants of transcription factor binding*. [1 Jun. 2020 – virtual]
23. Invited speaker, **University of Southern California, Dept. of Biological Sciences** (Los Angeles, CA), *Characterizing the sequence and chromatin predeterminants of induced transcription factor binding with bimodal neural networks*. [23 Apr. 2020 – postponed due to COVID19]
22. Invited speaker, **Princess Margaret Cancer Center, University of Toronto** (Toronto, Canada), *Using neural networks to characterize the predeterminants of induced transcription factor binding sites*. [6 Feb. 2020]
21. Invited lecturer, **Cold Spring Harbor Laboratory Course: Computational Genomics**, *Genomics of gene regulation*. [8 – 9 Dec., 2019]
20. Invited speaker, **Summer Symposium in Molecular Biology at The Pennsylvania State University, 2019** (University Park, PA), *Characterizing sequence and chromatin predeterminants of transcription factor binding using deep neural networks*. [2 Aug., 2019]

19. Invited lecturer, **Cold Spring Harbor Laboratory Course: Foundations of Computational Genomics**, *Genomics of gene regulation*. [2 – 3 Dec., 2018]
18. Invited speaker, **National University of Ireland, Galway, Chromosome Biology Center**, *Understanding transcription factor binding dynamics during neuronal programming*. [8 Aug., 2018]
17. Invited speaker, **Penn State College of Medicine, Stem Cell Seminar Series**, *Programming Neurons*. [14 Jun., 2018]
16. Invited speaker, **University of Wisconsin, Madison, Genome Center**, *Understanding transcription factor binding dynamics during neuronal programming*. [8 Feb., 2018]
15. Invited lecturer, **Cold Spring Harbor Laboratory Course: Foundations of Computational Genomics**, *Genomics of gene regulation*. [3 Dec., 2017]
14. Invited workshop speaker, **University of Rochester, Epigenomics Workshop**, *Computational analysis of ChIP-seq data*. [12 Jun., 2015]
13. Invited speaker, **Oregon State University, Dept. of Biochemistry & Biophysics**, *Characterizing context-dependent transcription factor activity during cellular programming*. [6 May, 2015]
12. Invited speaker, **Statistical Methods for Post Genomic Data** (Munich, Germany), *Characterizing context-dependent transcription factor binding using an integrated model of multi-condition ChIP-seq data*. [12 Feb., 2015]
11. Invited speaker, **Intelligent Systems in Molecular Biology (ISMB) 2014, Regulatory Genomics SIG** (Boston, MA), *Characterizing context-dependent transcription factor activity*. [12 Jul., 2014]
10. Invited speaker, **Penn State University College of Medicine, Institute for Personalized Medicine**, *Characterizing context-dependent transcription factor activity during cellular programming*. [24 Apr., 2014]
9. Invited speaker, **National University of Ireland, Galway, Dept. of Mathematics, Statistics, & Applied Mathematics**, *Characterizing context-dependent transcription factor activity during direct motor neuron programming*. [17 Oct., 2013]
8. Invited speaker, **Albert Einstein College of Medicine, Dept. of Genetics**, *Combinatorial binding of transcription factors during direct motor neuron programming*. [20 Feb., 2013]
7. Invited keynote speaker, **Virtual Institute of Bioinformatics & Evolution (VIBE) 2012 symposium** (Dublin, Ireland), *Combinatorial binding of transcription factors during direct motor neuron programming*. [2 Nov., 2012]
6. Invited speaker, **Penn State University, Dept. of Biochemistry & Molecular Biology**, *Combinatorial binding of transcription factors during direct motor neuron programming*. [Apr., 2012]
5. Invited speaker, **Louisiana State University, Dept. of Biological Sciences**, *Combinatorial binding of transcription factors during direct motor neuron programming*. [Mar., 2012]
4. Invited speaker, **University at Buffalo, Center of Excellence in Bioinformatics & Life Sciences**, *Combinatorial binding of transcription factors during direct motor neuron programming*. [Feb., 2012]
3. Invited speaker, **Merrimack Pharmaceuticals**, *Transcriptional networks in motor neuron differentiation*. [Feb., 2009]
2. Invited speaker, **Whitehead Institute Forum**, *Chromatin changes and transcriptional regulation during motor neuron development*. [Apr., 2008]
1. Invited speaker, **University of British Columbia, Centre for Molecular Medicine & Therapeutics**, *Adventures with familial binding profiles*. [Jan., 2007]

Contributed presentations at international meetings (* denotes presenter):

23. *Hox binding specificity is directed by DNA sequence preferences and differential abilities to engage inaccessible chromatin*
D Srivastava*, M Bulajić, E Mazzoni, S Mahony
Intelligent Systems in Molecular Biology (ISMB) 2020 [15 Jul. 2020 – virtual]
22. *Hox binding specificity is directed by DNA sequence preferences and differential abilities to engage inaccessible chromatin*
S Mahony*

- Systems Biology: Global Regulation of Gene Expression, 2020** (Cold Spring Harbor, NY). [10 Mar. 2020 – virtual]
21. *Cross-species transcription factor binding prediction via domain-adaptive neural networks*
K Cochran*, D Srivastava, A Balsubramani, A Kundaje, S Mahony
Machine Learning in Computational Biology (MLCB) 2019 (Vancouver, Canada). [14 Dec. 2019, 8% of submitted abstracts were selected for presentation]
 20. *Characterizing the sequence and chromatin predeterminants of induced transcription factor binding with bimodal neural networks*
S Mahony*
RECOMB/ISCB Conference on Regulatory & Systems Genomics 2019 (New York, NY). [5 Nov. 2019]
 19. *Characterizing the organization of protein-DNA complexes in a comprehensive epigenome*
S Mahony*
Intelligent Systems in Molecular Biology (ISMB) / European Conference on Computational Biology (ECCB) 2019 (Basel, Switzerland). [23 Jul. 2019]
 18. *Direct prediction of regulatory elements from partial data without imputation*
Y Zhang, S Mahony*
Great Lakes Bioinformatics (GLBIO) 2019 (Madison, WI). [21 May, 2019]
 17. *Analysis of ChIP-exo read profiles reveals spatial organizations of protein complexes*
N Yamada*, N Farrell, BF Pugh, S Mahony
Great Lakes Bioinformatics (GLBIO) 2019 (Madison, WI). [21 May, 2019]
 16. *Topic modeling enables identification of regulatory complexes in a comprehensive epigenome*
G Kuzu*, N Rossi, N Yamada, P Kuntala, C Mittal, N Badjatia, G Kellogg, BF Pugh, S Mahony
Great Lakes Bioinformatics (GLBIO) 2019 (Madison, WI). [21 May, 2019]
 15. *Cross-species transcription factor binding prediction via domain adapted neural networks*
K Cochran*, D Srivastava, A Balsubramani, A Kundaje, S Mahony
Great Lakes Bioinformatics (GLBIO) 2019 (Madison, WI). [20 May, 2019]
 14. *Characterizing protein-DNA binding event subtypes in ChIP-exo data using read distribution shapes and DNA sequences*
N Yamada*, S Mahony
International Conference of the ERCIM WG on Computational and Methodological Statistics 2018 (Pisa, Italy). [15 Dec. 2018]
 13. *Deep neural networks for characterizing sequence and chromatin pre-determinants of transcription factor binding*
S Mahony*, D Srivastava, B Aydin, A Kakumanu, EO Mazzoni
Intelligent Systems in Molecular Biology (ISMB) 2018 (Chicago, IL) [10 Jul. 2018]
 12. *Identification of locus-specific changes in chromosome conformation between cell types reveals enrichment of enhancers*
L Rieber*, S Mahony
Intelligent Systems in Molecular Biology (ISMB) 2018 (Chicago, IL). [7 Jul. 2018]
 11. *Characterizing protein-DNA binding event subtypes in ChIP-exo data*
N Yamada*, WKM Lai, N Farrell, BF Pugh, S Mahony
Research in Computational Molecular Biology (RECOMB), 2018 (Paris, France). [22 Apr. 2018, 19% of submitted abstracts were selected for presentation]
 10. *Characterizing sequence and chromatin pre-determinants of transcription factor binding using deep neural networks*
D Srivastava*, B Aydin, EO Mazzoni, S Mahony
CSHL Systems Biology: Global Regulation of Gene Expression, 2018 (Cold Spring Harbor, NY). [21 Mar. 2018]
 9. *miniMDS: 3D structural inference from high-resolution Hi-C data*
L Rieber*, S Mahony
Intelligent Systems for Molecular Biology (ISMB), 2017 (Prague, Czech Republic). [23 Jul. 2017, 16% of submitted abstracts were selected for presentation]
 8. *Deconvolving sequence features associated with transcription factor binding dynamics during direct motor neuron programming*

- A Kakumanu, S Velasco, EO Mazzone, S Mahony*
Intelligent Systems for Molecular Biology (ISMB), 2017 (Prague, Czech Republic). [22 Jul. 2017]
7. *Visualizing and understanding chromatin organization using the Self-Organizing Map*
 T Kunz*, S Mahony
Great Lakes Bioinformatics Conference (GLBIO), 2017 (Chicago, IL). [17 May 2017]
 6. *Cooperative transcription factor binding dynamics underlie direct motor neuron programming*
S Mahony*, EO Mazzone
CSHL Systems Biology: Global Regulation of Gene Expression, 2016 (Cold Spring Harbor, NY).
 [16 Mar. 2016]
 5. *Characterizing context-dependent transcription factor activity during cellular programming*
S Mahony*, EO Mazzone
Summer Symposium in Molecular Biology at The Pennsylvania State University, 2015 (University
 Park, PA). [22 Jul. 2015]
 4. *An integrated model of multiple-condition ChIP-seq data reveals predeterminants of Cdx2 binding*
S Mahony*, MD Edwards, EO Mazzone, RI Sherwood, A Kakumanu, CA Morrison, H Wichterle, DK
 Gifford
Research in Computational Molecular Biology (RECOMB), 2014 (Pittsburgh, PA). [2 Apr. 2014, 23%
 of submitted abstracts were selected for presentation]
 3. *Inferring protein-DNA dependencies using motif alignments and mutual information*
S Mahony*, PE Auron, PV Benos
Intelligent Systems for Molecular Biology (ISMB), 2007 (Vienna, Austria). [21 Jul. 2007, 15% of
 submitted abstracts were selected for presentation]
 2. *Integrating self-organizing neural networks in the search for DNA binding motifs*
S Mahony*, TJ Smith, A Golden
Workshop on Self-Organizing Maps, 2005 (Paris, France). [5 Sept. 2005]
 1. *Improved detection of DNA motifs using a self-organized clustering of familial binding profiles*
S Mahony*, A Golden, TJ Smith, PV Benos
Intelligent Systems for Molecular Biology (ISMB), 2005 (Detroit, MI). [25 Jun. 2005, 13% of submitted
 abstracts were selected for presentation]

AWARDS AND HONORS

- 2006 **Best Ph.D. Thesis Award**, *Irish Society for Scientific & Engineering Computation*
 Irish nomination to the ECCOMAS prize for best Ph.D. thesis.
- 2005 **Honorable Mention for a Student Paper**, *ISMB 2005*.
- 2004 **Computer Science Research Achievement Award** (1st place), *Embark / Engineers Ireland*
- 2003 **Education Abroad Program Reciprocity Award**, *University of California*
- 2002–2005 **Embark Ph.D. Scholarship**, *Irish Research Council for Science, Engineering & Technology*
- 2002 **Nortel Networks prize for undergraduate research** (2nd place), *NUI, Galway*