

Nic Herndon

Research Interests

Big Data, Artificial Intelligence, Machine Learning (in particular, Domain Adaptation), Data Mining and Knowledge Discovery, Bioinformatics, and Computational Biology.

Education

- 2016 **Doctor of Philosophy in Computer Science**, Kansas State University
Thesis title: *Domain Adaptation Algorithms for Biological Sequence Classification*
Advisor: Doina Caragea
- 2008 **Master of Science in Computer Science**, University of Nevada at Reno
Thesis title: *ATTITUDE: A Tidy Touchscreen Interface to a UML Development Environment*
Advisor: Sergiu Dascalu
- 2004 **Bachelor of Science in Computer Science**, University of Nevada at Reno
Minor in Mathematics

Professional Experience

- 2016 - now **Postdoctoral Fellow**, *Plant Computational Genomics Lab*, University of Connecticut.
◦ Lead the development of CartograTree (<http://cartogratree.org>), an open repository and open-source analytic framework for genomic, phenotypic, and environmental data for forest trees.
- 2012 - 2016 **Bioinformatics Specialist – Full-time**, *Bioinformatics Center*, Kansas State University.
◦ Improved genome assembly for *T.castaneum*; collaborated with researchers on genomics projects ranging from assembling and annotating genomes, to differential gene expression.
- 2008 - 2011 **Programmer Analyst – Full-time**, *Office of Undergraduate Admissions*, Kansas State University.
◦ Developed SQL scripts to import data into customer relationship management database and to generate views requested by colleagues; developed GUI applications to manage database imports; developed an application to create customized information packet for potential undergraduate students.
- Summer 2010 **Bioinformatics Intern**, *Bioinformatics Center*, Kansas State University.
◦ Configured and ran MAKER to generate gene models for *T.castaneum*.
◦ Installed and ran tRNAscan-SE to predict genes that encode for tRNA for *T.castaneum*, then converted the output to GFF format to use it with Apollo and Augustus.
- 2008 **Software Product Assurance Engineer II – Full-time**, *International Game Technology*, Reno, Nevada.
◦ Proposed changes to the Gaming Standards Association for the Game to System (G2S) communication protocol used by slot machines/Electronic Gaming Machines (EGMs) to exchange information with back-of-house systems.

- 2007 - 2008 **Software Product Assurance Engineer I – Full-time**, *International Game Technology*, Reno, Nevada.
 - Developed a GUI application to test the correct implementation of the G2S protocol.
- 2004 - 2007 **Local Area Network Administrator – Full-time**, *Barnes & Noble, Inc.*, Reno Distribution Center, Nevada.
 - Modified the ladder logic programs for the Allen-Bradley programmable logic controllers (PLCs) to improve the flow of totes and packages, and to accommodate the extension of the conveyor system.
 - Designed and implemented an application to control the shipping of packages; the application received the barcode data from scanners, queried the AS/400 DB2 database to determine the destination, passed the lane assignment to the PLC, and displayed the information about each package in a GUI.
- 2000 - 2004 **Information & Technology Assistant – Full-time**, *Barnes & Noble, Inc.*, Reno Distribution Center, Nevada.
 - Performed systems administration tasks.

Teaching Experience

- Spring 2016 **Secondary Instructor** for BIOL/CIS 734 – Introduction to Genomics and Bioinformatics, *Kansas State University*.
 - Taught labs and graded lab assignments.
- Summer 2015 **Co-instructor** for BIOL/CIS 890 – NGS Analysis on Beocat and Introduction to Perl programming for Bioinformatics, *Kansas State University*.
 - Prepared and delivered lectures; helped students with in-class hands-on programming assignments.
- Summer 2014 **Teaching Assistant** for BIOL/CIS 890 – NGS Analysis on Beocat and Introduction to Perl programming for Bioinformatics, *Kansas State University*.
 - Graded assignments and helped students during office hours.
- Spring 2014 **Secondary Instructor** for BIOL/CIS 734 – Introduction to Genomics and Bioinformatics, *Kansas State University*.
 - Taught labs and graded lab assignments.
- Summer 2013 **Co-instructor** for BIOL697 – Programming Perl for Bioinformatics, *Kansas State University*.
 - Prepared and delivered lectures; helped students with in-class hands-on programming assignments.
- Spring & Fall 2003 **Teaching Assistant** for Math, *Truckee Meadows Community College*, Reno, Nevada.
 - Helped students use ALEKS assessment and learning software and explained math concepts when students needed clarification.
- Spring & Summer 2001 **Math Tutor**, *Truckee Meadows Community College*, Reno, Nevada.
 - Tutored introductory college math in 1-on-1 and small group settings (up to five students).

Publications

Doctor Thesis

Herndon, N. (2016). *Domain Adaptation Algorithms for Biological Sequence Classification*. Kansas State University.

Master Thesis

Herndon, N. (2008). *ATTITUDE: A Tidy Touchscreen Interface to a UML Development Environment*. University of Nevada at Reno.

Refereed Journal Articles

1. Kanost, M. R., Arrese, E. L., Cao, X., Chen, Y.-R., Chellapilla, S., Goldsmith, M. R., Grosse-Wilde, E., Heckel, D. G., **Herndon, N.**, Jiang, H., Papanicolaou, A., Qu, J., Soulages, J. L., Vogel, H., Walters, J., Waterhouse, R. M., Ahn, S.-J., Almeida, F. C., An, C., Aqrawi, P., Bretschneider, A., Bryant, W. B., Bucks, S., Chao, H., Chevignon, G., Christen, J. M., Clarke, D. F., Dittmer, N. T., Ferguson, L. C., Garavelou, S., Gordon, K. H., Gunaratna, R. T., Han, Y., Hauser, F., He, Y., Heidel-Fischer, H., Hirsh, A., Hu, Y., Jiang, H., Kalra, D., Klinner, C., König, C., Kovar, C., Kroll, A. R., Kuwar, S. S., Lee, S. L., Lehman, R., Li, K., Li, Z., Liang, H., Lovelace, S., Lu, Z., Mansfield, J. H., McCulloch, K. J., Mathew, T., Morton, B., Muzny, D. M., Neunemann, D., Ongeri, F., Pauchet, Y., Pu, L.-L., Pyrousis, I., Rao, X.-J., Redding, A., Roesel, C., Sanchez-Gracia, A., Schaack, S., Shukla, A., Tetreau, G., Wang, Y., Xiong, G.-H., Traut, W., Walsh, T. K., Worley, K. C., Wu, D., Wu, W., Wu, Y.-Q., Zhang, X., Zou, Z., Zucker, H., Briscoe, A. D., Burmester, T., Clem, R. J., Feyereisen, R., Grimmelikhuijzen, C. J., Hamodrakas, S. J., Hansson, B. S., Huguet, E., Jermiin, L. S., Lan, Q., Lehman, H. K., Lorenzen, M., Merzendorfer, H., Michalopoulos, I., Morton, D. B., Muthukrishnan, S., Oakeshott, J. G., Palmer, W., Park, Y., Passarelli, A. L., Rozas, J., Schwartz, L. M., Smith, W., Southgate, A., Vilcinskas, A., Vogt, R., Wang, P., Werren, J., Yu, X.-Q., Zhou, J.-J., Brown, S. J., Scherer, S. E., Richards, S., and Blissard, G. W. (2016). *Multifaceted biological insights from a draft genome sequence of the tobacco hornworm moth, Manduca sexta*. *Insect Biochemistry and Molecular Biology* 76 (2016): 118-147.
2. **Herndon, N.**, and Caragea, D. (2016). *An evaluation of approaches for using unlabeled data with domain adaptation*. *Network Modeling Analysis in Health Informatics and Bioinformatics*, 5(25):1-12.
3. Raithel, S., Johnson, L., Galliard, M., Brown, S. J., Shelton, J. M., **Herndon, N.**, and Bello, N. M. (2016). *Inferential considerations for low-count RNA-seq transcripts: a case study on an edaphic subspecies of dominant prairie grass Andropogon gerardii*. *BMC Genomics*, 17(140):1-16.
4. **Herndon, N.** and Caragea, D. (2016). *A Study of Domain Adaptation Classifiers Derived from Logistic Regression for the Task of Splice Site Prediction*. *IEEE Transactions on NanoBioscience*, PP(99):1-9.
5. Tangirala, K., **Herndon, N.**, and Caragea, D. (2016). *A Comparative Analysis between k-mers and Community Detection-based Features for the Task of Protein Classification*. *IEEE Transactions on NanoBioscience*, PP(99):1-9.
6. Shelton, J. M., Coleman, M. C., **Herndon, N.**, Lu, N., Lam, E. T., Anantharaman, T., Sheth, P., and Brown, S. J. (2015). *Tools and pipelines for BioNano data: molecule assembly pipeline and FASTA super scaffolding tool*. *BMC Genomics*, 16(1):734.
7. Zhao, C., Escalante, L., Chen, H., Benatti, T., Qu, J., Chellapilla, S., Waterhouse,

R., Wheeler, D., Andersson, M., Bao, R., Batterton, M., Behura, S., Blankenburg, K., Caragea, D., Carolan, J., Coyle, M., El-Bouhssini, M., Francisco, L., Friedrich, M., Gill, N., Grace, T., Grimmelhuijzen, C., Han, Y., Hauser, F., **Herndon, N.**, Holder, M., Ioannidis, P., Jackson, L., Javaid, M., Jhangiani, S., Johnson, A., Kalra, D., Korchina, V., Kovar, C., Lara, F., Lee, S., Liu, X., Löfstedt, C., Mata, R., Mathew, T., Muzny, D., Nagar, S., Nazareth, L., Okwuonu, G., Ogeri, F., Perales, L., Peterson, B., Pu, L.-L., Robertson, H., Schemerhorn, B., Scherer, S., Shreve, J., Simmons, D., Subramanyam, S., Thornton, R., Xue, K., Weissenberger, G., Williams, C., Worley, K., Zhu, D., Zhu, Y., Harris, M., Shukle, R., Werren, J., Zdobnov, E., Chen, M.-S., Brown, S., Stuart, J., and Richards, S. (2015). *A Massive Expansion of Effector Genes Underlies Gall-Formation in the Wheat Pest* *Mayetiola destructor*. *Current Biology*, 25(5):613 - 620.

Refereed Book Chapters

1. **Herndon, N.** and Caragea, D. (2015). *Empirical Study of Domain Adaptation Algorithms on the Task of Splice Site Prediction*. In *Biomedical Engineering Systems and Technologies*, ser. *Communications in Computer and Information Science*, Springer International Publishing, 2015, vol. 511, pp. 195-211.
2. **Herndon, N.** and Caragea, D. (2014). *Predicting Protein Localization Using a Domain Adaptation Approach*. In *Biomedical Engineering Systems and Technologies*, ser. *Communications in Computer and Information Science*, Springer Berlin Heidelberg, 2014, vol. 452, pp. 191-206.

Refereed Conference Papers

1. **Herndon, N.**, Grau, E. S., Batra, I., Demurjian Jr., S. A., Vasquez-Gross, H. A., Staton, M. E., and Wegrzyn, J. L. (2016). *CartograTree: Enabling Landscape Genomics for Forest Trees*. In *Proceedings of the Open Source Geospatial Research & Education Symposium (OGRS 2016)*, Perugia, Italy, pp. 1-7. [Short paper]
2. **Herndon, N.**, and Caragea, D. (2016). *Ab initio Splice Site Prediction with Simple Domain Adaptation Classifiers*. In *Proceedings of the 7th International Conference on Bioinformatics Models, Methods and Algorithms (BIOINFORMATICS 2016)*, Rome, Italy, pp. 245-252. [Short paper]
3. Roy, S., DeLoach, J., Li, Y., **Herndon, N.**, Caragea, D., Ou, X., Ranganath, V. P., Li, H., and Guevara, N. (2015). *Experimental Study with Real-world Data for Android App Security Analysis using Machine Learning*. In *Proceedings of the 2015 Annual Computer Security Applications Conference (ACSAC 2015)*, Los Angeles, CA, pp. 81-90. [Regular paper. Acceptance rate: 25%]
4. **Herndon, N.**, and Caragea, D. (2015). *An Evaluation of Self-training Styles for Domain Adaptation on the Task of Splice Site Prediction*. In *Proceedings of the 4th International Symposium on Network Enabled Health Informatics, Biomedicine and Bioinformatics (HI-BI-BI 2015)*, Paris, France, pp. 1042-1047. [Regular paper. Acceptance rate: 35%. **Best paper award**]
5. **Herndon, N.**, and Caragea, D. (2015). *Domain Adaptation with Logistic Regression for the Task of Splice Site Prediction*. In *Proceedings of the 11th International Symposium on Bioinformatics Research and Applications (ISBRA 2015)*, Norfolk, VA, pp. 125-137. [Regular paper. Acceptance rate: 35%]
6. Tangirala, K., **Herndon, N.**, and Caragea, D. (2015). *Community Detection-Based Feature Construction for Protein Sequence Classification*. In *Proceedings of the 11th*

- International Symposium on Bioinformatics Research and Applications (ISBRA 2015), Norfolk, VA, pp. 331-342. [Regular paper. Acceptance rate: 35%]
7. Li, H., Guevara, N., **Herndon, N.**, Caragea, D., Neppalli, K., Caragea, C., Squicciarini, A., and Tapia, A. (2015). *Mining for Disaster Response: A Domain Adaptation Approach*. In Proceedings of the 12th International Conference on Information Systems for Crisis Response and Management (ISCRAM 2015), Kristiansand, Norway. [Short paper. Acceptance rate: 70%]
 8. **Herndon, N.**, Tangirala, K., and Caragea, D. (2014). *Predicting Protein Localization Using a Domain Adaptation Naïve Bayes Classifier with Burrows Wheeler Transform Features*. In Proceedings of the 6th IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2014), Belfast, UK, pp. 501-504. [Short paper. Acceptance rate: 38%]
 9. **Herndon, N.** and Caragea, D. (2014). *Empirical Study of Domain Adaptation with Naïve Bayes on the Task of Splice Site Prediction*. In Proceedings of the 5th International Conference on Bioinformatics Models, Methods and Algorithms (BIOINFORMATICS 2014), Angers, France, pp. 57-67. [Regular paper. Acceptance rate: 14%. **Nominated for best paper award**]
 10. **Herndon, N.** and Caragea, D. (2013). *Naïve Bayes Domain Adaptation for Biological Sequences*. In Proceedings of the 4th International Conference on Bioinformatics Models, Methods and Algorithms (BIOINFORMATICS 2013), Barcelona, Spain, pp. 62-70. [Regular paper. Acceptance rate: 10%. **Nominated for best student paper award**]
 11. Vert, G. and **Herndon, N.** (2006). *Secure Simultaneous Search of Distributed, Heterogeneous Bioinformatics Databases*. In Proceedings of the 2006 International Conference on Security & Management (SAM 2006), Las Vegas, NV, USA, pp. 384-389.

Posters and Presentations

1. **Herndon, N.**, Wynne, M., Grau, E. S., Ficklin, S., Staton, M. E., Jung, S., Main, D., Feltus, A., Gessler, D., and Wegrzyn, J. L. (2017). *Association mapping with CartograTree and Tripal API*. Poster presentation at the 2017 Gordon Research Conference on Ecological and Evolutionary Genomics, July 16-21, 2017, Biddeford, ME.
2. **Herndon, N.**, Lin, Q., Wynne, M., Grau, E. S., Ficklin, S., Staton, M. E., Jung, S., Main, D., Feltus, A., Gessler, D., and Wegrzyn, J. L. (2017). *CartograTree workflows with Tripal API for association mapping in forest trees*. Computer demonstration, and poster presentation at the 25th International Plant and Animal Genome Conference (PAG XXV), January 14-18, 2017, San Diego, CA.
3. Grau, E. S., **Herndon, N.**, Demurjian Jr., S. A., Lin, Q., Wynne, M., Gessler, D., Feltus, A., Staton, M. E., Ficklin, S., Main, D., and Wegrzyn, J. L. (2017). *TreeGenes: Genetic and Genomic Resources for Forest Trees*. Poster presented by E. S. Grau at the 25th International Plant and Animal Genome Conference (PAG XXV), January 14-18, 2017, San Diego, CA.
4. Lin, Q., **Herndon, N.**, Grau, E. S., Ficklin, S., Staton, M. E., Jung, S., Main, D., Feltus, A., and Wegrzyn, J. L. (2017). *A Novel Tripal Database Module and Workflow to Facilitate Variant Mapping and Detection in Non-Model Plant Species*. Poster presented by Q. Lin at the 25th International Plant and Animal Genome Conference (PAG XXV), January 14-18, 2017, San Diego, CA.
5. **Herndon, N.**, Grau, E. S., Batra, I., Demurjian Jr., S. A., Vasquez-Gross, H. A., Staton,

- M. E., and Wegrzyn, J. L. (2016). *CartograTree: Enabling Landscape Genomics for Forest Trees*. Oral presentation at the Open Source Geospatial Research & Education Symposium (OGRS 2016), October 12-14, 2016, Perugia, Italy.
6. **Herndon, N.** and Caragea, D. (2016). *Ab initio Splice Site Prediction with Simple Domain Adaptation Classifiers*. Oral presentation at the 7th International Conference on Bioinformatics Models, Methods and Algorithms (BIOINFORMATICS 2016), February 21-23, 2016, Rome, Italy.
 7. **Herndon, N.**, and Caragea, D. (2015). *Domain Adaptation Algorithms for ab initio Splice Site Prediction*. Poster presentation at the First Annual Midwest Bioinformatics Conference, October 15-16, 2015, Kansas City, MO.
 8. **Herndon, N.**, and Caragea, D. (2015). *An Evaluation of Self-training Styles for Domain Adaptation on the Task of Splice Site Prediction*. Oral presentation at the 2015 International Symposium on Network Enabled Health Informatics, Biomedicine and Bioinformatics (HI-BI-BI 2015), August 26-27, 2015, Paris, France.
 9. Donghum, K., **Herndon, N.**, Cheng, C., Nai, A. D. S., Jaworski, D., Ganta, R., and Park, Y. *Transcriptome of the lone star tick, Amblyomma americanum, revealing the molecular interaction between the vector and the pathogen Ehrlichia chaffeensis*. Poster presented by K. Donghum at the 9th Arthropod Genomics Symposium (AGS 2015), June 17-19, 2015, Manhattan, KS.
 10. **Herndon, N.**, and Caragea, D. (2015). *Domain Adaptation with Logistic Regression for the Task of Splice Site Prediction*. Oral presentation at the 11th International Symposium on Bioinformatics Research and Applications (ISBRA 2015), June 7-10, 2015, Norfolk, VA.
 11. Tangirala, K., **Herndon, N.**, and Caragea, D. (2015). *Community Detection-Based Feature Construction for Protein Sequence Classification*. Oral presentation at the 11th International Symposium on Bioinformatics Research and Applications (ISBRA 2015), June 7-10, 2015, Norfolk, VA.
 12. **Herndon, N.**, Tangirala, K., and Caragea, D. (2014). *Predicting Protein Localization Using a Domain Adaptation Naïve Bayes Classifier with Burrows Wheeler Transform Features*. Oral presentation at the 6th IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2014), November 2-5, 2014, Belfast, UK.
 13. Stanescu, A. and Caragea, D. (2014). *Ensemble-based semi-supervised learning approaches for imbalanced splice site datasets*. Regular paper presented by **N. Herndon** at the 6th IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2014), November 2-5, 2014, Belfast, UK.
 14. **Herndon, N.** and Caragea, D. (2014). *Empirical Study of Domain Adaptation with Naïve Bayes on the Task of Splice Site Prediction*. Oral presentation at the 5th International Conference on Bioinformatics Models, Methods and Algorithms (BIOINFORMATICS 2014), March 3-6, 2014, Angers, France.
 15. Tangirala, K. and Caragea, D. (2014). *Generating Features Using Burrows Wheeler Transformation for Biological Sequence Classification*. Short paper presented by **N. Herndon** at the 5th International Conference on Bioinformatics Models, Methods and Algorithms (BIOINFORMATICS 2014), March 3-6, 2014, Angers, France.
 16. **Herndon, N.**, Shelton, J. M., Andrews, W., Wang, W., and Brown, S. J. (2014). *Improving the Tribolium draft Assembly with Physical Maps Based on Imaging Ultra-Long Single DNA Molecules*. Poster presentation at 22nd International Plant and Animal

- Genome Conference (PAG XXII), January 11-15, 2014, San Diego, CA.
17. Shelton, J. M., **Herndon, N.**, Gray, M. M., Liang, H., Durrett, T., Johnson, L., Akhunova, A., and Brown, S. J. (2014). *Multi-K-Mer de novo Transcriptome Assembly, Validation, and Count Summarizing for Four Plant Taxa*. Poster presented by J. M. Shelton at the 22nd International Plant and Animal Genome Conference (PAG XXII), January 11-15, 2014, San Diego, CA.
 18. Giraldo, M. C., Dalby, M., **Herndon, N.**, Zhou, X., Jayasundera, K. B., Tao, A., Xu, J. R., and Valent, B. (2013). *Identification of Rice Proteins Interacting with Magnaporthe oryzae Effector Proteins*. Poster presented by M. C. Giraldo at the 6th International Rice Blast Conference (IRBC 2013), August 20-24, 2013, Jejudo, South Korea.
 19. **Herndon, N.** and Caragea, D. (2013). *Naïve Bayes Domain Adaptation for Biological Sequences*. Oral presentation at the 4th International Conference on Bioinformatics Models, Methods and Algorithms (BIOINFORMATICS 2013), February 11-14, 2013, Barcelona, Spain.
 20. **Herndon, N.** and Brown, S. J. (2013). *Improving the T.castaneum genome assembly with 3 mate pairs jumping libraries*. Oral presentation at K-INBRE Bioinformatics Core Minisymposium, January 2013.
 21. Shelton, J. M., Gray, M., Brown, S. J., Chellapilla, S., **Herndon, N.**, Akhunova, A., Akhunov, E., Liang, H., and Johnson, L. C. (2013). *De novo Transcriptome of Two Edaphically and Phenotypically Divergent Grasses: Dominant Forage Grass Big Bluestem Andropogon gerardii ssp. gerardii and Drought-Tolerant Sand Bluestem Andropogon gerardii ssp. hallii*. Poster presented by J. M. Shelton at the 21st International Plant and Animal Genome Conference (PAG XXI), January 12-16, 2013, San Diego, CA.
 22. **Herndon, N.** and Caragea, D. (2012). *Domain Adaptation for Genome-Wide Splice Site Prediction*. Oral presentation at K-INBRE Bioinformatics GRA summit, January, 2012.
 23. **Herndon, N.**, Osei-Boadi, K., Jiang, D., Caragea, D., and Brown, S. J. (2010). *MAKER and Apollo: tools for genome annotation*. Oral presentation at the Fourth K-INBRE Bioinformatics GRA Summit, July 2010, Manhattan, KS.

Paper Refereeing

Journals: PLoS One (three articles), Network Modeling Analysis in Health Informatics and Bioinformatics (one article), Social Network Analysis and Mining (one article), F1000Research (one article).

Conferences: SEDE'17 (three papers), SEDE'16 (three papers).

Professional Development

- Mar 2017 Participated in the *NCBI Genomics Hackathon* focused on advanced bioinformatics analysis of next generation sequencing data and metadata.
- Jan 2017 Participated in the *Tripal Hackathon* focused on making existing open-source code sharable, and implementing common download formats using the Tripal Download API.
- Fall 2016 Took the *Science Communication* course at University of Connecticut focused on improving the communication skills of scientists for better communicating science with the general public.

- Sep 2015 Attended the talk *Taking a Scientific Approach to Science and Engineering Education* by Professor Carl E. Wieman. A presentation as part of the Provost's Excellence in Scholarship Lecture Series at Kansas State University.
- Sep 2015 Attended the talk *Finding Joy in Teaching Students of Diverse Backgrounds: Culturally Responsive and Socially Just Practices in U.S. Classrooms* by Professor Emerita Sonia Nieto. A presentation as part of the College of Education's Distinguished Educational Research Lecture Series at Kansas State University.
- Mar 2014 Attended the interactive talk about the benefits of diversity, *Diversity re-considered: Social justice, compelling national need of global imperative* by Dr. Orlando Taylor. Sponsored by the Diversity Programming Committee, the Graduate School, and the Graduate Student Council at Kansas State University.
- Sep 2013 Attended the *Grant Writing Basics Workshop* at Kansas State University presented by James Guikema, Ph.D. Topics included: tips and tricks to find funding, develop the budget, prepare the proposal, and submit them correctly to get the grants.
- Jan 2013 Attended the *Time Management and Productivity Workshop for Graduate Students* at Kansas State University presented by Kerry Ann Rockquemore, Ph.D. Topics included: time management, writing productivity, long and short term goals, and transitioning to faculty positions.
- Sep 2012 Attended the presentation *The Art and Science of Teaching* by Bryce Lane, Ph.D. Organized by the Faculty Exchange for Teaching Excellence at Kansas State University.
- Jan 2011 Attended the NSF workshop *Science: Becoming the Messenger* at University of Kansas. The training focused on building skills for communicating effectively to a broad audience, using blogging, social media, and video presentations.
- Sep 2010 Attended the presentation *The Element: How finding your passion changes everything* by Sir Ken Robinson at Kansas State University.