

Rosemary Braun (Ph.D., M.P.H)

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1. Education

Date	Institution	Degree	Discipline
1996	Stony Brook University (SUNY Stony Brook)	BS	Physics
2004	University of Illinois, Urbana-Champaign (UIUC)	PhD	Physics
2006	Johns Hopkins—Bloomberg School of Public Health	MPH	Biostatistics

2. Training

Dates	Institution	Title	Field of research
06/2004–07/2005	U. Illinois, Urbana-Champaign	Postdoctoral Research Assoc.	Computational biophysics
07/2005–07/2009	Nat'l Cancer Institute, NIH	Cancer Prevention Fellow	Computational biology
07/2009–10/2011	Nat'l Cancer Institute, NIH	Research Fellow	Computational biology

3. Licensure/Certification

N/A

4. Academic Appointments

Dates	Title	Institution	Department
10/2011–	Assistant Professor	Northwestern University	Biostatistics, Dept of Preventive Medicine R.H.Lurie Comprehensive Cancer Center Northwestern Institute on Complex Systems
08/2014–	Assistant Professor	Northwestern University	Engineering Sciences and Applied Mathematics

5. Hospital Appointments

N/A

6. Honors and Awards

Date	Name of award
2009	Complex Systems Summer School (competitive admission), Santa Fe Institute.
2009	NIH Fellows Award for Research Excellence
2009	Poster Award, 12th International MGED Meeting

7. Professional Organizations

Role	Society
Member	International Society for Computational Biology

8. Professional Activities

Institutional Service

Dates	Activity
02/2013	Scientific Review Committee (SRC) Robert H. Lurie Cancer Ctr
2013	PhD Deliberation Ctte Biostatistics Division, Dept. of Preventive Medicine
2014–2015	Admissions Interviewer DGP Graduate Program
2014–	co-Director NICO Quantitative Biology working group
2015–	Executive Committee Northwestern Institute on Complex Systems

Teaching

Dates	Role	Course Title/Institution
1994–1995	Instructor	Calculus II Stony Brook University (SUNY Stony Brook)
1994–1996	Tutor	Math Learning Center Stony Brook University (SUNY Stony Brook)
1996–1997	Instructor	University Physics: Mechanics University of Illinois, Urbana–Champaign
2003	Instructor	Computational Biology Summer School University of Illinois, Urbana–Champaign
2007	Instructor	Computational Biophysics Workshop National Institutes of Health
2009–2010	Course Director	Math 127/128: Calculus I & II Foundation for Advanced Education in the Sciences Graduate School, NIH
06/2012	Invited Instructor	Statistical Analysis of Genome Scale Data Summer School Cold Spring Harbor Laboratory
07/2012	Course Director	Genomic Data Analysis Summer School Skolkovo Tech, Moscow, Russia
07/2012	Lecturer	Population Science, Northwestern Medical Scholars Summer Cardiology Academy Northwestern University
08/2013	Invited Instructor	q-Bio Summer School on predictive modeling of cellular regulatory systems LANL & New Mexico Consortium, Santa Fe, NM
08/2014	Invited Instructor	q-Bio Summer School on predictive modeling of cellular regulatory systems LANL & New Mexico Consortium, Santa Fe, NM

Trainees

Dates	Name	Status/Accomplishments
06/2014–	Phan Nguyen	PhD Candidate, Engineering Sciences & Applied Mathematics
08/2014–	Sahil Shah	PhD Candidate, Engineering Sciences & Applied Mathematics Fishel Graduate Research Fellowship, 2014–2015 1 publication & 2 poster abstracts to date
01/2014–04/2014	Daniel Cook	PhD Rotation, Driskill Graduate Program
01/2014–	Gary Wilk	PhD Candidate, Chemical & Biological Engineering Defended PhD Preliminary Proposal, October 2014
05/2014–	M. Harris Khan	Undergraduate, McCormick School of Engineering Summer Research Fellow (2014), Chemistry of Life Processes
10/2014–	Quan Mai	MSEB student thesis Topic: does gene expression predict response to taxol in ovarian cancer?
03/2015–	Marta Iwanaszko	Postdoctoral Fellow

Extramural Membership

- Erwin Shroedinger Fellowship, Austrian Science Fund, 2012–2013
- NIH Informatics SBIR Study Section (ad-hoc), 06/2014
- NIH Informatics SBIR Study Section (ad-hoc), 03/2015

Editorial Responsibilities

- Nature Scientific Reports

Review Responsibilities

Year	Reviewer for:
2010	Fellows Award for Research Excellence, NIH
2011	PLoS One; Fellows Award for Research Excellence, NIH
2012	PLoS One; Source Code for Biology and Medicine; Current Bioinformatics; IEEE/ACM Transactions on Computational Biology & Bioinformatics
2013	PLoS One; PLoS Genetics; IEEE/ACM Transactions on Computational Biology & Bioinformatics; Journal of the American Chemical Society (JACS); Journal of the American Medical Association (JAMA)
2014	PLoS One; IEEE/ACM Transactions on Computational Biology & Bioinformatics; Journal of the American Chemical Society (JACS); Journal of the American Medical Association (JAMA); Bioinformatics

9. Grant Awards

Agency	Award Title (Type)	Role	Period	Directs
NCI (NIH)	Cancer Prevention Fellowship	PI	2005–2009	
NCI (NIH)	Novel Pathway Analysis Methods for Identifying Genomic Causes of Cancer (K22)	PI	2012–2015	\$486,000
JS McDonnell Fnd	Modeling Biocomplexity: from molecular interactions to population genetics (Complex Systems Scholar Award)	PI	2015–2020	\$450,000

10. Invited Talks

Date	Title	Venue
08/2012	Hearing the Shape of Cancer	Spotlight Talk, q-Bio Conference on Cellular Information Processing
10/2012	Hearing the Shape of Complex Disease	Northwestern Institute on Complex Systems, Northwestern University
12/2012	Hearing the Shape of Complex Disease	Applied Physics Seminar, Northwestern University
10/2013	Mapping Gene Regulatory Networks	Applied Mathematics Colloquium, Northwestern University
10/2013	Gene Regulatory Dynamics: From Network Structure to Network Function	Mathematics Colloquium, West Virginia University
12/2013	Form and Function in the Architecture of Intracellular Networks	Network Frontiers Workshop, Northwestern University
04/2014	Hearing the Shape of Biological Dynamics	Physics Colloquium, University of Illinois, Chicago
08/2014	Inferring Aberrant Network Dynamics	Research Lecture, q-Bio Summer School on Cellular Information Processing
01/2015	TimeStamp Analysis (inferring circadian disruption from gene expression)	DARPA BioChronicity Meeting

11. Publications

Original Investigations

- [1] J. Gullingsrud, R. Braun, and K. Schulten, “Reconstructing potentials of mean force through time series analysis of steered molecular dynamics simulations,” *J. Comp. Phys.*, vol. 151, pp. 190–211, 1999.
- [2] R. Braun, M. Sarikaya, and K. Schulten, “Genetically engineered gold-binding polypeptides: Structure prediction and molecular dynamics,” *J. Biomat. Sci.*, vol. 13, pp. 747–758, 2002.
- [3] R. Braun, D. M. Engelman, and K. Schulten, “Molecular dynamics simulations of micelle formation around dimeric glycoporphin-A transmembrane helices,” *Biophys. J.*, vol. 87, pp. 754–763, 2004.
- [4] J. C. Phillips, R. Braun, W. Wang, J. Gumbart, E. Tajkhorshid, E. Villa, C. Chipot, R. D. Skeel, L. Kale, and K. Schulten, “Scalable molecular dynamics with NAMD,” *J. Comp. Chem.*, vol. 26, pp. 1781–1802, 2005.
- [5] J. Cohen, A. Arkhipov, R. Braun, and K. Schulten, “Imaging the migration pathways for O₂, CO, NO, and Xe inside myoglobin,” *Biophys. J.*, vol. 91, pp. 1844–1857, 2006.
- [6] R. Braun, L. Cope, and G. Parmigiani, “Identifying differential correlation in gene/pathway combinations,” *BMC Bioinformatics*, vol. 9, p. 488, 2008.
- [7] E. A. Mathé, G. H. Nguyen, E. D. Bowman, Y. Zhao, A. Budhu, A. J. Schetter, R. Braun, M. Reimers, K. Kumamoto, D. Hughes, N. K. Altorki, A. G. Casson, C.-G. Liu, X. W. Wang, N. Yanaihara, N. Hagiwara, A. J. Dannenberg, M. Miyashita, C. M. Croce, and C. C. Harris, “MicroRNA expression in squamous cell carcinoma and adenocarcinoma of the esophagus: associations with survival,” *Clin. Cancer Res.*, vol. 15, pp. 6192–6200, 2009.
- [8] R. Braun, W. Rowe, C. Schaefer, J. Zhang, and K. Buetow, “Needles in the haystack: Identifying individuals present in pooled genomic data,” *PLoS Genet.*, vol. 5(10), p. e1000668, 2009.
- [9] R. Braun and K. Buetow, “Pathways of Distinction Analysis: a new technique for multi-SNP analysis of GWAS data,” *PLoS Genet.*, vol. 7, no. 6, p. e1002101, 2011.
- [10] R. Braun, G. Leibon, S. Pauls, and D. Rockmore, “Partition decoupling for multi-gene analysis of gene expression profiling data,” *BMC Bioinformatics*, vol. 12, no. 497, 2011.

- [11] R. Braun, R. Finney, C. Yan, Y. Hu, Q.-R. Chen, M. Edmonson, D. Meerzaman, and K. Buetow, “Discovery analysis of TCGA data reveals association between germline genotype and survival in ovarian cancer patients,” *PLoS One*, vol. 8, no. 3, p. e0055037, 2013.
- [12] Q.-R. Chen, R. Braun, Y. Hu, C. Yan, E. M. Brunt, D. Meerzaman, A. J. Sanyal, and K. Buetow, “Multi-SNP analysis of GWAS data identifies pathways associated with nonalcoholic fatty liver disease,” *PLoS One*, vol. 8, no. 7, p. e65982, 2013.
- [13] R. Braun, “Systems analysis of high-throughput data,” *Advances in Experimental Medicine and Biology*, vol. 844, p. 153, 2014.
- [14] R. Braun and S. Shah, “Network methods for pathway analysis of gene expression data,” *Computational and Structural Biotechnology Journal*, (in press; arXiv preprint: <http://arxiv.org/abs/1411.1993>) 2014.
- [15] R. Braun, “Hearing the Shape of Cancer: A spectral graph theoretic approach for identifying altered gene regulatory networks,” *Under Review*, 2014.
- [16] R. Braun, “BioPartite: A flexible representation framework for multipartite pathway models,” *Under Review*, 2015.

Reviews, Case Reports, Letters, Editorials

- [1] R. Amaro, F. Autentieth, J. Baudry, Rosemary Braun, and Z. Luthey-Schulten, “Determining force fields,” *Instructional Material, Theoretical and Computational Biophysics Group*, 2003.
- [2] A. Arkhipov, Rosemary Braun, and Y. Yin, “Case study: Myoglobin,” *Instructional Material, Theoretical and Computational Biophysics Group*, 2008.
- [3] Rosemary Braun and E. Mathé, “LHCchip: Software for preprocessing custom LHC microarray data,” *Laboratory of Human Carcinogenesis, National Cancer Institute, NIH*, 2008.

Books and Book Chapters

- [1] R. Braun, “Systems analysis of high-throughput data,” in *Blood: A Systems Biology Approach* (S. Corey *et al.*, eds.), Springer-Verlag, 2014.

Abstracts (recent)

- [1] R. Braun, “Hearing the Shape of Cancer: Spectral graph theory for pathway analysis of gene expression data,” in *qBio Conference on Cellular Information Processing, Sixth Annual, LANL*, 2012.
- [2] B. Nabet, R. Braun, R. Popovic, and J. Licht, “Investigating the role of epigenetic mechanisms upon aberrant signaling network activation,” *AACR Annual Meeting (American Association of Cancer Research)*, 2013.
- [3] R. Braun, “A spectral approach for identifying altered gene regulatory networks,” *NetSci2013 International Conference on Network Science*, 2013.