Shaun Mahony

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EDUCATION

2002 – 2006 **Ph.D., Information Technology (Computational Biology),** *University of Galway*
Thesis: "Self-organizing neural networks for biological sequence analysis"

1998 – 2002 **B.E., Electronic & Computer Engineering,** *University of Galway*
First class honors.

RESEARCH EXPERIENCE

2021 – **Associate Professor of Biochemistry & Molecular Biology,** *The Pennsylvania State University*
2024 – **Eberly Distinguished Senior Scholar in Genomics**
2016 – 2021 **Assistant Professor (tenure track)**
2012 – 2016 **Assistant Professor (fixed term)**
Center for Eukaryotic Gene Regulation
Center for Computational Biology and Bioinformatics
Department of Biochemistry & Molecular Biology, Eberly College of Science
College of Information Sciences and Technology (Affiliate Associate Professor)

2011 – 2012 **Visiting Scientist,** *Harvard University*
Department of Stem Cell and Regenerative Biology

2010 – 2012 **Research Scientist,** *Massachusetts Institute of Technology*
2007 – 2010 **Postdoctoral Research Associate**
Computer Science and Artificial Intelligence Laboratory

2005 – 2007 **Postdoctoral Research Associate,** *University of Pittsburgh*
Fall 2004 **Visiting Researcher**
Department of Computational & Systems Biology

Fall 2003 **Visiting Researcher,** *University of California, Berkeley*
Department of Molecular Cell Biology and Joint Genome Institute

2002 – 2005 **Research Assistant,** *University of Galway*
National Centre for Biomedical Engineering Science

LEADERSHIP POSITIONS

2024 – **Associate Department Head for Research and Strategic Initiatives**
Department of Biochemistry & Molecular Biology, Eberly College of Science, Penn State University

2024 – 2025 **Chair, Next STEPS Committee on Best Practices in Faculty Hiring and Retention**
Eberly College of Science, Penn State University

2022 – **PLOS Computational Biology**
Section Editor (2025 –)
Academic Editor (2022 – 2025)

2023 – **Great Lakes Bioinformatics (GLBIO) Conference Organization**
GLBIO Steering Committee Co-Chair (2025 –)
Conference Chair, GLBIO, Pittsburgh, PA (2024)
Conference Co-Chair, GLBIO, Montreal, Canada (2023)

2020 – 2024 **Intelligent Systems in Molecular Biology (ISMB) Conference Organization**
Co-Chair, Regulatory and Systems Genomics (RegSys) Program Area (2020 – 2024)
Program Area Chair – Regulatory & Functional Genomics (2020 – 2021)

2019 – 2021 **Chair, Junior Principal Investigator Community of Special Interest**
International Society for Computational Biology

PUBLICATIONS

63. *Chromatin state dynamics during the Plasmodium falciparum intraerythrocytic development cycle*
AS Brown, M Llinás, S Mahony
BMC Genomics (2026) *in press*

62. *Optimized ChIP-exo for mammalian cells and patterned sequencing flow cells*
DQ James, S Mukherjee, CC Cannon, S Mahony
G3 Genes|Genomes|Genetics (2025) 16(1):jkaf270

61. *Perspective on recent developments and challenges in regulatory and systems genomics*
J Zeitlinger, S Roy, F Ay, A Mathelier, A Medina-Rivera, S Mahony, S Sinha, J Ernst
Bioinformatics Advances (2025) 5(1):vbaf106 [review article]

60. *Intragenomic conflict underlies extreme phenotypic plasticity in queen-worker caste determination in honey bees (Apis mellifera)*
ST Bresnahan, S Mahony, K Anton, B Harpur, CM Grozinger
Genome Biology (2025) 26(1):171

59. *Sized-based expectation maximization for characterizing nucleosome positions and subtypes*
J Yang, K Yen, S Mahony
Genome Research (2024) 34(9):1334-1343

58. *Systematic dissection of sequence features affecting the binding specificity of a pioneer factor reveals binding synergy between FOXA1 and AP-1*
C Xu, H Kleinschmidt, J Yang, E Leith, J Johnson, S Tan, S Mahony, L Bai
Molecular Cell (2024) 84(15):2838-2855.e10

57. *Accurate allocation of multi-mapped reads enables regulatory element analysis at repeats*
A Morrissey, J Shi, DQ James, S Mahony
Genome Research (2024) 34(6):937-951

56. *DNA sequence context and the chromatin landscape differentiate sequence-specific transcription factor binding in the human malaria parasite, Plasmodium falciparum*
V Bonnell, Y Zhang, A Brown, J Horton, G Josling, T-P Chiu, R Rohs, S Mahony, R Gordân, M Llinás
Nucleic Acids Research (2024) 52(17):10161-10179

55. *Cross-species regulatory landscapes and elements revealed by novel joint systematic integration of human and mouse blood cell epigenomes*
G Xiang, X He, BM Giardine, KJ Weaver, DJ Taylor, RC McCoy, C Jansen, CA Keller, AQ Wixom, A Cockburn, A Miller, Q Qi, Y He, Y Li, J Lichtenberg, EF Heuston, SM Anderson, J Luan, MW Vermunt, F Yue, MEG Sauria, MC Schatz, J Taylor, B Göttgens, JR Hughes, DR Higgs, MJ Weiss, Y Cheng, GA Blobel, D Bodine, Y Zhang, Q Li, S Mahony, RC Hardison
Genome Research (2024) 34(7):1089-1105

54. *The ENCODE Imputation Challenge: A critical assessment of methods for cross-cell type imputation of epigenomic profiles*
JM Schreiber, CA Boix, …, S Mahony (23rd of 41 authors), Z Zhang, …, MP Snyder, M Kellis, WS Noble, AB Kundaje
Genome Biology (2023) 24(1):79

53. *Synthetic genomic reconstitution reveals principles of mammalian Hox cluster regulation*
S Pinglay, M Bulajić, DP Rahe, E Huang, R Brosh, S German, JA Cadley, L Rieber, N Easo, S Mahony, MT Maurano, LJ Holt, EO Mazzoni, JD Boeke
Science (2022) 377(6601):eabk2820

52. *PEGR: a flexible management platform for reproducible epigenomic and genomic research*
D Shao, GD Kellogg, A Nematbakhsh, P Kuntala, S Mahony, BF Pugh, WKM Lai
Genome Biology (2022) 23(1):99

51. *Domain adaptive neural networks improve cross-species prediction of transcription factor binding*
K Cochran, D Srivastava, A Shrikumar, A Balsubramani, RC Hardison, A Kundaje, S Mahony
Genome Research (2022) 32:512-523

50. *Foxa2 and Pet1 direct and indirect synergy drive serotonergic neuronal differentiation*
B Aydin, M Sierk, M Moreno-Estelles, L Tejavibulya, N Kumar, N Flames*, S Mahony*, E Mazzoni*
Frontiers in Neuroscience (2022) 16:903881 (* corresponding authors)

49. *The BTB transcription factors ZBTB11 and ZFP131 maintain pluripotency by repressing pro-differentiation genes*
G Garipler, C Lu, A Morrissey, LS Lopez-Zepeda, SE Vidal, B Aydin, M Stadtfeld, U Ohler, S Mahony, NE Sanjana, EO Mazzoni
Cell Reports (2022) 38(11):110524

48. *High resolution protein architecture of the budding yeast 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
Nature (2021) 592(7853):309-314

47. *S3V2-IDEAS: a package for normalizing, denoising and integrating epigenomic datasets across different cell types*
G Xiang, BM Giardine, S Mahony, Y Zhang, RC Hardison
Bioinformatics (2021) 37(18):3011-3013

46. *An interpretable bimodal neural network characterizes the sequence and preexisting chromatin predictors of induced transcription factor binding*
D Srivastava, B Aydin, EO Mazzoni, S Mahony
Genome Biology (2021) 22(1):20

45. *The PfAP2-G2 transcription factor is a critical regulator of gametocyte maturation*
S Singh, JM Santos, LM Orchard, N Yamada, R van Biljon, HJ Painter, S Mahony, M Llinas
Molecular Microbiology (2021) 115(5):1005-1024

44. *Assessing relationships between chromatin interactions and regulatory genomic activities using the self-organizing map*
T Kunz, L Rieber, S Mahony
Methods (2021) 189:12-21

43. *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
Development (2020) 147(22):dev194761 (* equal contribution)

42. *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) 48(20):11215-11226 [*NAR Breakthrough Article*]

41. *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

40. *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

39. *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]

38. *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]

37. *Direct prediction of regulatory elements from partial data without imputation*
Y Zhang & S Mahony
PLoS Computational Biology (2019) 15(11):e1007399

36. *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

35. *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)*

34. *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 [ISCB RegSys "top 10 reading papers of 2019"]

33. *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

32. *Deconvolving sequence features that discriminate between overlapping regulatory annotations*
A Kakumanu, S Velasco, EO Mazzoni, S Mahony
PLoS Computational Biology (2017) 13(10):e1005795

31. *miniMDS: 3D structural inference from high-resolution Hi-C data*
L Rieber, S Mahony
Bioinformatics (2017) 33 (14): i261-i266

30. *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)*

29. *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

28. *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

27. *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

26. *Protein-DNA binding in high resolution*
    S Mahony, BF Pugh
    Critical Reviews in Biochemistry and Molecular Biology (2015) 50(4):269-283 [review article]

25. *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

24. *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)*

23. *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

22. *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)*

21. *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)*

20. *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

19. *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)*

18. *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

17. *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

16. *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)*

15. *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)*

14. *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

13. *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

12. *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

11. *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

10. *Inferring protein-DNA dependencies using motif alignments and mutual information*
S Mahony, PE Auron, PV Benos
Bioinformatics (2007) 23(13): i297-i304

9. *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

8. *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

7. *STAMP: a web tool for exploring DNA-binding motif similarities*
S Mahony, PV Benos
Nucleic Acids Research (2007) 35:W253-W258

6. *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

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 McInerney, TJ Smith, A Golden
   BMC Bioinformatics (2004) 5:23

Conference Proceedings (full manuscripts, peer reviewed)

3. *PEGR: a management platform for ChIP-based next generation sequencing pipelines*
   D Shao, G Kellogg, S Mahony, W Lai, BF Pugh
   Practice and Experience in Advanced Research Computing (2020) 285-292

2. *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

1. *Gene prediction in metagenomic libraries using the self-organising map and high performance computing techniques*
   N McCoy, S Mahony, A Golden
   Distributed, High-Performance and Grid Computing in Computational Biology (GCCB 2007). Lecture Notes in Computer Science (2007) 4360: 99-109

Preprints & Submitted Manuscripts

4. *Widespread regulatory turnover across human segmental duplications*
   A Morrissey, AS Brown, J Yang, S Mahony
   bioRxiv https://doi.org/10.64898/2026.01.21.700947

3. *TPCAV: Interpreting deep learning genomics models via concept attribution*
   J Yang, S Mahony
   bioRxiv https://doi.org/10.64898/2026.01.20.700723

2. *Human CCR4-NOT suppresses pervasive transcription and retrotransposable elements*
   S Kulkarni, A Morrissey, A Sebastian, OT Akinniyi, CA Keller, I Albert, S Mahony, JC Reese
   bioRxiv https://doi.org/10.64898/2026.01.16.699749

1. *Joint sequence & chromatin neural networks characterize the differential abilities of Forkhead transcription factors to engage inaccessible chromatin*
   S Arora*, J Yang*, T Akiyama, DQ James, A Morrissey, TR Blanda, N Badjatia, WKM Lai, MSH Ko, BF Pugh, S Mahony
   bioRxiv https://doi.org/10.1101/2023.10.06.561228

RESEARCH FUNDING

Active Funding

Grant	Title	Grant Period	Funding	
			Direct	Total
NIH NIGMS MIRA (R35-GM144135) PI: S Mahony	Understanding the predeterminants of transcription factor regulatory activity	01/2022 – 12/2026	$1,500,000	$2,304,983
	(Equipment supplement)	07/2023	$113,683	$113,683
NSF DBI CAREER (2045500) PI: S Mahony	CAREER: Predicting transcription factor binding dynamics across cell types and species	06/2021 – 05/2026	$541,700	$839,567
NSF NCEMS Working Group Co-Lead: S Mahony Co-Lead: M Konkel	Transposable Elements and the Emergence of Genomic Innovation	04/2025 – 04/2027	In-kind support, including computational scientist effort and computational resource allocations.	

Completed Funding

Grant	Title	Grant Period	Funding	
			Direct	Total
Huck Innovative and Transformational Seed Fund PI: S Mahony Co-I: X Lian	Designing 3′ UTRs to convert pancreatic exocrine cells into insulin-producing beta cells	07/2022 – 06/2023	$56,173	$56,173
NIH NIGMS R01 (R01-GM125722)	Genome-wide structural organization of proteins within human gene regulatory complexes	01/2018 – 12/2022	$840,000	$1,280,459

PI: S Mahony PI: BF Pugh				
	(Equipment supplement)	09/2018	$61,750	$61,750
	(Open software tool development supplement)	09/2020	$147,509	$233,064
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	$450,000	$685,035
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 (R01-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 courses I developed)

- **BMB-400: Molecular Biology of the Gene**
  Penn State University, Dept. of Biochemistry & Molecular Biology.
  Lecturer: Spring 2024 (76 students); Fall 2025 (111 students)
- *__BMB-482: Computational Biology__
  Penn State University, Dept. of Biochemistry & Molecular Biology.
  Lecturer: Fall 2013 (24 students); Fall 2014 (21 students); Fall 2015 (10 student); Fall 2017 (22 students); Fall 2018 (19 students); Fall 2019 (22 students); Fall 2020 (16 students); Spring 2024 (16 students); Spring 2025 (8 students)
- **BMMB-554: Foundations in Data-Driven Life Sciences**
  Penn State University, Dept. of Biochemistry & Molecular Biology.
  Lecturer: Spring 2022 (23 students)

- **BGEN-541: Critical Analysis of Literature in Bioinformatics and Genomics**
  Penn State University, Dept. of Biochemistry & Molecular Biology.
  Lecturer: Fall 2018 (12 students); Fall 2019 (21 students); Fall 2020 (13 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 2015 (9 students); Fall 2016 (17 students); Fall 2017 (16 students)
- **6.874: Computational Systems Biology**
  Massachusetts Institute of Technology, CSAIL.
  Co-Lecturer: Spring 2011 (13 students)
- **CT523: Object Oriented Design**
  University of Galway, Department of Information Technology.
  Lecturer: Spring 2003 (17 students)
- **CT470: Object-Oriented Programming**
  University of Galway, Department of Information Technology.
  Teaching Assistant: 2002 – 2004
- **C, C++, Java, and Network Programming laboratory classes**
  University of 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

- **BMMB-541: Molecular Biology of Animal Development,** *Guest lectures:* Spring 2021
- **BIOE-509: Mechanobiology,** *Guest lecture:* Fall 2019
- **DS-200: Introduction to Data Sciences,** *Guest lecture:* Fall 2018
- **BMMB-554: Foundations in Data Driven Life Sciences,** *Guest lectures:* Spring 2014, Spring 2015, Spring 2016, Spring 2017
- **MICRB-416: Microbial Biotechnology,** *Guest lectures:* Fall 2017, Fall 2019
- **MICRB-450: Microbial & Molecular Genetics,** *Guest lecture:* Fall 2017
- **MCIBS-596: Orientation and Teaching Assistant Training,** *Guest lectures:* Spring 2013, Fall 2013, Fall 2014, Fall 2015, Fall 2016, Fall 2017
- **CSE-598C/BMMB-598F: Algorithms and Data Structures in Bioinformatics,** *Guest lecture:* Spring 2013
- **BMMB-597D: Analyzing High Throughput Sequencing Data,** *Guest lecture:* Fall 2012
- **BIN219: Bioinformatics,** St. Vincent College, *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 teachers: Janet Magargal, Upper Darby High School, PA (Summer 2020); Rebecca Torres, Milton Hershey School, Hershey, PA (Summer 2023); Jason Gvazdauskas, Scranton City School District, PA (Summer 2023)

RESEARCH MENTORING

Ph.D. thesis direction

Student	Advisor	Location / Graduate Program	Dates
Ishika Verma	Mahony	Penn State (Bioinformatics & Genomics)	2025 – .
Salaar Khan	Mahony	Penn State (Bioinformatics & Genomics)	2023 – .
Sohini Mukherjee	Mahony	Penn State (BMMB)	2023 – .
Jianyu Yang	Mahony	Penn State (Bioinformatics & Genomics)	2021 – .
Alan Brown	Mahony	Penn State (Bioinformatics & Genomics)	2021 – .
Alexis Morrissey	Mahony	Penn State (Bioinformatics & Genomics)	2019 – 2025
Divyanshi Srivastava	Mahony	Penn State (Bioinformatics & Genomics)	2016 – 2021
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

Individual	Advisor(s)	Position	Dates
Daniela James	Mahony	Assistant Research Professor	2020 – .
Siddharth Ghule	Mahony	Postdoctoral Research Associate	2023 – 2024
Sonny Arora	Mahony	Computational Scientist	2019 – 2022
Kelly Cochran	Mahony	Research Technologist	2018 – 2019
Guray Kuzu	Mahony	Postdoctoral Research Associate	2017 – 2019
Belinda Giardine	Hardison & Mahony	Programmer / Analyst	2016 – 2021

Master's thesis direction

Student	Advisor	Location / Degree	Dates
Vandana Agarwala	Mahony	Penn State (M.S. Bioinf. & Genomics)	2019 – 2022
Rachel Cooper	Mahony	Penn State (M.S. Bioinf. & Genomics)	2019 – 2021
Natalie Zesati	Mahony	Penn State (M.S. Bioinf. & Genomics)	2019 – 2020
Siddarth Wekhande	Mahony	Penn State (M.S. Bioinf. & Genomics)	2018 – 2019
Guanjue Xiang	Mahony	Penn State (M. Biotechnology)	2014

Undergraduate honors thesis direction

Student	Advisor	Location / Degree	Dates
Jeffrey Shi	Mahony	Penn State (BMB B.Sc.)	2021 – 2024
Radha Patel	Mahony	Penn State (Statistics B.Sc.)	2020 – 2023
Anna Leon	Mahony	Penn State (Data Sciences & Math B.Sc.)	2020 – 2022
Tim Kunz	Mahony	Penn State (BMB B.Sc.)	2014 – 2017

Undergraduate research supervision

Katie Barfield (SROP, 2025), Nicholas Oses (SROP, 2025), Krisha Patel (WISER program, 2025 –), Caiden Cannon (2024 –), Bea Ricafort (WISER program, 2024 – 2025), Aislynn Cross (2024), Totton Hollenbeak (2024), Ash Booth (2023 – 2024), Ann Zezyus (WISER program, 2023 – 2024), Jeffrey Shi (2021 – 2024), Emily Barrett (WISER program, 2022), Kevin Mouck (2022), Devyn Hauser (2021), Anna Leon (MURE program, 2020 – 2022), Radha Patel (2020 – 2023), Vandana Agarwala (2019 – 2022), Zheng Zhang (2019), Aishan Liu (2018 – 2019), Connor Heaton (2018 – 2019), Steven Spak (2018 – 2019), Rachel Cooper (WISER program, 2017 – 2019), Yuanyuan Xu (2018), Jessica Lee (WISER program, 2018), Saimun Shahee (2017 – 2018), Shunran Zhang (2017 – 2018), Kara Dally (WISER program, 2016 – 2018), Will Yoshida (2016), Kyle McIlroy (2016), Ryan Feng (2016), Tim Kunz (2014 – 2017), Christopher Roth (2013 – 2015), Nathan Oakes (2013 – 2014).

Ph.D. thesis committees

Student	Advisor(s)	Location / Graduate Program	Dates
S. Rezwan Hosseini	Chikini	University of Pittsburgh (Comp. Biology)	2026 – .
Soheil Behravesh	Shriver	Penn State (Anthropology)	– .
Hanh Tran	Davenport	Penn State (Biology)	2025 – .
Jeong Han	Kim	Penn State (Animal Science)	2025 – .
Niral Shah	Bai	Penn State (BMMB)	2025 – .
Ji Woo Kim	Paulson	Penn State (MCIBS)	2025 – .
Mariam Lawal	Reese	Penn State (BMMB)	2024 – .
Saswat Mohanty	Makova	Penn State (MCIBS)	2024 – .
Mitchell Godin	Bai	Penn State (BMMB)	2024 – .
Courtney Smith	Bai	Penn State (BMMB)	2024 – .
Zahin Tasfia	Shao	Penn State (CSE)	2023 – .
Neha Patwardhan	Bai	Penn State (BMMB)	2023 – .
Gerardo Mirizio	Iwafuchi	Cincinnati Children's HMC	2023 – .
Shane Stoeber	Bai	Penn State (BMMB)	2022 – .
Xi He	Li	Penn State (Bioinformatics & Genomics)	2022 – .
April Rich	Carvunis	University of Pittsburgh (Comp. Biology)	2022 – .
Priscilla Villalona	Okafor	Penn State (BMMB)	2022 – .
Holly Godin	Bai	Penn State (BMMB)	2021 – .
Qian Shi	Shao	Penn State (CSE)	2023 – 2025
Jordan Krebs	Pugh	Penn State (MCIBS)	2019 – 2024
Sophia Dewing	Showalter	Penn State (BMMB)	2021 – 2024
Alessandro Howells	Lian	Penn State (Bioengineering)	2021 – 2024
Sean Bresnahan	Grozinger	Penn State (MCIBS)	2021 – 2024
Victoria Sharp	Medina	Penn State (Biology)	2020 – 2024
Yi Li	Bai	Penn State (BMMB)	2020 – 2024
Catherine Douds	Bevilacqua	Penn State (BMMB)	2019 – 2024
Cheng Xu	Bai	Penn State (BMMB)	2017 – 2024
Zhihan Liu	Huang/Girirajan	Penn State (MCIBS)	2023 – 2023
Aswathy Sebastian	Albert	Penn State (Bioinformatics & Genomics)	2018 – 2023
Dynisty Wright	Schaeffer	Penn State (Biology)	2020 – 2023
Kathryn Weaver	Taylor & McCoy	Johns Hopkins University (Biology)	2020 – 2023
Victoria Bonnell	Llinas	Penn State (BMMB)	2019 – 2023
Hengye Chen	Bai	Penn State (BMMB)	2018 – 2022
Ericka Surrett	Miyashiro	Penn State (BMMB)	2016 – 2022

Molly Rathbun	Szpara	Penn State (BMMB)	2018 – 2022
Adam Rork	Renner	Penn State (Entomology)	2019 – 2021
Jordan Hughey	Liu	Penn State (Bioinformatics & Genomics)	2019 – 2021
Fan Song	Yue	Penn State (Bioinformatics & Genomics)	2018 – 2021
Guanjue Xiang	Hardison	Penn State (Bioinformatics & Genomics)	2020 – 2020
Brendan Puls	Chen	Penn State (Neuroscience)	2017 – 2020
Derek Nye	Rolls	Penn State (MCIBS)	2016 – 2020
Suprita Singh	Llinas	Penn State (BMMB)	2018 – 2019
Tarik Salameh	Yue	Penn State (Bioinformatics & Genomics)	2017 – 2019
Xueyuan Jiang	Assis	Penn State (MCIBS)	2017 – 2019
Ningxin Ma	Chen	Penn State (Neuroscience)	2017 – 2019
Frank Shen	Li & Altman	Penn State (Statistics)	2015 – 2018
Tao Yang	Li & Yue	Penn State (Bioinformatics & Genomics)	2017 – 2018
Chao Yan	Bai	Penn State (BMMB)	2014 – 2018
Doug Baumann	Gilmour	Penn State (BMMB)	2017 – 2018
Anna Okula Basile	Ritchie	Penn State (BMMB)	2015 – 2018
Shefali Setia-Verma	Ritchie	Penn State (Bioinformatics & Genomics)	2014 – 2017
Mahmoud Ibrahim	Mazzoni & Ohler	NYU / Max Delbruck Center, Berlin	2013 – 2017
Ruowang Li	Ritchie	Penn State (Bioinformatics & Genomics)	2014 – 2016
Rohit Reja	Pugh	Penn State (Bioinformatics & Genomics)	2013 – 2016
Qingyu Wang	Altman & Girirajan	Penn State (Bioinformatics & Genomics)	2014 – 2015

Ph.D./Master's thesis external evaluations

Student	Advisor	Location	Dates
Hesam Hafezalseheh (M.Sc.)	Cremona	Université Laval, Canada	2024
Aseel Awdeh (Ph.D.)	Perkins	University of Ottowa, Canada	2022
Gherman Novakovskiy (Ph.D.)	Wasserman	University of British Columbia, Canada	2022
Tomasz Szczesnik (Ph.D.)	Ho	University of New South Wales, Australia	2018
Marzia Cremona (Ph.D.)	Secchi	Politecnico di Milano, Italy	2015
John Healy (Ph.D.)	Chambers	University of Galway, Ireland	2013
Nung Kion Lee (Ph.D.)	Wang	La Trobe University, Australia	2011

Ph.D. candidacy examination committees

Bioinformatics & Genomics program: Ewura-Esi Manful, Lujia Song, Akshatha Nayak, Fan Zhang, Ioannis Mouratidis, Deepro Banerjee, Natashia Benjamin, Aswathy Sebastian, Xi He, Fan Song, Ayaan Hossain, Matthew Jensen, Xinyuan Zhang, Israel Rivera Colon, Tao Yang, Wilfried Guiblet, Yong Jung, Akshay Kakumanu, Samarth Rangavittal

BMMB program: Sophia Dewing, Victoria Bonnell, Andrew Renda, Melanie Yap, Mackenzie Shipley

MCIBS program: Sean Bresnahan, Xueyuan Jiang, Jacob Heldenbrand, Kai Hu, Mengyang Fang, Haining Chen

Awards & honors for mentored individuals

Individual	Award	Dates
Jianyu Yang	ICDS Rising Researcher Fellowship	2025
Alan Brown	Glaxosmithkline Graduate Fellowship	2024 – 2025
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* (2025)
NIH MIRA ZRG1 MGG-F SEP, *ad hoc reviewer* (2025)
NIH MRAF Study Section, *ad hoc reviewer* (2025)
National Science Foundation, BIO Directorate, *Panelist* (2024)
NIH Transformative Research Award SEP, *mail reviewer* (2024)
NIH RM1 ZRG1 MBBC-G SEP, *mail reviewer* (2023)
NIH K99/R00 MOSAIC Study Section, *ad hoc reviewer* (2023)
NIH K99/R00 MOSAIC Study Section, *ad hoc reviewer* (2022)
European Research Council, *ad hoc reviewer* (2022)
NIH MG Study Section, *ad hoc reviewer* (2022)
National Science Foundation, BIO Directorate, *ad hoc reviewer* (2021)
NIH MRAA Study Section, *ad hoc reviewer* (2021)
NIH GCAT Study Section, *ad hoc reviewer* (2019)
National Science Foundation, *Panelist* (2018)
Israeli Science Foundation, *ad hoc reviewer* (2016)

Journal editorial duties

PLoS Computational Biology, *Academic Editor* (2022 – 2025), *Section Editor* (2025 –)
Biochimica et Biophysica Acta - Gene Regulatory Mechanisms, *Editorial Board Member* (2019 –)

Ad-hoc manuscript peer reviewer *[210+ manuscripts, 2 textbooks]*

Bioinformatics (2008-2025), Nucleic Acids Research (2012-2025), Nature (2023, 2025), Cell (2018), Nature Genetics (2019-2021, 2024), Nature Machine Intelligence (2021), Nature Methods (2014-2017, 2025), Nature Biotechnology (2024), Nature Reviews Genetics (2022), Cell Systems (2024), Genome Research (2020-2024), Genome Biology (2015-2025), eLife (2018), PLoS Computational Biology (2013-2021), Molecular Systems Biology (2016), Gene (2021), BMC Bioinformatics (2008, 2012-2014), PLoS Genetics (2017), Cell Genomics (2023), Cell Reports (2014, 2017), PLoS ONE (2012-2013, 2016-2017), Nature Communications (2016), Nucleic Acids Research Genomics & Bioinformatics (2023), Methods (2020), BMC Genomics (2008-2009), BMC Molecular Biology (2009), RECOMB (2011-2012), ECCB (2012-2013), Biostatistics (2021), BioData Mining (2015), BBA Gene Regulatory Mechanisms (2015-2022), G3 (2018, 2022), Scientific Reports (2018), Quantitative Biology (2015), IEEE Transactions on Neural Networks (2006, 2010, 2014), IEEE Transactions on Computational Biology and Bioinformatics (2006, 2021), 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 member

Intelligent Systems in Molecular Biology (Montreal, Canada), 2024 – *RegSys Program Chair*
Great Lakes Bioinformatics Conference (Pittsburgh, PA), 2024 – *Conference Chair*
Intelligent Systems in Molecular Biology (Lyon, France), 2023 – *RegSys Program Chair*
Great Lakes Bioinformatics Conference (Montreal, Canada), 2023 – *Conference Co-Chair*
38th Summer Symposium in Molecular Biology at The Pennsylvania State University, 2023 – *Organizer*
Intelligent Systems in Molecular Biology (Madison, WI), 2022 – *RegSys Program Co-Chair*

Intelligent Systems in Molecular Biology (virtual conference), 2021
- *Program Area Chair – Regulatory & Functional Genomics*
- *RegSys Program Co-Chair*

Great Lakes Bioinformatics Conference (virtual conference), 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 – *Organizer*
Workshop on Emerging Methods for Sequence Analysis (Penn State University), 2018 – *Organizer*
34th Summer Symposium in Molecular Biology at The Pennsylvania State University, 2015 – *Organizer*

Conference program committee member

ISMB/ECCB 2025
RECOMB/ISCB Conference on Regulatory and Systems Genomics, 2024
ISMB 2024
ISMB/ECCB 2023
RECOMB/ISCB Conference on Regulatory and Systems Genomics, 2022
ISMB 2022
Machine Learning in Computational Biology, 2020
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

Great Lakes Bioinformatics Conference, 2021
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

Eberly College of Science Next STEPS Committee (2021 – 2025; Committee Chair 2024 – 2025)
BMB Dept., Associate Head for Research and Strategic Initiatives (2024 –)
BMB Dept., Standing Faculty Advisory Committee (Committee Chair 2025 –)
BMB Dept., Graduate Student Recruitment Committee (2016 – 2018, 2023 –)
Bioinformatics & Genomics Graduate Admissions Committee (2013 – 2016, 2018 – 2022, 2024 –)
BMB Dept., Promotion & Tenure Committee (2024 –)
BMB Dept., Faculty Search Committees (2019 – 2024)
BMB Dept., Undergraduate Program Events & Scholarship (2022 – 2024)
BMB Dept., Undergraduate Program Steering Committee (2018 – 2021)
BMB Dept., Graduate Program Steering Committee (2021 – 2022)
Eberly College of Science IT Committee (2018 – 2020)
Institute for CyberScience Coordinating Committee (2018 – 2020)
BMB Dept., Honors & Awards Committee (2018 – 2019)
BMB Dept., Curricular Affairs and Assessment Committee (2018 – 2019)
BMB Dept., Undergraduate Affairs Committee (2017 – 2018)
BMB Dept., Distinguished Lecture Committee (2015 – 2018)
BMB Dept., Climate & Diversity Committee (2013 – 2014, 2016 – 2018)
BMB Dept., Undergraduate Professional Development (2015 – 2016)
Penn State Schreyer Honors College Admissions Evaluator (2016, 2017, 2019, 2024)

International Society for Computational Biology

ISCB Senior Member (2025 –)
Chair, Junior PI Community of Special Interest (2019 – 2021)
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:

41. Invited speaker, **Rules of Protein-DNA Interactions** (Cancún, Mexico), *TBD* [13 Oct. 2025]
40. Invited keynote speaker, **Genomic Education Partnership National Faculty Workshop** (virtual), *How to predict genomic regulatory regions using neural networks* [22 Jun. 2025]
39. Invited speaker, **Cornell University, Molecular Biology & Genetics Seminar Series** (Ithaca, NY), *Understanding transcription factor binding determinants using neural networks.* [28 Feb. 2025]
38. Invited speaker, **Genomic Education Partnership Research Seminar Series** (virtual), *Understanding the sequence and chromatin determinants of transcription factor binding specificity.* [5 Dec. 2024]
37. Invited speaker, **University at Buffalo, Department of Biochemistry** (Buffalo, NY), *Understanding the sequence and chromatin determinants of transcription factor binding specificity.* [29 Oct. 2024]
36. Invited keynote speaker, **RECOMB/ISCB Conference on Regulatory & Systems Genomics with DREAM Challenges** (Madison, WI), *Understanding the sequence and chromatin determinants of transcription factor binding specificity.* [4 Oct. 2024]
35. Invited speaker, **Royal College of Surgeons in Ireland, Dept. of Physiology and Medical Physics** (Dublin, Ireland), *Interpreting and predicting transcription factor binding patterns using neural networks.* [20 Jun. 2024]

34. Invited speaker, **Washington University of St. Louis School of Medicine, Dept. of Genetics** (St. Louis, MO), *Understanding the sequence and chromatin predeterminants of induced transcription factor binding with neural networks*. [7 Dec. 2023]

33. Invited speaker, **New York University School of Medicine, Institute for Systems Genetics** (New York, NY), *Predicting and interpreting transcription factor binding patterns using neural networks.* [10 Apr. 2023]

32. Invited speaker, **New York University, Dept. of Biology** (New York, NY), *Predicting and interpreting transcription factor binding patterns using neural networks*. [29 Mar. 2023]

31. Invited speaker, **University of Southern California, Dept. of Quantitative & Computational Biology** (Los Angeles, CA), *Understanding the sequence and chromatin determinants of transcription factor binding.* [3 Nov. 2022]

30. Invited speaker, **ASBMB: Evolution and core processes in gene expression** (Kansas City, MO), *Paralogous transcription factors diversify their DNA-binding targets via differential abilities to engage inaccessible chromatin* [21 Jul. 2022]

29. Invited speaker, **Stony Brook University, Biomedical Informatics Grand Rounds Seminar** (Stony Brook, NY), *Using neural networks to understand the DNA-binding specificity of transcription factors* [20 Apr. 2022 – virtual]

28. Invited speaker, **University of Pittsburgh, Dept. of Computational & Systems Biology** (Pittsburgh, PA), *Understanding transcription factor binding specificity during cell fate decisions* [20 Oct. 2020 – virtual]

27. Invited speaker, **University of Melbourne, Melbourne Integrative Genomics Seminar Series** (Melbourne, Australia), *Understanding transcription factor binding specificity during cell fate decisions* [15 Oct. 2020 – virtual]

26. Invited speaker, **University of Colorado, Anschutz Medical Campus, Computational Bioscience Program** (Denver, CO), *Using machine learning to understand transcription factor binding dynamics during neuronal programming.* [5 Oct. 2020 – virtual]

25. Invited speaker, **University of Oslo, Sven Furberg Seminars in Bioinformatics and Statistical Genomics** (Oslo, Norway), *Characterizing sequence and chromatin predeterminants of transcription factor binding.* [17 Sept. 2020 – virtual]

24. Invited speaker, **Indiana University, Center for Bioinformatics Research** (Bloomington, IN), *Using neural networks to characterize the predeterminants of induced transcription factor binding sites.* [17 Sept. 2020 – virtual]

23. Invited speaker, **Cincinnati Children's Hospital Medical Center** (Cincinnati, OH), *Characterizing sequence and chromatin predeterminants of transcription factor binding.* [1 Jun. 2020 – virtual]

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):

27. *Accurate allocation of multi-mapped reads enables regulatory element analysis at repeats*
A Morrissey, S Mahony*
Intelligent Systems in Molecular Biology (ISMB) 2024 (Montreal, Canada). [14 Jul. 2024]

26. *Joint sequence and chromatin neural networks characterize the differential abilities of Forkhead transcription factors to engage inaccessible chromatin*
S Arora, J Yang, T Akiyama, J Yang, D James, T Blanda, N Badjatia, WKM Lai, BF Pugh, M Ko, S Mahony*
Intelligent Systems in Molecular Biology (ISMB) / European Conference on Computational Biology (ECCB) 2023 (Lyon, France). [25 Jul. 2023]

25. *Forkhead transcription factors diversify their DNA-binding targets via differential abilities to engage inaccessible chromatin*
S Arora, T Akiyama, J Yang, D James, T Blanda, N Badjatia, WKM Lai, BF Pugh, M Ko, S Mahony*
RECOMB/ISCB Conference on Regulatory & Systems Genomics 2022 (New York, NY). [11 Nov. 2022]

24. *Domain adaptive neural networks improve cross-species prediction of transcription factor binding*
K Cochran*, D Srivastava, A Shrikumar, A Balsubramani, A Kundaje, S Mahony
Intelligent Systems in Molecular Biology (ISMB) / European Conference on Computational Biology (ECCB) 2021 [26 Jul. 2021 – virtual]

23. *Hox binding specificity is directed by DNA sequence preferences and differential abilities to engage inaccessible chromatin*
D Srivastava*, M Bulajiç, 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 Mazzoni, 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 Mazzoni
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 Mazzoni
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 Mazzoni, 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

2024 –	**Eberly Distinguished Senior Scholar in Genomics,** *Penn State University*
2023	**Daniel R. Tershak Teaching Award,** *Penn State University*
2021	**NSF CAREER Award**
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), *University of Galway*