

CURRICULUM VITAE
The Johns Hopkins University School of Medicine

Michael F. Ochs

October 15, 2012

Date of version

DEMOGRAPHIC AND PERSONAL INFORMATION

Current Appointments:

Associate Professor of Oncology, Division of Biostatistics and Bioinformatics
School of Medicine, The Johns Hopkins University, Baltimore, Maryland

Joint Appointment, Department of Health Science Informatics, School of Medicine,
The Johns Hopkins University, Baltimore, Maryland

Director, Bioinformatics Shared Resource, The Sidney Kimmel Comprehensive Cancer
Center at Johns Hopkins, Baltimore, Maryland

Personal Data:

Business Address: The Sidney Kimmel Cancer Center
 at Johns Hopkins Division of Oncology
 Biostatistics/Bioinformatics
 550 North Broadway, Suite 1101
 Baltimore, MD 21205-2013

Phone: (410) 955-8830

Fax: (410) 955-0859

Email: mfo@jhu.edu

Education and Training:

1982 B.A., Haverford College, Chemistry

1985 A.M., Harvard University, Celtic Languages and Literatures

1991 M.A., Brandeis University, Physics

1995 Ph.D., Brandeis University, Physics

Professional Experience:

1981 – 1982 Undergraduate Research, Haverford College, Haverford PA

1982-1983 Associate Scientist, Solar Energy Systems, Newark, DE

1985-1986	Associate Scientist, Raytheon, Lexington, MA
1986- 1988	Research Assistant II, Harvard Medical School, Southborough, MA
1989- 1995	Graduate Research, Brandeis University, Waltham, MA
1993-1996	Instructor/Departmental Assistant, Haverford College, Haverford, PA
1996-2000	Sr. Programmer/Analyst, Fox Chase Cancer Center, Philadelphia, PA
2000	Project Leader, Fox Chase Cancer Center, Philadelphia, PA
2000-2002	Manager, Bioinformatics, Fox Chase Cancer Center, Philadelphia, PA
2001-2006	Member, Bioinformatics Working group, Fox Chase Cancer Center, Philadelphia, PA
2002-2006	Director, Bioinformatics, Fox Chase Cancer Center, Philadelphia, PA
2005-2006	Visiting Associate Research Professor, Drexel University, Philadelphia, PA
2006-2008	Visiting Associate Professor of Oncology, Johns Hopkins School of Medicine, Baltimore, MD
2008-	Associate Professor Oncology, School of Medicine, Johns Hopkins University, Baltimore, MD
2009-	Director, Bioinformatics Shared Resource, Sidney Kimmel Comprehensive Cancer Center, Baltimore, MD
2009-	Joint Appointment Health Science Informatics, School of Medicine, Johns Hopkins University, Baltimore, MD

RESEARCH ACTIVITIES

Peer- Reviewed Publications

1. Kestler HW, 3rd, Li Y, Naidu YM, Butler CV, **Ochs MF**, Jaenel G, King NW, Daniel MD and Desrosiers RC. Comparison of simian immunodeficiency virus isolates. *Nature*. 1988; **331**: 619-22.
2. **Ochs MF**, Stoyanova RS, Arias-Mendoza F and Brown TR. A new method for spectral decomposition using a bilinear Bayesian approach. *J Magn Reson*. 1999; **137**: 161-76.
3. Golemis EA, **Ochs MF** and Pugacheva EN. Signal transduction driving technology driving signal transduction: factors in the design of targeted therapies. *J Cell Biochem Suppl*. 2001; **37**: 42-52.
4. **Ochs MF**, Stoyanova RS, Brown TR, Rooney WD and Springer CS Jr. A Bayesian Markov chain Monte Carlo solution of the bilinear problem. in *Bayesian Inference and Maximum Entropy Methods in Science and Engineering: 19th International Workshop*. Rychert, J. T., Erickson, G. J. and Smith, C. R. Melville, American Institute of Physics: 2001; 274 - 284.
5. Grant JD, Broccoli D, Muquit M, Manion FJ, Tisdall J and **Ochs MF**. Telometric: a tool providing simplified, reproducible measurements of telomeric DNA from constant field agarose gels. *Biotechniques*. 2001; **31**:1314-6, 1318.
6. Bidaut G, Moloshok TD, Grant JD, Manion FJ and **Ochs MF**. Bayesian Decomposition analysis of gene expression in yeast deletion mutants. in *Methods of Microarray Data Analysis II*. Johnson, K. and Lin, S. Boston, Kluwer Academic. 2002; 105-122.
7. Moloshok TD, Klevecz RR, Grant JD, Manion FJ, Speier WF and **Ochs MF**. Application of Bayesian Decomposition for analysing microarray data. *Bioinformatics*. 2002; **18**:566-75.

8. Grant JD, Dunbrack RL, Manion FJ and **Ochs MF**. BeoBLAST: distributed BLAST and PSI-BLAST on a Beowulf cluster. *Bioinformatics*. 2002; **18**:765-6.
9. Moloshok TD, Datta D, Kossenkov AV and **Ochs MF**. Bayesian Decomposition classification of the Project Normal data set. in *Methods of Microarray Data Analysis III*. Johnson, K. F. and Lin, S. M. Boston, Kluwer Academic. 2003; 211 - 232.
10. Frolov A, Chahwan S, **Ochs M**, Arnoletti JP, Pan ZZ, Favorova O, Fletcher J, Mehren M von, Eisenberg B and Godwin AK. Response markers and the molecular mechanisms of action of Gleevec in gastrointestinal stromal tumors. *Mol Cancer Ther*. 2003; **2**: 699-709.
11. Kossenkov A, Manion FJ, Korotkov E, Moloshok TD and **Ochs MF**. ASAP: automated sequence annotation pipeline for web-based updating of sequence information with a local dynamic database. *Bioinformatics*. 2003; **19**: 675-676.
12. Grant JD, Somers LA, Zhang Y, Manion FJ, Bidaut G and **Ochs MF**. FGDP: functional genomics data pipeline for automated, multiple microarray data analyses. *Bioinformatics*. 2004; **20**: 282 - 283.
13. **Ochs MF**, Goralczyk EM, Grant JD, Manion FJ, Yeung A, Seeholzer S, Mathew G, Hardy RR and Beck JR. A unified laboratory information management system for research data. *Medinfo 2004*: 1784.
14. Bidaut G and **Ochs MF**. ClutrFree: cluster tree visualization and interpretation. *Bioinformatics*. 2004; **20**: 2869-71.
15. Kossenkov A, Bidaut G and **Ochs MF**. Genes associated with prognosis in adenocarcinoma across studies at multiple institutions. in *Methods of Microarray Data Analysis IV*. Johnson, K. and Lin, S. Boston, Kluwer Academic. 2005; 239.
16. Bidaut G, Suhre K, Claverie JM and **Ochs MF**. Bayesian decomposition analysis of bacterial phylogenomic profiles. *Am J Pharmacogenomics*. 2005; **5**: 63-70.
17. Favorov AV, Andreewski TV, Sudomoina MA, Favorova OO, Parmigiani G and **Ochs MF**. A Markov chain Monte Carlo technique for identification of combinations of allelic variants underlying complex diseases in humans. *Genetics*. 2005; **171**: 2113-21.
18. Ertel A, Verghese A, Byers SW, **Ochs M** and Tozeren A. Pathway-specific differences between tumor cell lines and normal and tumor tissue cells. *Mol Cancer*. 2006; **5**: 55.
19. Tchuvatkina, Shimoni L, **Ochs MF** and Moloshok T. Proteomics LIMS: A caBIG project, year 1. *AMIA Annu Symp Proc*. 2006; 1116.
20. Bidaut G, Manion FJ, Garcia C and **Ochs MF**. WaveRead: automatic measurement of relative gene expression levels from microarrays using wavelet analysis. *J Biomed Inform*. 2006; **39**: 379-88.
21. Bidaut G, Suhre K, Claverie JM and **Ochs MF**. Determination of strongly overlapping signaling activity from microarray data. *BMC Bioinformatics*. 2006; **7**: 99.
22. Favorova OO, Favorov AV, Boiko AN, Andreewski TV, Sudomoina MA, Alekseenkov AD, Kulakova OG, Gusev EI, Parmigiani G and **Ochs MF**. Three Allele Combinations Associated with Multiple Sclerosis. *BMC Med Genet*. 2006; **7**: 63.
23. Wang G, Kossenkov AV and **Ochs MF**. LS-NMF: A modified non-negative matrix factorization algorithm utilizing uncertainty estimates. *BMC Bioinformatics*. 2006; **7**: 175.

24. Spidlen J, Gentleman RC, Haaland PD, Langille M, Meur NL, **Ochs MF**, Schmitt C, Smith CA, Treister AS and Brinkman RR. Data standards for flow cytometry. *Omics*. 2006 **10**: 209-14.
25. Patel AA, Gilbertson JR, Showe LC, London JW, Ross E, **Ochs MF**, Carver J, Lazarus A, Parwani AV, Dhir R, Beck JR, Liebman M, Garcia FU, Prichard J, Wilkerson M, Herberman RB, Becich MJ and a PCABC."A novel cross-disciplinary multi-institute approach to translational cancer research: Lessons learned from Pennsylvania Cancer Alliance Bioinformatics Consortium (PCABC). *Cancer Informatics* **3**: 255 - 274 2007.
26. Kossenkov AV, Peterson AJ and **Ochs MF**. Determining transcription factor activity from microarray data using Bayesian Markov Chain Monte Carlo sampling. *Medinfo*. 2007; **12**.
27. **Ochs MF** and Casagrande JT. Information systems for cancer research. *Cancer Invest*. 2008; **26**: 1060-7.
28. Belinsky MG, Rink L, Cai KQ, **Ochs MF**, Eisenberg B, Huang M, Mehren M von and Godwin AK. The insulin-like growth factor system as a potential therapeutic target in gastrointestinal stromal tumors. *Cell Cycle*. 2008; **7**: 2949-55.
29. Smith IM , Glazer CA , Mithani SK, **Ochs MF** , Sun W , Bhan S , Vostrov A , Abdullaev Z, Lobanekov V , Gray A , Liu C , Chang SS , Ostrow KL , Westra WH , Begum S , Dhara M and Califano J . Coordinated activation of candidate proto-oncogenes and cancer testes antigens via promoter demethylation in head and neck cancer and lung cancer. *PLoS ONE*. 2009; **4**: e4961.
30. AV Kossenkov and **MF Ochs**. Matrix factorization methods applied in microarray analysis. *Int J Data Mining Bioinfo*. 2010; **4**: 72-90.
31. O'Doherty C, Favorov A, Heggarty S, Graham C, Favorova O, **Ochs M**, Hawkins S, Hutchinson M, O'Rourke K and Vandebroek K. Genetic polymorphisms, their allele combinations and interferon- β treatment response in Irish multiple sclerosis patients. *Pharmacogenomics*. 2009; **10**: 1177-86.
32. Rink L, Skorobogatko Y, Kossenkov A, Belinsky MG, Pajak T, Heinrich MC, Mehren M von, **Ochs MF**, Eisenberg B and Godwin AK. Genetic Signatures Indicate Predictable Rapid Response to Imatinib Mesylate Treatment in Gastrointestinal Stromal Tumors. *Mol Cancer Therapeutics*. 2009; **8**: 2172-2182.
33. Parfenov MG, Titov BV, Sudomoina MA, Martynov M, Favorov AV, **Ochs MF**, Gusev EI and Favorova OO. [Complex analysis of genetic predisposition to ischemic stroke in Russians]. *Mol Biol (Mosk)*. 2009; **43**: 937-45.
34. **Ochs MF**, Rink Lori, Tarn C, Mburu S, Taguchi T, Eisenberg B, and Godwin AK. Detection of Treatment-Induced Changes in Signaling Pathways in Gastrointestinal Stromal Tumors Using Transcriptomic Data. *Canc Res*. 2009; **69**: 9125-32.
35. Glazer CA, Smith IM, **Ochs MF**, Begum S, Westra W, Chang SS, Sun W, Bhan S, Khan Z, Ahrendt S and Califano JA. Integrative discovery of epigenetically derepressed cancer testis antigens in NSCLC. *PLoS One*. 2009; **4**: e8189.
36. Kent OA, Mullendore M, Wentzel EA, Lopez-Romero P, Tan AC, Alvarez H, West K, **Ochs MF**, Hidalgo M, Arking DE, Maitra A and Mendell JT. A resource for analysis of microRNA expression and function in pancreatic ductal adenocarcinoma cells. *Cancer Biol Ther*. 2009; **8**: 2013-24.
37. **Ochs MF**. Knowledge-based data analysis comes of age. *Brief Bioinfo*. 2010; **11**: 30-9.

38. Sudomoina MA, Sukhinina T, Barsova RM, Favorov AV, Sakhnovich RM, Titov BV, NA Matveeva, IN Rybalkin, TN Vlasik, **MF Ochs**, MYa Ruda, OO Favorova. Complex analysis of association of inflammation gene polymorphisms with myocardial infarction. *Molecular Biology*. 2010; **44**: 407-14.
39. Ibragimova I, I Ibáñez de Cáceres, Hoffman AM, Potapova A, Dulaimi E, Al-Saleem T, Hudes GR, **Ochs MF**, Cairns P. Global reactivation of epigenetically silenced genes in prostate cancer. *Cancer Prev Res (Phila)*. 2010; **3**: 1084-92.
40. Fertig EJ, Ding J, Favorov AV, Parmigiani G, **Ochs MF**. CoGAPS: an R/C++ package to identify patterns and biological process activity in transcriptomic data. *Bioinformatics*. 2010; **26**: 2792-3.
41. Yörük E, **Ochs MF**, Geman D, Younes L. A Comprehensive Statistical Model for Cell Signaling. *IEEE/ACM Trans Comput Biol and Bioinfo*. 2011; **8**:592-606.
42. Hennessey PT, **Ochs MF**, Mydlarz WW, Hsueh W, Cope L, Yu W, Califano JA. Promoter methylation in head and neck squamous cell carcinoma cell lines is significantly different than methylation in primary tumors and xenografts. *PLoS One*. 2011; **6**: e20584.
43. Favorov A, Lvovs D, Speier W, Parmigiani G, **Ochs MF**. OnionTree XML: A Format to Exchange Gene-Related Probabilities. *J Biomol Structure Dynamics*. 2011; **29**:1-7.
44. Fertig EJ, Danilova LV, Favorov AV, **Ochs MF**. Hybrid modeling of cell signaling and transcriptional reprogramming and its application in *C. elegans* development. *Front Gene*, 2011; **2**: 77.
45. Tsareva EI, Kulakova OG, Makarycheva OIu, Boiko AN, Shchur SG, Lashch NIu, Popova NF, Gusev EI, Bashinskaia VV, L'vov DV, Favorov AV, **Ochs MF**, Favorova OO. [Pharmacogenomics of multiple sclerosis: association of immune response genes polymorphism with copaxone treatment efficacy]. [Article in Russian] *Mol Biol (Mosk)*. 2011; **45**:963-72.
46. Hennessey PT, Sanford T, Choudhary A, Mydlarz WW, Brown D, Adai AT, **Ochs MF**, Ahrendt SA, Mambo E, Califano JA. Serum microRNA Biomarkers for Detection of Non-Small Cell Lung Cancer. *PLoS One*. 2012; **7**: e32307.
47. Fertig EJ, Ren Q, Cheng H, Hatakeyama H, Dicker A, Rodeck U, Considine M, **Ochs MF**, Chung CH. Gene expression signatures modulated by epidermal growth factor receptor activation and their relationship to cetuximab resistance in head and neck squamous cell carcinoma. *BMC Genomics*, 2012; **13**: 160.
48. **Ochs MF**, Fertig EJ. Matrix Factorization for Transcriptional Regulatory Network Inference, *IEEE Symposium on Computational Intelligence in Bioinformatics and Biology*, 2012:387-396.
49. Fertig EJ, Favorov AV, **Ochs MF**. Identifying context-specific transcription factor targets from prior knowledge and gene expression data, *IEEE Conference on Bioinformatics and Biomedicine*, In Press.
50. Speier W, **Ochs MF**. Updating annotations with the distributed annotation system and the automated sequence annotation pipeline, *Bioinformatics*, In Press.

Patents

US Patent pending: Methods of Decomposing Complex Data with coinventors M.F. Ochs, I.R. Brown, R. Stoyanova, and C. Patriotis

Extramural FundingGrants:**Current**

- 09/01/2012 – 08/31/2014 Modeling Transcriptional reprogramming by Markov Chain Monte Carlo Sampling
NLM
R01LM011000
\$200,000
PI, 25%
- 09/30/2010 – 09/29/2013 Innovative Approaches to Therapeutic Target Identification in High Risk Pediatric
NCI (Subcontract)
20303
\$1,004,654
PI: Arceci
Co-Investigator, 5%
- 07/01/2011 – 06/30/2016 JHU ICMIC Program: Biostatistics Core
NCI
P50CA103175
\$1,028,228
PI: Bhujwalla / Huang
Co-Investigator, 5%
- 05/07/1997 – 04/30/2012 Regional Oncology Research Center: Bioinformatics Core
P30CA006973
NCI
\$493,370
PI: Nelson/Ochs
Co-Investigator, 15%
- 09/17/2007 – 07/31/2012 SPORE in Head & Neck Cancer: Biostatistics and Bioinformatics Core
P50DE0109032
NCI
\$103,232

Curriculum Vitae

7

Michael F. Ochs

PI: Sidransky/Rosner
Co-Investigator, 5%

- 05/01/2008 – 02/28/2013 The Role of CDK5 in Metastasis
R01CA085567
NCI
\$213,725
PI: Nelkin
Co-Investigator, 10%
- 09/25/2009 – 08/31/2012 Validation of Epigenetic Biomarkers of Head and Neck Cancer Progression
RC2DE020789
NCI
\$280,998 (NCE)
PI: Califano
Co-Investigator, 5%
- 09/22/2009 – 08/31/2012 Integrative Pathway Analysis of Epigenomic/transcriptional Alteration in HNSCC
RC1DE020324
NIDCR
\$266,093 (NCE)
PI: Califano
Co-Investigator, 5%
- 07/01/2009 – 05/31/2014 Image-guided Prodrug and SiRNA Targeting of Cancer
R01CA138515
NCI
\$207,500
PI: Bhujwala
Co-Investigator, 5%
- 07/01/2010 – 06/30/2012 Tools for Detecting Biologically Important Sequence Variation in Cancer
NCI
R21CA152432
\$220,115
PI: Karchin
Co-Investigator, 7%
- 07/20/2007 – 05/31/2012 Molecular signatures on HNSCC in Response to Targeted Therapies
NIDCR
R01DE017982
\$237,434

PI: Chung
Co-Investigator, 5%

Pending

- 04/01/2012 – 03/31/2017 Defining Signatures for risk Classification and Therapeutic Targeting in AML
Fred Hutchinson Cancer Research Center/NIH
ID
\$164,000
PI: Arceci
Co-Investigator, 5%
- 07/01/2012- 06/30/2017 Novel Epigenetic Mechanisms of Gene Regulation in Oral Cancer
NIH
R01CA169371
\$250,000
PI: Califano
Co-Investigator, 5%
- 07/01/2012 – 06/30/2017 Biomarkers for Identification of Relapse Risk and Therapeutic Targets in Childhood AML
Fred Hutchinson Cancer Research Center
ID
\$121,785
PI: Arceci
Co-Investigator, 5%
- 07/01/2012 – 06/30/2016 Pathway-Based Integrated analysis to Isolate Epigenetic Drivers in HNSCC (PQ10)
NCI
\$807,261
PI, 25%

Previous

- 05/06/2005 – 04/30/2007 Gene Expression in Circulating Tumor Cells
NIH
R42CA099410
\$50,000
PI: Terstappen / Immunicon
Co-Investigator, 5%

Curriculum Vitae

9

Michael F. Ochs

- 04/01/2005 – 03/31/2009 Bioinformatics Standards for Flow Cytometry
NIH
ID
\$23,000
PI: Brinkman
Co-Investigator, 5%
- 07/01/2004 – 06/30/2008 The Johns Hopkins Institutions Statewide Academic Health Center
Grant
MCRF
CH844CRF
PI: Parmigiani
Co-Investigator, 5%
- 07/01/2006 – 06/30/2008 Identification of Signaling Activity in Tumor Cells
MCRF
CH8666CRF
PI, 20%
- 04/10/2007 – 04/09/2010 Identifying Genetic Factors for Predisposition in Polygenic Diseases
R03LM008932
NLM
\$48,550
PI, 2%
- 09/01/2008 – 08/31/2010 An Open-Source Algorithm Isolating Signatures in Microarray Data
R21LM009382
NLM
\$112,500
PI: 18%
- 09/09/2008 – 08/31/2010 Tools for Large-Scale Analysis of Driver Pathways
R21CA135877
NCI
\$112,500
PI: Karchin
Co-Investigator, 7%
- 09/30/2009 – 09/29/2011 An Open-Source Algorithm Isolating Overlapping Signatures in
Microarray Data
R21LM009382
NLM (ARRA)
\$38,042 (equipment only)
PI: 0%

Curriculum Vitae 08/01/2008 – 05/31/2013	10	Michael F. Ochs
	Signal Transduction in the Heart after Cancer Therapy R01HL088649 NHLBI \$250,000 PI: Gabrielson Co-Investigator, 4%	
08/01/2009 – 07/31/2014	The Molecular Actions of Imatinib Mesylate in GISTs R01CA106588 Fox Chase Cancer Center (Subgrant) \$24,023 PI: Godwin/Ochs, 7.5%	
09/22/2011 – 06/30/2016	Johns Hopkins Pediatric Obesity Research and Training Center NICHD U54HD070725 \$2,913,378 PI: Wang Co-Investigator, 10%	
09/01/2010 – 08/31/2011	A Randomized, Open Label, Multicenter Study to Evaluate the Efficacy and Safety of Decitabine as Epigenetic Priming with Induction Chemotherapy in Pediatric Acute Myelogenous Leukemia (AML subjects) E7373-G000-202 EISAI America INC \$1,015,099 PI: Arceci Co-Investigator, 5%	

EDUCATIONAL ACTIVITIES

Educational Publications:

Solicited Reviews and Chapters

1. EA Golemis, **MF Ochs** and EN Pugacheva. "Signal transduction driving technology driving signal transduction: factors in the design of targeted therapies." *J Cell Biochem Suppl Suppl 37*: 42-52 2001.
2. **MF Ochs**. comment on "A statistical framework for expression-based molecular classification in cancer". *Journal of the Royal Statistical Society, B 64*: 756 - 757 2002.
3. **MF Ochs** and G Bidaut. Microarray data normalization. in *Microarray Image Analysis - Nuts and Bolts*. Shah, S. and Kamerova, G. London, DNA Press, LLC: 131-154 2002.
4. **MF Ochs** and EA Golemis. The biology behind gene expression: a basic tutorial. in *Methods of Microarray Data Analysis III*. Johnson, K. F. and LIn, S. M. Boston, Kluwer Academic: 9 - 24 2003.

5. **MF Ochs**. Bayesian Decomposition. in *The Analysis of Gene Expression Data: Methods and Software*. Parmigiani, G., Garrett, E., Irizarry, R. and Zeger, S. New York, Springer Verlag 2003.
6. **MF Ochs** and AK Godwin. "Microarrays in cancer: research and applications."*Biotechniques* **34**: S4-S15 2003.
7. **MF Ochs**, TD Moloshok, G Bidaut and G Toby. "Bayesian Decomposition: Analyzing microarray data within a biological context."*Annals of the New York Academy of Sciences* **1020**: 212 - 226 2004.
8. A Kossenkov, G Bidaut and **MF Ochs**. Estimating cellular signaling from transcription data. in *Bayesian Inference for Gene Expression and Proteomics*. Do, K.-A., Mueller, P. and Vannucci, M. Cambridge, Cambridge University Press 2006.
9. G Wang and **MF Ochs**. Estimating gene function with least squares nonnegative matrix factorization. in *Methods in Molecular Biology: Gene Function Analysis*. Ochs, M. F. Totowa, Humana Press: 35 - 48 2007.
10. **MF Ochs**, AJ Peterson, A Kossenkov and G Bidaut. Incorporation of gene ontology annotations to enhance microarray data analysis. in *Methods in Molecular Biology: Microarray Data Analysis*. Korenberg, M. J. Totowa, Humana Press: 243 - 254 2007.
11. **MF Ochs**. "Gene function analysis. Preface."*Methods Mol Biol* **408**: vii-ix 2007.
12. **MF Ochs** and JT Casagrande. "Information systems for cancer research."*Cancer Invest* **26**: 1060-7 2008.
13. MG Belinsky, L Rink, KQ Cai, **MF Ochs**, B Eisenberg, M Huang, M von Mehren and AK Godwin. "The insulin-like growth factor system as a potential therapeutic target in gastrointestinal stromal tumors."*Cell Cycle* **7**: 2949-55 2008.
14. AV Kossenkov and **MF Ochs**. "Matrix factorization methods applied in microarray analysis."*Int J Data Mining Bioinfo* **4**: 72-90, 2010.
15. AV Kossenkov and **MF Ochs**. Matrix Factorization for Recovery of Biological Processes from Microarray Data."*Methods in Enzymology* **467**: 59-77, 2009.
16. **MF Ochs**. "Knowledge-Based Data Analysis Comes of Age."*Brief Bioinfo* **11**: 30-9, 2010.
17. E Fertig, L Danilova, and **MF Ochs**. "Cancer Systems Biology" in HH Lu, B Schölkopf, H Zhao (eds): *Handbook of Computational Statistics: Statistical Bioinformatics*, Springer, New York, 2011.
18. L Danilova and **MF Ochs**. "Biomarkers of System Response to Therapeutic Intervention, in Daniel A. Casciano and Saura C. Sahu (Eds) *Handbook of Systems Toxicology*, Wiley, 2011.
19. **MF Ochs**, R Karchin, H Ransom, R Gentleman. "Identification of aberrant pathway and network activity from high-throughput data."*Pac Symp Biocomput.* 364-8, 2011.
20. **MF Ochs**. "Gene sets for pathways" in W Dubitzky, O Wolkenhauer, H Yokota, K-H Cho (Eds.) *Encyclopedia of Systems Biology*. Springer, New York, 2013.
21. R Karchin, **MF Ochs**, JM Stuart, JS Bader. "Identification of aberrant pathway and network activity from high-throughput data."*Pac Symp Biocomput.* 2012;17:1-6.

Book Chapters

1. **M. F. Ochs**, D.H. Roberts, L.F. Brown, J.F.C. Wardle. "Milliarcsecond polarization structure of the quasars 3C273 and 3C345 at two frequencies", *Bulletin of the American Astronomical Society*, **24**, 732, 1992.
2. **M. F. Ochs**, R. S. Stoyanova, T. R. Brown, W. D. Rooney, and C. S. Springer, Jr.: "A Bayesian Markov chain Monte Carlo solution of the bilinear problem", in J. T. Rychert, G. J. Erickson, and C. R. Smith (eds): *Bayesian Inference and Maximum Entropy Methods in Science and Engineering*, 19th International Workshop, AIP Conference Proceedings, Melville (NY), 2001.
3. G. Bidaut, K. Suhre, J.-M. Claverie, **M. F. Ochs**: "Analysis of phylogenetic profiles using Bayesian Decomposition", *Proceedings of the 2003 IEEE Computer Society Bioinformatics Conference (CSB '03)*, 480, 2003.
4. A.V. Favorov, O.O Favorova, T.V. Andreevski, M.A. Sudomoina, A.D Alekseenkov, O.G. Kulakova, A.N. Boiko, E.I Gusev, G. Parmigiani, **M.F.Ochs**. "MCMC Method Has Found That Multiple Sclerosis is Associated With Two Three-Genes Combinations", *Proc Fourth Intl Conf Bioinformatics of Gen Reg Struct*, v.2, pp 189-192, 2004.

Books

1. **MF Ochs** (editor). *Gene Function Analysis. Methods in Molecular Biology, vol 408*. Humana Press, Totowa, 2007.
2. **MF Ochs**, JT Casagrande, RV Davuluri (editors). *Biomedical Informatics for Cancer Research*. Springer-Verlag Press, New York, 2010.
3. **MF Ochs** (editor). *Gene Function Analysis, 2nd Edition. Methods in Molecular Biology, vol 408*. Humana Press, Totowa, expected 2013.

Teaching:

Course Taught

Co-Instructor

140.637.01 BIOLOGICAL DATABASES AND DISTRIBUTED COMPUTING

Term 2 – October – December 2008, Johns Hopkins School of Public Health

Term 2 – October – December 2009, Johns Hopkins School of Public Health

Term 2 – October – December 2011, Johns Hopkins School of Public Health

Mentoring

Predoctoral / Postdoctoral Trainees

2010 - 2011 Yingying Wei: Graduate Student, Johns Hopkins School of Public Health.

2008 - 2009 Jie Ding: Postdoctoral Fellow, Johns Hopkins University School of Medicine and Harvard University Dana Farber Cancer Institute.

- 2008 - 2010 Ludmila Danilova: Postdoctoral Fellow, Johns Hopkins University School of Medicine
- 2008 - 2012 Elana Fertig: Instructor, Department of Oncology, K25 Fellow, formerly Postdoctoral Fellow, Johns Hopkins University School of Medicine
- 2000 – 2010 Alexander Favorov: Postdoctoral Fellow, Johns Hopkins University School of Medicine (50%) and Russian Academy of Sciences (50%); visiting graduate student, Fox Chase Cancer Center (2000 – 2005).
- 2001 - 2004 Ghislain Bidaut: Team Leader (tenured), Integrative Bioinformatics, Institut Paoli-Calmettes, INSERM, Marseille; postdoctoral associate 2007 with Benno Schwikowski, Pasteur Institute; postdoctoral associate 2004-2007 with Chris Stoeckert, University of Pennsylvania; predoctoral trainee 2001-2004, completed Ph.D. work in Bioinformatics at Fox Chase Cancer Center in December, 2004 in collaboration with Jean-Michel Claverie, CNRS-Marseille; received Ph.D. with highest honors from the Faculté des Sciences de Luminy, Marseille, France.
- 2003 - 2007 Andrew Kossenkov: presently postdoctoral associate with Louise Showe, Wistar Institute; predoctoral trainee 2003-2007, completed Ph.D. work in Bioinformatics at Fox Chase in March, 2007 in collaboration with Aydin Tozeren, Drexel University; predoctoral trainee, 2003, completed M.S. work in Bioinformatics at Fox Chase Cancer Center in collaboration with Eugene Korotkov, Russian Academy of Sciences; received M.S. from Moscow Engineering Physics Institute in January, 2004.
- 2003-2004 Aidan Peterson: presently postdoctoral associate with Michael O'Connor, HHMI/University of Minnesota; postdoctoral associate in Bioinformatics at Fox Chase 2003-2004.
- 2002 Vladimir Minayev: predoctoral trainee, 2003, completed M.S. work in Bioinformatics at Fox Chase in collaboration with Eugene Korotkov, Russian Academy of Sciences; received M.S. from Moscow Engineering Physics Institute in June, 2004; presently a predoctoral trainee at the Moscow Engineering Physics Institute.
- 2005 - 2006 Yan Zhou: presently a research associate in Immunology and Bioinformatics at Fox Chase Cancer Center
- 2005-2006 Guoli Wang: presently a research associate in Structural Biology at Fox Chase Cancer Center; research associate in bioinformatics, 2005-2006

ORGANIZATIONAL ACTIVITIES

Institutional Administrative Appointments

2009- Director, Sidney Kimmel Comprehensive Cancer Center Bioinformatics Shared Resource

Other Appointments/Responsibilities

2009- Joint Appointment, Associate Professor, Department of Health Science Informatics, School of Medicine

SKCC Administrative Committees

2011- Commonwealth Foundation Committee
2011- Research Information Technology Services (RITS) Core Prioritization Committee
2012 Personalized Medicine Working Group

Editorial Activities

2002 Guest Editor, Bio Techniques
2004 Editorial Board, Cancer Informatics
2005-2006 Editor, Methods in Molecular Biology: Gene Function Analysis
2008-2009 Editor, Biomedical Informatics for Cancer Research, Springer
2009-2012 Associate Editor, BMC Bioinformatics
2011 – 2012 Associate Editor, Frontiers in Bioinformatics and Computational Biology
2011 – 2012 Editorial Board, Chemotherapy: Open Access
2012 – 2013 Editor, Methods in Molecular Biology: Gene Function Analysis, 2nd Ed.
2012 – 2013 Editor-in-Chief, Chemotherapy-Open Access

Journal Peer Reviewer Activities

2001 Reviewer, BioTechniques
2001 Reviewer, Kluwer Scientific
2001 Reviewer, Cancer Research
2002 Reviewer, Bioinformatics
2003 Reviewer, Journal of VLSI Signal Processing
2003 Reviewer, Molecular Cancer Therapeutics
2003 Reviewer, Journal of Biotechnology
2003 Reviewer, Clinical Cancer Research
2003 Reviewer, Journal of the American Statistical Association
2003- Reviewer, BMC Bioinformatics
2003- Reviewer, Bioinformatics
2004 Reviewer, Journal of Bioinformatics and Computational Biology
2004 Reviewer, Proceedings of the National Academy of Sciences
2004- Reviewer, BMC Bioinformatics

2005	Reviewer, Trends in Biotechnology
2005	Reviewer, Nucleic Acids Research
2005	Reviewer, Journal of Biomedical Informatics
2005	Reviewer, Magnetic Resonance in Medicine
2005	Reviewer, American Medical Informatics Association
2005	Reviewer, BMC Biotechnology
2005	Reviewer, Interface, Journal of the Royal Statistical Society
2006	Reviewer, Physiological Genomics
2007	Reviewer, MedInfo2007
2009	Reviewer, Biometrics
2009	Reviewer, Lung Cancer
2009	Reviewer, Nature Methods
2009	Reviewer, Cancer Research
2010	Reviewer, Nature
2010	Reviewer, Nature Immunology

Advisory committees, Review Groups, Study Sections

2000	Bioinformatics Postdoctoral Training Program, Member
2000-2001	Department of Defense Breast Cancer Training Program, Member
2001	Scientific Steering Committee, Critical Assessment of Microarray Data Analysis Conference, Member
2005	City of Hope Information Management Strategic Plan, External Reviewer

Peer Review Study Sections

2002	Ad hoc Reviewer, NIH/NCI GRB(O3), Basic and Preclinical Study Section
2003	Ad hoc Reviewer, NIAID Bioinformatics Resource Centers for Biodefense and Emerging/Re-emerging Infectious Disease
2003-	Reviewer, Philip Morris External Research Program
2004	Ad hoc Reviewer, NIAID Genomics of Human Transplantation
2004	Ad hoc Reviewer, NCI Special Emphasis Panel, NCI-C RPRB (G1)
2004	Ad hoc Reviewer, NCI Hematological Oncology 1
2004	Ad hoc Reviewer, CCSG Oregon Health Sciences University
2004	Ad hoc Reviewer, NIDDK Proteomic and Metabolomic Approaches to Diagnose Diabetes and Pre-Diabetes
2004	Ad hoc Reviewer, NCI Subcommittee A, Cancer Center Support Grant
2005	Ad hoc Reviewer, Louisiana Board of Regents Grant Program
2005	Ad hoc Reviewer, CCSG USC/Norris Cancer Center
2005 - 2006	Ad hoc Reviewer, NIH ZRG1 Shared Instrumentation Grant
2005 - 2006	Ad hoc Reviewer, NLM ZLM1 Special Emphasis Panel
2006	Ad hoc Reviewer, NIAID Special Emphasis Panel
2006	Ad hoc Reviewer, CCSG Moffitt Cancer Center
2006	Ad hoc Reviewer, MABS Study Section

Curriculum Vitae	16	Michael F. Ochs
2007	Ad hoc Reviewer, NIH Metabolomics Special Emphasis Panel	
2007	Ad hoc Reviewer, NCI Molecular Oncology P01 Panel	
2007	Ad hoc Reviewer, NLM ZLM1 Special Emphasis Panel	
2007 - 2009	Ad hoc Reviewer, NIH GCAT Study Section	
2009	Ad hoc Reviewer, NLM EUREKA Special Emphasis Panel	
2010	Ad hoc Reviewer, NCI Nanotechnology Special Emphasis Panel	
2010	Ad hoc Reviewer, National Centers for Biomedical Computing SEP2010	
2010	Ad hoc Reviewer, ARRA RC4 Genomics Grants	
2010	Ad hoc Reviewer, ZRG1 OTC-LCDDT SBIR/STTR Panel	
2010	Ad hoc Reviewer, CCSG OHSU Knight Cancer Center	
2011	Ad hoc Reviewer, NIH SBIR Cancer Development and Therapeutics	
2012	Ad hoc Reviewer, NIH AREA Grant Study Section	

Professional Societies (National and International)

2000 -	Institute of Electronics and Electrical Engineers (IEEE), Member
2006 -	Eastern North American Region, International Biometric Society
2007 -	International Society for Computational Biology (ISCB)

Conference Organizer, Symposia, Session Chair

2003	Greater Philadelphia Bioinformatics Alliance Short Course on Microarray Data Analysis, Lecturer
2004	APIII 9 th International Conference, Conference Organizer
2005	NCI Proteomic Technologies Informatics Workshop, Attendee
2008-2009	Knowledge Driven Data Analysis and Integration, Pacific Symposium on Biocomputing, Originator and Co-Chair
2008-	Biological Databases, Johns Hopkins School of Public Health, Instructor
2008 – 2012	Program Committee, Annual IEEE Conference on Bioinformatics and Biomedicine
2009	Medical Informatics and Translational Bioinformatics 3 rd Annual IEEE Conference on Bioinformatics and Biomedicine, Program Vice-Chair
2011	Identification of Aberrant Pathway and Network Activity from High-Throughput Data, Pacific Symposium on Biocomputing, Workshop Co-Chair
2012	Identification of Aberrant Pathway and Network Activity from High-Throughput Data, Pacific Symposium on Biocomputing, Co-Chair

- 2012 IEEE Conference on Bioinformatics and Biomedicine, Session Chair
- 2013 Identification of Aberrant Pathway and Network Activity from High-Throughput Data, Pacific Symposium on Biocomputing, Co-Chair
- 2013 World Biotechnology Conference, Track Chair Medical Biotechnology

RECOGNITION

Awards Honors

- 1978 - 1982 Tektronix Fellow
- 1978 - 1982 National Merit Scholar
- 1982 Elected Member of Phi Beta Kappa
- 1982 B.A. received cum laude: Chemistry Departmental Honors
- 1990 - 1993 Air Force Laboratory Graduate Fellow
- 2004 Medical Informatics MBL/NLM Course Fellow
- 2012 IEEE Bioinformatics and Biomedicine Annual Meeting, Best Paper Award

Invited Seminars

- 10/2001 Critical Assessment of Microarray Data Analysis Second Annual Conference
- 03/2002 ENAR Meeting, International Biometrics Society
- 05/2002 Basic Research Institutions Information Technology Exchange Conference
- 05/2002 Mediterranean Agronomic Institution of China
- 08/2002 NCI Applications of Bioinformatics in Cancer Detection Workshop
- 11/2002 Critical Assessment of Microarray Data Analysis Third Annual Conference, Duke University
- 12/2002 Basic Research Institutions Information Technology Exchange Conference
- 05/2003 10th Annual Hewitt Symposium, University of Connecticut
- 07/2003 6th International Engelhardt conference of the Russian Academy of Science
- 10/2003 Institute for Mathematics and its Applications Workshop
- 10/2004 APIII 9TH International Conference

12/2004 American Statistical Association, New York Chapter

01/2005 2nd International IMS/ISBA Joint Meeting

04/2005 Thomas Jefferson University Computational Biology Seminar

04/2005 caBIG 2nd Annual Meeting Plenary Session

04/2005 Nebraska EPSCoR Expo, Bioinformatics Tract

07/2005 Moscow Conference on Computational Molecular Biology

10/2005 Greater Philadelphia Bioinformatics Alliance Retreat

10/2005 American Medical Informatics Association Annual Meeting Semi-Plenary

06/2006 Second Scientific Meeting of the Metabolomics Society, Informatics Workshop

05/2007 39th Symposium on the Interface: Computing Science and Statistics

06/2007 Department of Health Science Informatics, Johns Hopkins University

08/2007 University of Technology, Sydney, Australia

08/2007 Telethon Institute for Child Health Research, Perth, Australia

02/2008 Lombardi Cancer Center, Georgetown University

04/2008 Rutgers University

09/2009 CRC-Marseille, INSERM, Marseille, France

09/2010 West Virginia University

04/2011 Dana Farber Cancer Institute, Harvard University

08/2011 Gordon Research Conference: Mechanisms of Cell Signaling

11/2011 Lupin Pharmaceuticals, Pune, India

02/2012 Metabolomics and Systems Biology Conference, San Francisco

05/2012 FDA Office of Applied Research and Safety Assessment, Laurel, MD

10/2012 IEEE Annual Conference on Bioinformatics and Biomedicine, Philadelphia

10/2012 Association of Molecular Pathology, Industry Seminar: micro-RNA Assays in Clinical Oncology, Long Beach, CA

Conference Presentations

- 05/1992 Milliarcescond polarization structure of the quasars 3C273 and 3C345, American Astronomical Society Annual Meeting
- 03/1998 Spectral decomposition by Bayesian methods, Experimental Nuclear Magnetic Resonance Conference
- 07/1999 Pattern recognition in gene expression data using a novel Bayesian approach, 2nd International Engelhardt Conference on Molecular Biology
- 08/1999 A Bayesian Markov chain Monte carlo solution of the bilinear problem, Bayesian Inference and Maximum Entropy Methods in Science and Engineering 19th International Workshop
- 04/2000 CSImage: an extensible and flexible Java tool for data visualization, Visual Development Environments 2000
- 03/2001 Gene Expression Analysis: discovering multiple pathways and encoding prior information, 3rd International Meeting on Microarray Data Standards Annotations, Ontologies, and Databases
- 08/2001 Encoding biological prior information into gene expression analysis, Bioinformatics Gordon Research Conference
- 10/2001 Bayesian Decomposition applied to microarray data, Critical Assessment of Microarray Data Analysis Second Annual Conference
- 02/2002 Waveread: automatic measurement of relative gene expression levels from microarrays using wavelet analysis, 3rd International Meeting on Microarray Data Standards, Annotations, Ontologies and Databases
- 03/2002 Encoding biological prior information into gene expression analysis, Transcriptome 2002
- 03/2002 Gene expression analysis using a Bayesian method which encodes biological prior information, ENAR 2002 Meeting of the International Biometric Society

- 05/2002 A data pipeline for functional genomics, Cold Spring Harbor Genome Sequencing and Biology 2002
- 07/2002 MCMC method for identification of allelic pattern in data with quantitatively describable phenotypic features, 3rd International Conference on Bioinformatics of Genome Regulation and Structure
- 08/2003 Analysis of phylogenetic profiles using Bayesian Decomposition, 2003 IEEE Computer Society Bioinformatics Conference
- 08/2003 A laboratory information management system for flow cytometry, 2003 IEEE Computer Society Bioinformatics Conference
- 08/2003 Leveraging biological knowledge in the analysis of functional genomics data, 2003 Gordon Conference on Bioinformatics
- 11/2003 Retrieving Bacterial Functional Units by Bayesian Decomposition Analysis of Phylogenetic Profiles, BISTI Symposium, Digital Biology: The Emerging Paradigm
- 11/2003 Bayesian Decomposition classification analysis of the CAMDA2003 data set, Critical Assessment of Microarray Data Analysis, 4th Annual Conference
- 11/2003 Applying multiple clustering techniques to adenocarcinoma data, Critical Assessment of Microarray Data Analysis, 4th Annual Conference
- 11/2003 ClutrFree: Cluster tree visualization and interpretation, Critical Assessment of Microarray Data Analysis, 4th Annual Conference
- 04/2004 Identification of Gene Groups Linked to Biological Functions in Pathogenic Bacteria, Keystone Meeting: Biological Discovery Using Diverse High-Throughput Data
- 09/2004 A Unified Laboratory Information Management System for Research Data, MedInfo 2004
- 10/2004 Identification of Signaling Pathways from Microarray Data, Greater Philadelphia Bioinformatics Alliance Retreat
- 11/2004 Linking Gene Expression Patterns and Transcriptional Regulation in *Plasmodium falciparum*, Critical Assessment of Microarray Data Analysis, 5th Annual Conference
- 04/2005 Defining and Characterizing Early B Lineage Cell Fractions in Mouse Bone Marrow, Keystone Conference on B Cell Development, Function and Disease

- 11/2005 LSNMF: A modified non-negative matrix factorisation algorithm with uncertainty measurements, Greater Philadelphia Bioinformatics Alliance Retreat
- 10/2006 Estimating Targeting of Signaling Inhibitors using Probabilistic Boolean Networks and Transcriptional Data, Society for Medical Decision Making 2006 Annual Meeting
- 11/2006 Proteomics LIMS: a caBIG™ Project, Year 1, Annual Symposium, American Medical Informatics Association
- 03/2007 Probabilistic Boolean Network Models for Estimating Signaling Activity, Cold Spring Harbor Computational Cell Biology Meeting
- 08/2008 Detecting Signaling Network Modification during Therapy, Gordon Research Conference: Cancer Models and Mechanisms
- 04/2009 Gene expression signatures and response to imatinib mesylate in gastrointestinal stromal tumor, AACR Annual Meeting
- 08/2009 Detection of Treatment-Induced Changes in Signaling Pathways using Transcriptomic Data, Gordon Research Conference: Mechanisms of Cell Signaling
- 11/2009 Biomarkers of Cell Signaling in Cancer, IEEE BIBM 2009
- 01/2011 Inferring coordinated gene activity in pattern sets. Pacific Symposium on Biocomputing
- 01/2011 Hybrid stochastic modeling of phenotypic decisions by cell signaling and transcriptional reprogramming. Gordon Conference on Stochastic Physics in Biology
- 04/2010 Identification of novel epigenetically silenced genes by a global reactivation screen of prostate cancer, AACR Annual Meeting
- 04/2011 5-Aza-2'-deoxycytidine and cytarabine mediate distinct effects on clonogenic growth, genome wide methylation and RNA expression in AML, AACR Annual Meeting
- 08/2011 Improved Inference of Signaling Activity through Genomic and Epigenetic Data Integration, Gordon Research Conference: Mechanisms of Cell Signaling
- 10/2011 Predicting cellular fate decisions in *C. elegans* by integrating a graphical model of cellsignaling with a continuous model of transcriptional reprogramming, ASCMB

Conference: Chemical, Synthetic And Systems Biology: New Directions Of Biochemistry

- 01/2012 Identifying context-specific transcription factor targets from prior knowledge and gene expression data. Cold Spring Harbor Meeting on Systems Biology: Global regulation of gene expression
- 02/2012 Integration of epigenomic and genomic data elucidates pathways in head and neck squamous cell carcinoma, Metabolomics and Systems Biology Conference
- 04/2012 Integrative analysis of epigenetic and transcriptional alterations in head and neck squamous cell carcinomas, AACR Annual Meeting
- 04/2012 Smad4 inactivation correlates with EMT and cetuximab resistance in head and neck squamous cell carcinoma, AACR Annual Meeting
- 05/2012 Matrix Factorization for Transcriptional Regulatory Network Inference, IEEE Conference on Computational Intelligence in Bioinformatics and Computational Biology
- 10/2012 Fundamental patterns of gene expression in the developing human brain, Society of Neuroscience Nanosymposium
- 10/2012 MicroRNAs in Early Detection of Lung Cancer, AMP Workshop: MicroRNAs in Clinical Oncology