

CURRICULUM VITAE
Jan.2020
Dr. Jennifer Walsh Weller

Current Position

Associate Professor
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Dept. of Bioinformatics and Genomics
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Professional experience:

- *June 2007-present.* Associate Professor in the Bioinformatics and Genomics department, as well as member of the Bioinformatics Research Center, at UNC-Charlotte.
 - My research and teaching are focused on the design, generation and analysis of genomic and gene expression data from high-throughput platforms, both microarrays and sequencing. Specifically, I am interested in understanding and controlling sources of technical variation in the data by understanding biophysical behavior that affects microarray and NGS sequence assay performance exclusive of the genetic differences.
 - To enhance the utility of our data I have also conducted research into the storage, organization, and integration of multiple data types (genetic, phenotypic, environmental, clinical etc.) in biological databases.
 - I have applied much of my research to molecular marker/biomarker discovery.
 - A special project included bringing the BSL3 lab up to standard for certification, including outfitting the lab, testing its function and writing the required manuals and other documentation.
 - I have been recognized as a professional development mentor, partly through outreach at UNCC and NSF thanks to a varied professional background and partly through work with the ADVANCE program, again through engagement at NSF and UNCC. This year that outreach has included seminars for the Biology Department at UNCC, at NC A&T, at Duke University and at The Ohio State University (in March).
- *Aug 2015 – Aug 2019.* Program Officer at the National Science Foundation, as an IPA on leave of absence from UNC Charlotte.
 - My primary responsibilities were for the Advances in Biological Informatics program (bioinformatics and computational biology applications in the Innovation, Development and Sustaining tracks).

- I was a Working Group member for the ADVANCE, GRFP, PRFG, BigData, Rules of Life and other cross-directorate and cross-division co-funding initiatives, as well as interagency working groups.
- Outreach activities were extensive and included Tribal Colleges and Universities as well as HBCUs and MSIs– they are listed at the end of this document with Seminars.
- DBI was been concerned with guiding Development Track proposals towards better management practices, as they affect large communities, so I had extensive Project Management the goal of developing best practice guidelines and templates for the research community.
- Because of the programmatic changes that we introduced I participated extensive in outreach activities to both small colleges and Universities (seminars and one-on-one meetings) and as an invited speaker at professional society meetings (PAG, ISMB, RECOMB).
- The budget for which I shared management responsibility was \$30M USD per year.

Previous

Academic

- *June 2002 – May 2007*. Associate Professor in the School of Computational Science, and Bioinformatics and Computational Biology department, at George Mason University at the Prince William campus in Manassas VA.

Government

- *May 2002-June 2003*. Scientific Advisor and Director of Bioinformatics for the Epidemic Outbreak Surveillance project funded by the USAF/SGX. The project is described briefly below.
 - The EOS project designed and carried out prototype testing of a microarray to monitor the outbreak of several respiratory infections, including adenovirus and influenza virus causative agents, among basic military trainees. The study used standard clinical assessment, antibody, PCR and custom Affymetrix GeneChip™ platforms to establish the cause of illness.

Academic

- *September 2000- May 2002*. Research Assistant Professor at the Virginia Bioinformatics Institute at Virginia Tech University.
 - At the time I joined, this institute was being initiated so it was ‘virtual’. My primary roles were to
 - Oversee the design of the experimental laboratories with the team of 12 architects
 - Design core capabilities and hire personnel for the Core Genomics Laboratory (of which I was interim Director),
 - Recruit faculty and support personnel for the institute
 - Work with other new faculty to initiate programs and obtain funding. Six grants in which I played a major creative and writing role were funded in the first 18 months.
 - I also had a position as adjunct assistant professor in the Biology Department (desirable in order to meet collaborators and students).

- I was primary author and PI of an NSF grant for the ‘OpenGeneX’ project, awarded by the NSF in May 2002, which transferred to GMU with me

NFP

- *June 1999-August 2000.* Senior Research Scientist in the molecular genetics group at NCGR, the National Center for Genome Resources, in Santa Fe, NM,
 - Promoted in August, 1999 to Program Leader for Structural Genomics,
 - Acted as interim program leader for Gene Expression and then promoted to group leader of the Gene Expression group in February 2000.
 - The projects I managed included a large EST pipeline and analysis project for the SR Noble Foundation (‘MGI’ and ‘XGI’), and the internally-funded project for a gene expression information system (‘GeneX’).
 - I was primary author and PI on an NSF grant for the Gene Expression development, which was awarded in October of 2000 (transferred to NCGR at their request).
 - I oversaw one PhD student from the University of New Mexico, Peter Hraber, who successfully defended his thesis in May 2001.

Industry

- *1997-1999* Senior Research Scientist at PE GenScope, a Center of Excellence of PE Biosystems that had merged with Applied Biosystems, a developer of high-throughput sequencing technology.
 - The PE Genscope group provided transcript imaging data to the pharmaceutical industry, and molecular marker development and testing to a variety of entities including animal breeding data to the AKC.
 - Scientific duties included establishment of PCR protocols to meet standards of reproducibility for the cDNA-AFLP technology; protocol development for production of the samples for bulk cloning in a sequencing project that provided baseline sequence data and SNP information for rat, mouse and human tissues.
 - A major accomplishment was the production of 30,000 gene tags for the rat genome in six months, giving GenScope the largest such data-base in the world at that time.
 - Laboratory management duties included training of technical associates, maintaining day-to-day operations of the molecular biology laboratory, and maintenance of database entry, editing and updating for the sequencing project.
 - Production team duties included improving the sequencing project technology sufficiently to save half of the budgeted cost in two months; cutting the time to project completion by one-third, establishing ISO9000 accountability and GLP and GMP standards within our operating unit; writing SOPs, and working with software engineers to describe and implement sample handling, data flow and data processing and report production requirements into the LIMS and proprietary data analysis programs PE GenScope produced.

In January 1999 PE GenScope became part of Celera Applied Genomics, headed by Dr. Craig Venter.

- *1994-1997* Research Scientist at Perkin-Elmer/Applied Biosystems Division- Agricultural Applications Group in Foster City CA.

- Primary research and development duties were to convert the PCR-based molecular genetic markers called AFLPs from a manual, radioactive detection mode to a fluorescence-based automated system.
 - I provided support for data analysis in the technical manual in the form of tutorials.
 - Several extensive collaborations were undertaken, and data exchange managed, to demonstrate the utility of the technology. One such joint project was the generation of an *Arabidopsis thaliana* map having 1000 markers, of which I provided half.
 - A strong customer education component was a responsibility of the job, including providing research communications, giving scientific seminars, giving presentations at meetings, designing the training course for the Applications Specialists and the training of telephone support personnel to give knowledgeable and accurate help to customers. I was the sole R & D scientist involved in this effort.

Teaching

Graduate Courses Taught at UNCC

BINF 6211/8211* Design and Implementation of Bioinformatics Databases
 BINF 6350/ITSC8350* Genomic Biotechnology Laboratory

* Each has been offered annually from 2007-2020, both were developed and taught by me except while I was at the NSF.

Graduate Courses Taught at GMU

BINF 633 Molecular Biotechnology and Bioinformatics Tools*
 BINF 636 Microarray Design and Analysis
 BINF 637 DNA Forensics*
 BINF 702 Research Methods (Biostatistics)
 BINF 704 Graduate Research Colloquium
 BINF 705 Research Ethics
 BINF 733 Microarray Data Analysis
 BINF 739 Databases for Bioinformatics (now BINF650)

* Graduate courses also taught as Visiting Scientist at Korea University, Seoul, Korea Summer 2006.

Outreach Teaching/Training:

- From 2009-2017 I taught a summer science camp for high school students at Olympic High School in the CMS district with two teachers from the school (Ms. Jeanne Smith and Ms. Erica Putnam). From 2014-2017 we had funding from the Burroughs-Wellcome Education Fund.
 - We focused on purifying DNA and generating molecular markers or chloroplast sequence data from the American Chestnut samples for the first 5 years.
 - We expanded to include some bioinformatics lessons in the last two years, and included Illumina sequencing the last year.

Academic Training

Research

- 1990-1994 Postdoctoral Research Associate, MSU-DOE Plant Research Labs, Michigan State University and The Carnegie Institute for Plant Biology at Stanford University with Dr. Shauna Somerville. Two projects were initiated. The first was to generate subtractive cDNA and genomic libraries from near-isogenic barley lines that are resistant/susceptible to the powdery mildew disease, *Erysiphe graminis* f. sp. *hordei*, as a strategy for isolating the gene for resistance at the MI-a locus, using the RDA technology. The second project was the genetic and physical mapping of the MI-a locus using DNA fragment polymorphisms generated using random 10-mers as primers in the PCR reaction (RAPD or DAF markers).

Teaching

- 1987-1988 Instructor of Biochemistry, University of Montana. Courses taught:
 - Biochemistry 382
 - Biochemistry Lab 485,486,490
 - Biochemistry 483

Research

- 1986-1989. Graduate student in the laboratory of Dr. Walter E. Hill at the University of Montana. Research involved probing the detailed structure of specific regions of 16S rRNA *in situ* in the 30S ribosomal subunit of *E.coli*, using cDNA oligomers. Regions of interest were then tested for various functional activities in the presence and absence of the cDNA oligomers.
- 1979-1982. Graduate student in the laboratory of Dr. Kensal van Holde at Oregon State University. Structural changes occurring in chromatin during gene expression were investigated. Metabolically manipulatable genes in *Saccharomyces cerevisiae* allowed specific induction and repression of targeted genes.
- August 1979- September 1979. Graduate student with Dr. Barbara Hamkalo during the Woods Hole MBL Physiology post-course. Oocytes of the surf clam, *Spissula solidissima* were spread on em grids; areas active in transcription during early development were studied.
- 1976-1979 Undergraduate research assistant in the laboratory of Dr. Walter E. Hill at the University of Montana. Research involved physical studies of the 30S subunit of the *E. coli* ribosome, with and without the protein S1.

Educational Training:

B.Sc. Chemistry, 1979 - University of Montana

Marine Biological Laboratories Physiology Course, Woods Hole, MA. 1979

Cold Spring Harbor Laboratory Yeast Genetics Course, Cold Spring Harbor, New York. 1980

M.Sc. Biochemistry and Molecular Genetics - Oregon State University (1979-1982, degree awarded 1986)

Ph.D. Biochemistry - University of Montana, April, 1990

Postdoctoral experience- with Dr. Shauna Somerville at two institutions:

DOE-Plant Research Laboratories	The Carnegie Institute for Plant Biology
Plant Biology Building	290 Panama St.
Michigan State University	Stanford University
East Lansing, MI 48824 USA	Stanford CA 94305 USA
Telephone: (517)-353-9182	Telephone: 415-325-1521

Honors and Awards:

UM Regents Scholarship (1976-1977)

UM Honors Scholarship (1977-1978)

Hetler Memorial Award (1978)

Watkins-Morton Scholar (1978-1979)

Awardee on MBL Physiology Training Grant (1979)

ASM Presidents Fellowship (1981)

Bertha Morton Scholar (1987-1988)

Bertha Morton Scholar (1988-1989)

Fuson Award (1988)

ACS Divisional Award for outstanding student presentation at a meeting (1988).

Touchstone Award for the Northern California Technical Communication Competition (1997)

PE SPOT Award (1998) for technical contributions

NCGR Sustained Achievement Award (Mar. 2000)

Adjunct Professor of Biology at the University of New Mexico (Feb. 2000)

Adjunct Professor of Biology at Virginia Tech (March 2001)

Adjunct Professor of Bioinformatics and Computational Biology at GMU (2007, 2010)

Tenure at Rank (2012) University of North Carolina Charlotte

Graduate Teaching Award in the College of Computing and Informatics at UNCC (2015)

Membership in Professional Societies:

The American Society for Microbiology (ASM)

The International Society of Computational Biologists (ISCB/ISMB)

Association for Biosafety and Biosecurity (ABSA)

Board Member of the Functional Genomics Data (FGED) Society (elected 2012, reappointed in 2013, resigned 2013 to avoid COI with PIs applying to the NSF)

General Research Interests:

The biophysical properties of molecules, particularly shape, that affects measurements and function in both in vitro and in vivo roles. More specifically I study the interaction of biophysical characteristics of nucleic acids on molecular biology procedures and assays, and how that affects the interpretation of measurements and subsequent bioinformatics analyses. I have studied how these properties affect our interpretation of gene expression and regulation, primarily at the transcriptional level. I have participated in research teams examining ovarian cancer and ALS in humans. I continue to be interested in the application of molecular genetic markers in large or previously unmapped genomes for population, breeding and forensics applications. I have pursued a relationship with the American Chestnut Foundation and Dr. Paul Sisco, their geneticist, to map several blight-resistant crosses planted in North Carolina. I have worked on the development of databases and tools that allow the tracking, merging and multi-component analysis of biological and genetic information.

Publications

Articles in reviewed journals or proceedings:

1. Davie, J.R., Saunders, C.A., Walsh, J.M., and Weber, S., "Histone acetylation in the yeast, *S. cerevisiae*", *Nucleic Acids Research*, 9, 3205-3215 (1981).
2. Weller, R., Weller, J.W., and Ward, D.M. "16S rRNA Sequences Retrieved As Randomly Primed cDNA from a Hot Spring Cyanobacterial Mat Community", *Applied and Environmental Microbiology*, 57, 1146-1151 (1991).
3. Weller, J. and Hill, W.E. "Probing the initiation complex formation on *E. coli* ribosomes using short complementary DNA oligomers". *Biochimie*.73(7-8):971-81 (1991).
4. Weller, J.W. and Hill, W.E. "Using Complementary Oligodeoxyribonucleotides to 16S rRNA as Probes of Dynamic Changes in rRNA Conformation in the 30S Subunit of the *E. coli* Ribosome". *Biochemistry*, 31, 2748-2757 (1992).
5. Weller, J.W. and Hill, W.E., "The Structure of the Decoding Region of 16S rRNA in situ as Determined With Hexameric cDNAs". *Journal of Biological Chemistry*, 269 (30), 19369-19374 (1994).
6. DeCenzo, R., Engel, S.R., Gomez, G., Jackson, E., Munkvold, G., Weller, J., and Irelan, N. "Analysis of genetic diversity in *Eutypa lata* from California grape production regions using fluorescent AFLP and rDNA ITS sequence data. *Phytopath.* 89(10),884-893 (1999).
7. Iyoda S, Wada A, Weller J, Flood SJ, Schreiber E, Tucker B, Watanabe H. "Evaluation of AFLP, a high-resolution DNA fingerprinting method, as a tool for molecular subtyping of enterohemorrhagic *Escherichia coli* O157:H7 isolates". *Microbiol Immunol.* 1999;43(8):803-6.
8. Zhao S, Mitchell SE, Meng J, Kresovich S, Doyle MP, Dean RE, Casa AM, Weller JW. "Genomic typing of *Escherichia coli* O157:H7 by semi-automated fluorescent AFLP analysis". *Microbes Infect.* 2000 Feb;2(2):107-13.
9. Waugh, M., Hraber, P., Weller, J.W., Inman, J., Farmer, A. Sobrall, B.W. "The *Phytophthora* Genome Initiative" NAR Database Issue, 2000.

10. Harger, C., Chen, G., Farmer, A., Huang, W., Inman, J., Kiphart, D., Schilkey, F., Skupski, M.P., Weller, J. (2000). The genome sequence database. *Nucleic Acids Research* **28**, 31-32.
11. Bell, C.J., Dixon, R.A., Farmer, A.D., Flores, R., Inman, J., Gonzales, R.A., Harrison, M.J., Paiva, N.L., Scott, A.D., Weller, J.W. and May, G.D. (2001). The *Medicago* genome initiative: a model legume database. *Nucleic Acids Research*, 29(1): 114-117.
12. Inman, J.T., Flores, H.R., May, G.D., Weller, J.W., and Bell, C.J. (2001) "A High-Throughput Distributed DNA Sequence Analysis and Database System" *IBM Systems Journal*, 40(2) 464-486.
13. Mangalam, H., Stewart, J., Zhou, J., Schlauch, K., Waugh, M., Chen, G., Farmer, A., Colello, G., Weller, J. "GeneX: An Open Source gene expression database and integrated tool set" *IBM Systems Journal*, 40(2) 552-569.
14. Hraber, P.T. and Weller, J.W. "On the species of origin: diagnosing the source of symbiotic transcripts" *Genome Biology* 2001: 2(9) 37.1-37.13.
15. Gibas C.J., Sturgill D.M., Weller, J.W. *GenoMosaic: On-Demand Multiple Genome Comparison and Comparative Annotation*. 2003. In *Proceedings of the Third IEEE Symposium on BioInformatics and BioEngineering*, IEEE Press: 158-167.
16. Lee, J.K., Laudeman, T., Kanter, J., James, T., Siadaty, M.S., Knaus, W.A., Prorok, A., Bao, Y., Freeman, B., Puiu, D., Wen, L., Buck, G.A., Schlauch, K., Weller, J., Mangalam, H.J., Fox, J.W. "GeneX Va: VBC Open Source Microarray Database and Analysis Software for Multiple Users in Biomedical Research" *Benchmarks, Biotechniques*. 2004 Apr;36(4):634-8, 640, 642..
17. Mao, C., Cushman, J.C., May, G.D., Weller, J.W. "ESTAP – an automated system for the analysis of EST data" *Bioinformatics* (2003) 19: 1720-1722.
18. Ratushna, V., Weller, J., Gibas, C. "Secondary structure as a confounding factor in synthetic oligomer microarray design" *BMC Genomics*(2005) 6:31.
19. Higgs, B., J. Weller, et al. (2005). "On Spectral Embedding for Extraction of Structure in Biological Data". *Joint Statistical Meeting 2005 - Using Our Discipline to Enhance Human Welfare*, Minneapolis, Minnesota, ASA.
20. Higgs, B., J. Weller, et al. (2005). "Deriving Meaningful Structure from Spectral Embeddings and Clustering." *Interface 2005: Classification and Clustering 37th Symposium on the Interface*, St. Louis, Mo., Interface Foundation of North America.
21. Higgs BW., Solka JL., Weller J. (2005) Deriving Meaningful Biological Structure from Spectral Embedding and Clustering. *Computing Science and Statistics*. 37.
22. Higgs, B.W., Weller, J.W. and Solka, J.L. (2006) "Spectral Embedding Finds Meaningful (Relevant) Structure in Image and Microarray Data" *BMC Bioinformatics* **7**:74.
23. Overall, CC, Solka, JL, Weller, JW, Priebe, CE "Anomaly Detection in Genetic Networks." *Joint Statistical Meeting (JSM)*. Seattle, WA, August 6-10, 2006.
24. Overall, CC, Solka, JL, Weller, JW, Priebe, CE. "Using Scan Statistics for Anomaly Detection in Genetic Networks." *Classification Society of North America (CSNA)*. Rutgers, NJ, May 10-13, 2006.
25. Overall, CC, Solka, JL, Priebe, CE, Weller, JW, Using Scan Statistics for Anomaly Detection in Genetic Regulatory Networks. *Quantitative Methods in Defense and National Security (QMDNS)*. Fairfax, VA, February 7-8, 2007.
26. Kumari, S., Verma, L., and Weller, J, "AffyMAPSDetector: A Tool To Detect SNPs In Affymetrix GeneChip™ Expression Arrays" *BMC Bioinformatics* **8**:276.

27. Taylor, R.C., Singhal, M., Weller, J., Khoshnevis, S., Shi, L., McDermott, J. (2009) A Network Inference Workflow Reveals Functional Groups, Metabolic Pathways, and Regulons in *Salmonella typhimurium*. *Annals of the NY Academy of Science, Proceedings of the DREAM 2 conference*.1158:143-58.
28. Thompson, K.T., Deshmukh, H., Solka, J.L., Weller, J.W. (2010) “A Whitebox Approach to Microarray Probe response Characterization: the BaFL Pipeline” *BMC Bioinformatics* 10:449.
29. Gharaibeh, R.Z., Newton, J.M., Weller, J.W., Gibas, C.J. (2010)” Application of Equilibrium Models of Solution Hybridization to Microarray Design and Analysis” *PLoS ONE*: doi:10.1371/journal.pone.0011048.
30. Paszko, C. and Weller, J.W. (2011) “Computerized LIMS” *The European Pharmaceutical Contactor (EPC magazine)*, Spring 2011 pp 64-67 (invited).
31. Overall, C.C., Carr, D.A., Tabari, E.S., Thompson, K.J., Weller, J.W. (2011) “ArrayInitiative – a tool that simplified creating custom Affymetrix CDFs” *BMC Bioinformatics*.
32. Baciu C, Thompson KT, Mougeot JL, Brooks BR, Weller JW (2012) “The LO-BaFL method and ALS microarray expression analysis” *BMC Bioinformatics* 13:244.
33. Tickle, TL, and Weller, JW (2012) “Serous ovarian benign tumor and type II carcinoma data set for expression and paracrine signaling investigation” Major Revision
34. Thompson, KJ, and Weller, JW (2012) “Characterizing Normal Epithelial Transcript Signatures using Microarray Meta-Analysis”.
35. Review Paper with Purdue on Resilience submitted Dec 2019
36. MinSEQE paper with FGED group - final revision accepted

Book Chapters, Invited articles

Hill, W.E., Weller, J.W., Gluick, T., Merryman, C., Marconi, R.T., Tassanakajohn, A., Tapprich, W.E., “Probing Ribosome Structure and Function by Using Short Complementary DNA Oligomers” in The Ribosome. Structure, Function and Evolution.(Eds. Hill, W.E., Dahlberg, A., Garrett, R., Moore, P.B., Sclessinger, D., and Warner, J.R.) pp 253-261. 1990 ASM Publications, Washington, D.C.

Bates, S.R.E., Knorr, D.A., Weller, J.W. and Ziegler, J.S. “Instrumentation for Automated Molecular Marker Acquisition and Data Analysis.” in The Impact of Plant Molecular Genetics (Ed. Sobral, B.) 1996 Birkhauser, Boston

Weller, J.W. and Reddy, A.S., “Fluorescent Detection and Analysis of RAPD Amplicons Using the ABI Prism™ DNA Sequencers” in Fingerprinting Methods Based on Arbitrarily Primed PCR in the Springer Lab Manual series (Eds. Bova, R. and M.R. Micheli) pp 81-92. 1997 Springer-Verlag, Berlin Heidelberg New York.

Weller, J.W. and Robertson, J.R. , “An Introduction to PCR Primer Design and Optimization of Amplification Reactions” in Forensic DNA Profiling Protocols from the Methods in Molecular Biology series (Ed. Lincoln, P.J. and J.Thomson) pp121-154 . 1998 The Humana Press, Totowa, New Jersey.

Giese, H., Hippe-Sanwald,S., Somerville,S. and Weller,J. “*Eriyisiphe graminis*” in The Mycota series (Eds. Carroll,G.C. and Tudzynski,P.) Chapt 4 Part B, 1997 Springer-Verlag, Berlin Heidelberg.

Paszko, C. and Weller, J.W. (2011) "Computerized LIMS" The European Pharmaceutical Contactor (EPC magazine), Spring 2011 pp 64-67.

Selected Abstracts and Presentations

Chen, S. Yee, A., Weller, J., MacFadden, S., Read, S., Johnson, R., Gyles, C., De Grandis, S. (1996) "Molecular Typing of Verotoxigenic *Escherichia coli* Using Amplified Fragment Length Polymorphism (AFLP) Analysis". American Society of Microbiology. Miami, Florida, 1996.

Flood, S.J.A., Weller, J., Sharaf, M., Green, R., Wada, A., Izumiya, H., Watanabe, H., Paszko-Kolva, C. (1996) "Investigation of *E. coli* O157:H7 Epidemic Samples from Japan using Genomic Fingerprinting Techniques and Genetic Based Typing Methods" . American Society of Microbiology. Miami, Florida, 1996.

Casa, A.M., Mitchell, S.E., Dean, R., Kresovich, S.K. Jester, C., Weller, J.W. and Ferreira, M.E. (1997) "Fluorescence-Based AFLP Genotyping of Cultivated Rice and Its Wild Relatives" Plant Genome V, Abstract #74. San Diego CA, Jan 11-16, 1997.

Walsh-Weller, J., Johnston, E., and Millam, J. (1997) "AFLP Fluorescent Markers for Mapping a Family of Yellow-Naped Amazons: a Comparison of the Marker Density and Inheritance Patterns of Fluorescent AFLP Markers and VNTR-RFLP Markers" Plant Genome V, Abstract #83. San Diego CA, Jan 11-16, 1997.

Walsh-Weller, J., Sharaf, M., Inagaki, Y., Izumiya, H., and Watanabe, H. (1997) "Application of Fluorescent AFLP Analysis to the Classification and Identification of *E. coli* O157:H7 Strains from the Recent Outbreak in Japan" Plant Genome V, Abstract #84. San Diego CA, Jan 11-16, 1997.

Bodeau, J., Baumhueter, S., Spier, E., Weller, J., Hwang, S., Gilbert, D. (1998) "PE GenScope: Transcript Imaging", Functional Genomics meeting, Seattle, Washington Sept 10-11, 1998.

Sturgill, D., Weller, J.W., and Gibas, C. (2002) "Systematic Genomic Comparison of Three *Brucella* Spp. and a Data Model for Feature-Based Multiple Genome Analysis." ISMB Aug 2002, Edmonton Canada (Weller name inadvertently left off of printed abstract for poster 192A).

Deshmukh, H., Mangalam, H., Weller, J. (2004) "PyROOo: an interface to GeneX for Spreadsheet Functions" MGED 7, Toronto, Canada, Sept 8-11, 2004.

Carr, D.A., Deshmukh, H., Weller, J. (2005). ISMB 2005, Detroit MI. June 24-28, 2005

Deshmukh, H., Carr, D.A., Weller, J. (2005). ISMB 2005, Detroit MI. June 24-28, 2005
Kumari, S., Verma, L., Weller, J. (2005). ISMB 2005, Detroit MI. June 24-28, 2005

Weller, Jennifer. “AffyMAPSDetector: Finding and Applying SNP information for probes in Affymetrix GeneChips” Seminar at NCI Nov. 3rd, 2005.

Carr, D.A. and Weller, J.W. “DataFATE: A prototypic SIMS for Ontology Construction and Data Mining” ISMB. Toronto, Canada. July 18-23, 2008

North Carolina A & T, Mar 27th 2009 “Forensic Science: DNA Diagnostics and Bioinformatics”. Part of graduate recruiting effort with Elise Marshall.

Davidson College, April 1st 2009. “Bioinformatics and DNA Markers: Identifying Individual and their Environment Over Time”. Part of graduate recruiting effort with Elise Marshall.

Bioinformatics and Genomics Graduate Seminar Spring 2009, by request, a Friday seminar covering various types of jobs (government, academic, industrial, not-for-profit), how and when to apply, what to expect in different types of jobs.

Biology department at UNCC, Sept 2010” Non-statistical data cleansing for microarrays: how and why, and what then?”

CS department at UNCC, March 2011 “ArrayInitiative: a bioinformatics tools for studying transcriptomics”

Biology Department at Western Carolina University, April 2011 “ArrayInitiative: a bioinformatics tools for studying transcriptomics”

Some selected NSF outreach presentations in 2017-2019

- Rosetta Conference in Leavenworth WA, Aug 8-11, 2017
- Plant and Animal Genome XXVI, January 13-19, 2018. I attended presentations given by ABI-funded PIs and participated in a panel (with a short talk) for Sustaining Funding. I had individual meetings with 10 PIs.
- BioCreative workshop, seminar and panel of funding agencies Oct 18, 2017
- National Microbiome Data Consortium Workshop agency representative, at ASM headquarters in Washington DC Nov 9-10, 2017.
- USDA Genomes to Phenomes workshop, agency representative and panel participant, Nov 15, 2017
- AddGene presentations and meetings on sustainable resources for both wet-lab materials (BioBlocks, for example) and data and protocols, Feb 20, 2018
- NIFA -sponsored HSI PIs meeting at NSF, short talk on DBI programs and activities, Mar 19, 2018
- University and college outreach activities
 - 4 Tribal Colleges in Arizona and NM, Apr 23-27

- NAU seminars/visit, Apr 28, 2017
- OLPA-sponsored NSF Day Louisville KY, June 5-6, 2017
- Seattle Children's Hospital and Univ of WA seminar/visits Aug 7, 2017
- NCAT seminar/visit Sept 22, 2017
- Virginia Tech seminar/visit Oct 13, 2017
- George Mason Univ. informal visit Dec 8, 2017
- UC Riverside seminar/visit, Jan 18, 2018
- OLPA sponsored NSF day in Brookings, SD, Mar 28-30, 2018

Working Group Participation at NSF

- DBI RR Solicitation revision Working Group (started due to change to no-deadline and also for consolidation of programs)
 - Innovation solicitation revision and proposal with Steve Ellis and Rob Fleischman
- DBI Communication Working Group member
 - P drive organization (lead, because I care)
- Rules of Life Working Group and RoL FELS working group (i.e. PO for the EAGER/RAISE reviews and full proposal decision group).
 - DBI representative to the Rules of Life Working Group – completed the description of what the BIO emphasis will encompass.
 - DBI PO (with Steve Ellis) on the group assigned to review, bin and make decisions on the ~200 proposals received in response to the DCL.
 - BIO RoL co-review at request of other POs aiming for Venture Funds (reviewed 3 proposals at request of Karen Cone, none were competitive for ABI)
- ADVANCE Working group – BIO representative
 - I have attended ~every other biweekly meeting
 - Reviewed proposals for the HSI call and participated in the panel ranking proposals for funding decisions, Nov 7, 2017
- NSF-wide Broadening Participation Working Group – BIO representative
 - Attended 6 of the meetings (usually conflict with other meetings)
- NSF cross-cutting initiative for aDNA studies -an ad hoc group of POs interested in whether this is an area of interest for NSF
 - Rationale: there is little research in the US and a great deal in other countries, so this might be a competitive area in which we are losing out.
- NSF-wide Interagency Working Group on Animal Functional Annotation – DBI representative
 - Lakshmi Matukumalli of NIFA is the organizer. The intention is to write an MOU for co-funding cyberinfrastructure resources. I have been communicating with 3 PIs who will write a planning grant once the new solicitations go public.
- NSF Cross-cutting Initiatives panel service
 - PO for GRFP panel Jan 9, 12, 2018
 - PO for the Bio Big Data panel with Reed Beaman May 24-25, 2018

Funding History

Joint development project (VBI/U Nevada at Reno/SR Noble Foundation), PI J Weller “Collaborative development of an EST database and analysis pipeline: ESTAP”, 2000-2002, \$399,354.

NSF CISE, PI Ramakrishnan, “Espresso, a microarray experiment management system”, co-PI for 5% effort (salary recovery) 2001-2005.(not currently actively engaged)

NSF PGRP, PI Mendes, “ An Integrated Approach to Functional Genomics and Bioinformatics in a Model Legume”, senior personnel for 10% effort (salary recovery while at VBI, did not migrate to GMU), 2001-2005.

GenXpediter: An upload tool for gene expression data to the GeneX database Virginia Tech \$17,100 VT and \$5700 matching VBI 12/31/01-12/30/02. Current ASPIRES program and Virginia Tech

NSF-BDI “Open GeneX: Expanding the Toolkit of an Open Source Gene Expression Informatics System.” George Mason University. \$751,260 05/01/02 – 04/30/04 (two extensions granted).

NIH ZRG1 BST-D Gibas(PI) and Weller (coPI) “Biophysical Optimization of Oligonucleotide Microarrays” R01 GM072619-01. \$698,672. Aug 2006 – July 2011 (one extension granted).

NC Biotechnology Center (IDG). Clemons(PI) Dreau (Co-PI) Weller (Co-PI) \$157,245. “A laser capture microscope platform for the interdisciplinary biotechnology programs in Charlotte”. An Institutional Development Grant for a shared laser capture microscope (Arcturus) with laser capture, laser cutting and fluorescence imaging capabilities along with strong image tracking and image analysis software capabilities. 05/01/09.

Contract Advanced Technology Laboratories, Inc. Contract PI: Jennifer Weller. Project title: “A beta-test run of the SeqNFind algorithm”. This project involved testing a GPU processor implementation of several sequence-matching algorithms against an exhaustive search produced by a scanning method. Both accuracy and speed were measured. 04/15/2010-12/31/2011 \$11,000

North Carolina Biotechnology Center (2012) Education Enhancement Grant-6017) Schlueter, J (PI) and Weller (co-PI). \$58,670. “Genomic Technologies in Bioinformatics” A goal of this is to support learning-research in a genomics lab where students produce genome-scale data that they can take to courses in Statistics, Genomics and Sequence Analysis.

School of Computational Science (UNCC) and School of Medicine (WF) 2012 Deans Seed-Grant Initiative to support Collaborative Research Weller (PI-UNCC) and Guthold (WF). “Aptamer sequencing and protein binding on the Ion Torrent PGM – a proof of concept”.(\$24,500 from UNCC; \$30,000 from WF).

NIH-SBIR with small business Nanomedica (Cubicciotti) and Guthold (Wake Forest University and School of Medicine) as PIs and Weller as Contract personnel. “Adapting the Ion Torrent PGM

as a Lab-on-Bead for macrocycle screening”. Phase I has been approved (but not yet started). Weller lab is budgeted for \$20,000 to support sequencing costs each year.

FRG – UNCC Levens, S (PI) and Weller, J (PI) \$13,000 8/1/2012 – 7/31/2013

This is a faculty research grant to help advance the cross-disciplinary team between Psychology and Bioinformatics, looking at links between genetic and metagenomic traits and behaviors predictive of academic success.

IPA to NSF – grant to UNCC 8/3/2015-8/3/2019

This grant was to reimburse the University for my salary and benefits during the time I was on leave at the National Science Foundation. It was structured as an IPA. Four years is the maximum that such appointments are allowed to continue, it was very unusual that it was approved by the Director, Dr. France Cordova.

Research Advisor

PhD and MS students

Peter Hraber (primary advisor; PhD awarded June 2001, University of New Mexico).

Brandon Higgs (PhD awarded Dec 2005, GMU)

Thomas Heiman (PhD awarded Dec 2005, GMU)

Hrishikesh Deshmukh (PhD awarded May 2006, GMU)

Elo Leung (PhD awarded Dec 2007, GMU)

Kevin Thompson (PhD awarded Sept 2008, GMU)

James C. Diggans (PhD awarded Dec 2008, GMU)

Timothy Tickle (PhD awarded 2011, UNCC)

Cristina Baciú (PhD awarded 2012, UNCC)

Christopher Overall (PhD awarded 2012, UNCC)

Saeed Koshnevis (PhD awarded August 2013, UNCC)

Sushant Patil (PhD awarded June 2016, UNCC)

Yuying Tian (MS awarded May 2002 VPISU)

Sunita Kumari (MSc awarded May 2004, GMU)

Sarah Bittenbender (MSc awarded Aug 2005, GMU)

Karen Schwartz (MSc awarded May 2005 GMU)

Vasuki Palanigobu (MSc awarded Aug 2005 GMU)

Farhana Alam (MSc awarded Dec 2005, GMU)

Rachel Brower (MSc May 2006, GMU)

Shaun Rabah (MSc, May 2006, GMU)

Anthony Zukas (MSc, Dec 2007, GMU)

Saeed Khoshnevis (MSc, May 2007, GMU)

Krishna Kanchinadam (MSc, May 2008, GMU)

Postdoctoral Fellows

Dr. Karen Schlauch (now Director of Bioinformatics at U-Nevada Reno).

Dr. Sunita Kumari (now at CSHL in the Ware group)

Dr. Chris Bradburne (now at the Applied Physics Lab at Johns Hopkins University).

Dr. Andrew Carr (now Director of Bioinformatics at Accelerated Technology Labs)
Dr. Kevin Thompson (now at the Mayo Clinic in Rochester, MN).

Statement of Teaching Philosophy

Teaching is an activity that I find enjoyable as well as challenging, since it requires a lot of self-criticism and work to refine my logic and carry it into clear communication. I have always sought opportunities to design and present workshops, seminars, and short courses at my places of employment and for the local community, hence my involvement with the summer science program and visiting scientist programs at local high schools. My goal is to produce scientists who understand every aspect of the process of creating data, in addition to being confident in the analysis of that data. Because of that, at both Universities I have set up and run wet-lab courses for the computational students, to initiate them in the real-world limitations that arise from handling materials and using equipment. The question I constantly pose it – how would this affect your analysis, now that you know it might happen? What controls should you be seeing in the report so that you know you can ignore this problem? When students get to do real science while learning about it they work a lot harder without grumbling. I am very proud when students come back to visit after graduation and tell me that they resented how much work my classes were at the time they took them, and that because of it they outshine their peers in the workplace.

Curriculum Development

New courses developed

Microarray Methods, BINF 636 – a course aimed at teaching students the wet lab, instrumentation and manufacture, bioinformatics and experimental design methods required to construct a microarray that can answer fundamental scientific questions.

Data modeling for Bioinformatics, BINF 739 (with Dr. Curt Jamison) – a course emphasizing data models that meet basic design requirements of the scientific methods and implementation using the ER model and relational DBMS, as well as an introduction to the structure of the most widely used biological databases.

Academic programs developed or substantially modified

Molecular Biotechnology, BINF 633 – This course was previously taught as primarily a DNA molecular biology methods class, I added strong components of biochemistry and instrumentation with data readout and quality control as part of the analysts /bioinformaticians challenge.

Journal editing: ad hoc reviewer for a number of journals including Bioinformatics, Genome Research, Genome Biology, BMC Genetics, Functional Genomics, PLoS Bioinformatics, PLoS ONE and other PLoS titles, Folia Microbiologica.

Infrastructure Development

Throughout most of my scientific career I have lead efforts to bring new infrastructure to my places of work, from the beginning phases of deciding how requirements and budgets can be brought into alignment to making purchases, setting up facilities, hiring professionals, managing

use, maintenance and costs and writing reports. Specifics of past projects may be requested, I have only put my most recent efforts at UNCC in this CV.

Infrastructure Development at UNCC

I have had primary responsibility for designing and setting up a genomic biotechnology teaching lab for our department, which includes state of the art devices for creating libraries and carrying out sequencing on an Ion Torrent PGM, as well protocols and training methods for the related courses.

I have had primary responsibility for bringing the BSL3 facility housed in the Bioinformatics building to a state where it can be commissioned and to where faculty are prepared to use it to carry out experiments. These are parallel but not identical requirements, since a safe facility can be empty of anything but protective gear and decontamination solutions. A usable lab must have basic equipment and that equipment must have aerosol-safe and decontamination –safe characteristics. I have also compiled a prototype set of operating procedures and check-lists. While much of this will be turned over to the Biosafety Officer when hired, the goal is to have a fully operational facility when that individual is hired.

Service Contributions

Professional Meetings Organized

Oct 17, 2002 Organizer of the Virginia Bioinformatics Consortium Genex-dev meeting at George Mason University. Developers from Virginia, Cal Tech, and New Mexico met for a day to discuss progress and needs for continued progress in a gene expression database and information system.

Interface 2004, May 29-30, Baltimore MD (organized keynote and workshop speakers)

WiNGS (Workshop in Next Generation Sequencing), May 17-18th, 2012. Charlotte, NC. Six researchers from the SE region spoke of their research applications on the first day and conducted hands-on workshops on the second day, for ~80 attendees, 60 of whom were not from UNC Charlotte. I organized the entire meeting, from parking and food to recruiting speakers, computers, assistants and recording the sessions.

FGED 2013 June 20th – 23rd in Seattle WA. Co-organizer of the Galaxy and Kbase workshops.

Grant Review panelist for federal agencies

NIH; SSS-H ZRG1 (2004),BMDA ZRG1 (2004), BDMA (2006) 2019, 2020
NSF: PGRP (2004, 2005), INFORM (2003-2005), BDI (2006), CISE(2009), ABI (2007, 2009, 2010, 2011, 2014)

GMU SCS committees/ responsibilities

BINF Faculty hiring committee 2003-2004
BINF Graduate student admissions committee 2003- present)
BINF and SCS Weekly and BI-Semester Faculty meetings
BINF Laboratory Safety and Organization committee (2004- present)
BINF Curriculum Committee (2005- present, now chair)

Service to other universities (program review, etc.)

Nov 5, 2002 Invited panelist/advisor for the Louisiana CERT-CIBI group, an NSF-EPSCoR funded consortium in the planning grant stage of developing a medical bioinformatics program in their state.

NSF-EPSCoR program review as member of the scientific advisory board for UN-Reno. May 20, 2004 (I was a member of this Board in 2002 and 2003 as well).

NSF Maize Chromatin Scientific Advisory Board member (Mar 2005- present)

NSF workshop for Arabidopsis Data Integration (invited participant), meeting in April 2005 at TIGR, organized by Chris Town.

Office of Naval Research, NSWCDD B-10; external reviewer of in-house laboratory research (IHLR) projects, Oct 2004.

NSF-EPSCoR program external advisory board member for UN-Reno for the component lead by Dr. Sushil Louis. (Aug 2006)

UNC-Charlotte Professional Science Masters external advisory board member for program and curriculum development, lead by Dr. Cynthia Gibas and Dr. Larry Mays (Nov 2006).

Adjunct Professor Bioinformatics and Computational Biology at Wake Forest University (2012 – 2015)

Adjunct Professor Bioinformatics and Computational Biology at George Mason University (renewed for a third 3-year term in April 2017).

Entrepreneurial Activities

I have met with representatives from Celera Pharmacogenomics, MITRE Corp., GeneLogic Corp., IDD (a cancer diagnostics lab in San Antonio TX) and BoozAllenHamilton in order to discuss activities of mutual interest that might lead to funding of graduate students, transfer of research ideas to the industrial setting and to find out what computational tools scientists in industry most feel they need. This led to several jointly submitted grant proposals (SBIRs). I am consultant for AT Labs, InsituTec, and NanoMedica, all small bio/technology companies in North Carolina.

Synergistic and Outreach Activities:

1. Project Leader for the gene expression analysis system GeneX (<http://www.ncgr.org/research/genex>) currently funded by NSF-BDI. GeneX is an open source database and query/analysis interface developed at NCGR.

2. Project leader of an EST analysis system development team for collaborative EST sequencing projects at NCGR (<http://www.ncgr.org/research/mgi> and <http://www.ncgr.org/research/pgi>) and at the Virginia Bioinformatics Institute at the Virginia Polytechnic Institute and State University (<http://www.vbi.vt.edu/estap>).
3. Development of a high-density *Arabidopsis thaliana* genetic map using the Landsberg er. x Columbia gl. RI lines using AFLP markers (~1000 markers) has been made available to the community through the TAIR Web site (<http://www.arabidopsis.org>).
4. Lectured in “Dreamcatchers”, a three-evening mini-course in science (molecular genetics of corn, with hands-on sample prep and PCR) in June 2000, for Native American middle-school age children, an enrichment program sponsored by the AISES and Sandia National Labs.
5. Instructor in the “Database Design and Development for Genomics Research” course sponsored by the BioPharmaceutical Center Institute in Madison WI, June 29-July1, 2000. A beginners course for biologists interested in bioinformatics and for computer scientists interested in bioinformatics.
6. Organizing committee for an O’Reilly conference on Bioinformatics schedules for January 2002 (<http://conferences.oreilly.com/biocon/cfp.html>).
7. Workshop organizer and one of two instructors for a course titled “The analysis and informatics of gene expression data” funded by the NSF and the SR Noble Foundation, Aug 19-21, 2002 in Ardmore OK.
8. Scientific advisor on bioinformatics to the USAF Surgeon General’s office for the Epidemic Outbreak Surveillance project May 15, 2002 – June 30, 2003, Falls Church VA.
9. Conference organizer for Interface 2004, Baltimore, MD, May 26-29, 2004
10. Organizer and Instructor for a summer science camp for high school students at Olympic High School in Charlotte NC, to provide hands-on experience purifying DNA and producing molecular markers for the American Chestnut. With Jeanne Smith I sought and obtained funding for the program from several local sources. Periods: June 2010 (2 weeks full time), June 2011 (two weeks full time), June 2012 (3 weeks, part time).
11. Meeting organizer for WINGS 2012, Charlotte NC, May 17-18, 2012.
12. Workshop organizer for FGED 2013 in Seattle WA, June 19-22, 2013
13. Biodiversity, Biotechnology and Bioinformatics (B3) Olympic High School Summer Science Camp (2009-2017). See Web site for activities, pictures, protocols, etc. http://webpages.uncc.edu/~jeweller2/pages/BioinformaticsBootCamp2016/BioinformaticsBootCamp2016_Home.html