

Christopher J Mungall

Lawrence Berkeley National Laboratory
Genomics Division
1 Cyclotron Road
Berkeley CA 94720

Phone: (510) 486-4170
Email: cjmungall@lbl.gov

Education

2011 **Ph.D.** Bioinformatics, University of Edinburgh
1993 **BSc.** Artificial Intelligence and Computer Science, University of Edinburgh

Employment

2006-Present **Scientist** Genomics Division, Lawrence Berkeley National Laboratory
2001-2006 **Bioinformatics specialist** Howard Hughes Medical Institute, UC Berkeley
1999-2006 **Bioinformatician** Life Sciences Division, Lawrence Berkeley National Laboratory
1994-1999 **Bioinformatician.** Roslin Institute, Edinburgh, UK

Publications

Refereed Journal Articles

- | | |
|------|---|
| 2013 | Smedley, D., Oellrich, A., Köhler, S., Ruef, B., Westerfield, M., Robinson, P., Lewis, S., and Mungall, C. (2013). PhenoDigm: analyzing curated annotations to associate animal models with human diseases. <i>Database: the journal of biological databases and curation</i> , 2013 |
| | Meehan, T., Vasilevsky, N., Mungall, C. , Dougall, D., Haendel, M., Blake, J., and Diehl, A. (2013). Ontology based molecular signatures for immune cell types via gene expression analysis. <i>BMC Bioinformatics</i> , 14(1):263 |
| | Roncaglia, P., Martone, M. E., Hill, D. P., Berardini, T. Z., Foulger, R. E., Imam, F. T., Drabkin, H., Mungall, C. , and Lomax, J. (2013). The Gene Ontology (GO) Cellular Component Ontology: integration with SAO (Subcellular Anatomy Ontology) and other recent developments. <i>Journal of Biomedical Semantics</i> , 4(1):20 |
| | Köhler, S., Doelken, S. C., Ruef, B. J., Bauer, S., Washington, N., Westerfield, M., Gkoutos, G., Schofield, P., Smedley, D., Lewis, S. E., Robinson, P. N., and Mungall, C. J. (2013). Construction and accessibility of a cross-species phenotype ontology along with gene annotations for biomedical research. <i>F1000Research</i> , 2 |

- Hill, D. P., Adams, N., Bada, M., Batchelor, C., Berardini, T. Z., Dietze, H., Drabkin, H. J., Ennis, M., Foulger, R. E., Harris, M. A., Hastings, J., Kale, N. S., de Matos, P., **Mungall, C. J.**, Owen, G., Roncaglia, P., Steinbeck, C., Turner, S., and Lomax, J. (2013). Dovetailing biology and chemistry: integrating the Gene Ontology with the ChEBI chemical ontology. *BMC genomics*, 14(1):513
- Doelken, S. C., Köhler, S., **Mungall, C. J.**, Gkoutos, G. V., Ruef, B. J., Smith, C., Smedley, D., Bauer, S., Klopocki, E., Schofield, P. N., et al. (2013). Phenotypic overlap in the contribution of individual genes to CNV pathogenicity revealed by cross-species computational analysis of single-gene mutations in humans, mice and zebrafish. *Disease models & mechanisms*, 6(2):358–372
- Egaña Aranguren, M., Fernández-Breis, J. T., Antezana, E., **Mungall, C.J.**, Rodríguez González, A., and Wilkinson, M. D. (2013). OPPL-Galaxy, a Galaxy tool for enhancing ontology exploitation as part of bioinformatics workflows. *Journal of biomedical semantics*, 4(1):2
- Cooper, L., Walls, R. L., Elser, J., Gandolfo, M. a., Stevenson, D. W., Smith, B., Preece, J., Athreya, B., **Mungall, C. J.**, Rensing, S., Hiss, M., Lang, D., Reski, R., Berardini, T. Z., Li, D., Huala, E., Schaeffer, M., Menda, N., Arnaud, E., Shrestha, R., Yamazaki, Y., and Jaiswal, P. (2013). The plant ontology as a tool for comparative plant anatomy and genomic analyses. *Plant & cell physiology*, 54(2):e1
- 2012 **Mungall, C. J.**, Torniai, C., Gkoutos, G. V., Lewis, S. E., and Haendel, M. A. (2012). Uberon, an integrative multi-species anatomy ontology. *Genome Biology*, 13(1):R5
- Thomas, P. D., Wood, V., **Mungall, C. J.**, Lewis, S. E., and Blake, J. A. (2012). On the Use of Gene Ontology Annotations to Assess Functional Similarity among Orthologs and Paralogs: A Short Report. *PLoS computational biology*, 8(2):e1002386
- Osumi-Sutherland, D., Reeve, S., **Mungall, C. J.**, Neuhaus, F., Ruttenberg, A., Jefferis, G. S. X. E., and Armstrong, J. D. (2012). A strategy for building neuroanatomy ontologies. *Bioinformatics (Oxford, England)*, pages 1–10
- Walls, R. L., Athreya, B., Cooper, L., Elser, J., Gandolfo, M. A., Jaiswal, P., **Mungall, C. J.**, Preece, J., Rensing, S., Smith, B., and Stevenson, D. W. (2012). Ontologies as integrative tools for plant science. *American journal of botany*, pages ajb.1200222–
- Chen, C.-K., **Mungall, C. J.**, Gkoutos, G. V., Doelken, S. C., Köhler, S., Ruef, B. J., Smith, C., Westerfield, M., Robinson, P. N., Lewis, S. E., Schofield, P. N., and Smedley, D. (2012). MouseFinder: Candidate disease genes from mouse phenotype data. *Human mutation*, 33(5):858–66
- 2011 **Mungall, C.**, Torniai, C., Diehl, A., Haendel, M., Ireland, A., Manzoor, S., Meehan, T., and Osumi-Sutherland, D. (2011). Modularization for the Cell Ontology

- Meehan, T., Masci, A. M., Abdulla, A., Cowell, L., Blake, J., **Mungall, C. J.**, and Diehl, A. (2011). Logical Development of the Cell Ontology. *BMC Bioinformatics*, 12(1):6
- Tirmizi, S., Aitken, S., Moreira, D., **Mungall, C. J.**, Sequeda, J., Shah, N., and Miranker, D. (2011). Mapping between the OBO and OWL ontology languages. *Journal of Biomedical Semantics*, 2(Suppl 1):S3
- Kohler, S., Bauer, S., **Mungall, Chris J**, Carletti, G., Smith, C. L., Schofield, P., Gkoutos, G. V., and Robinson, P. N. (2011). Improving ontologies by automatic reasoning and evaluation of logical definitions. *BMC Bioinformatics*, 12(1):418
- Hoehndorf, R., Batchelor, C., Bittner, T., Dumontier, M., Eilbeck, K., Knight, R., **Mungall, Chris J**, Richardson, J. S., Stombaugh, J., Westhof, E., Zirbel, C. L., and Leontis, N. B. (2011). The RNA Ontology (RNAO): An ontology for integrating RNA sequence and structure data. *Applied Ontology*, 6(1):53–89
- 2010 Deegan, J., Dimmer, E., and **Mungall, C. J.** (2010). Formalization of taxon-based constraints to detect inconsistencies in annotation and ontology development. *BMC bioinformatics*, 11(1):530
- Mungall, C. J.**, Bada, M., Berardini, T. Z., Deegan, J., Ireland, A., Harris, M. A., Hill, D. P., and Lomax, J. (2011). Cross-product extensions of the Gene Ontology. *Journal of Biomedical Informatics*, 44(1):80–86
- Antezana, E., Venkatesan, A., **Mungall, C. J.**, Mironov, V., and Kuiper, M. (2010). ONTO-ToolKit: enabling bio-ontology engineering via Galaxy. *BMC Bioinformatics*, 11(Suppl 12):S8
- Alterovitz, G., Xiang, M., Hill, D. P., Lomax, J., Liu, J., Cherkassky, M., Dreyfuss, J., **Mungall, C.J.**, Harris, M. A., Dolan, M. E., Blake, J. A., and Ramoni, M. F. (2010). Ontology engineering. *Nature Biotechnology*, 28(2):128–130
- 2009 **Mungall, C. J.**, Gkoutos, G., Smith, C., Haendel, M., Lewis, S., and Ashburner, M. (2010). Integrating phenotype ontologies across multiple species. *Genome Biology*, 11(1):R2
- Skinner, M. E., Uzilov, A. V., Stein, L. D., **Mungall, C. J.**, and Holmes, I. H. (2009). JBrowse: A next-generation genome browser. *Genome Research*
- Hancock, J., Mallon, A.-M., Beck, T., Gkoutos, G., **Mungall, C. J.**, and Schofield, P. (2009). Mouse, man, and meaning: bridging the semantics of mouse phenotype and human disease. *Mammalian Genome*

- Schober, D., Smith, B., Lewis, S., Kusnierczyk, W., Lomax, J., **Mungall, C. J.**, Taylor, C., Rocca-Serra, P., and Sansone, S.-A. (2009). Survey-based naming conventions for use in OBO Foundry ontology development. *BMC Bioinformatics*, 10(1):125
- Masci, A., Arighi, C., Diehl, A., Lieberman, A., **Mungall, C.**, Scheuermann, R., Smith, B., and Cowell, L. (2009). An improved ontological representation of dendritic cells as a paradigm for all cell types. *BMC bioinformatics*, 10(1):70
- Diehl, A. D., Augustine, A. D., Blake, J. A., Cowell, L. G., Gold, E. S., Gondré-Lewis, T. A., Masci, A. M., Meehan, T. F., Morel, P. A., Group, N. C. O. W., Nijnik, A., Peters, B., Pulendran, B., Scheuerman, R. H., Yao, Q. A., Zand, M. S., and **Mungall, C. J.** (2010). Hematopoietic Cell Types: Prototype for a Revised Cell Ontology. *Journal of Biomedical Informatics*, Epub ahead
- 2008 Yandell, M., Moore, B., Salas, F., **Mungall, C. J.**, MacBride, A., White, C., and Reese, M. G. (2008). Genome-wide analysis of human disease alleles reveals that their locations are correlated in paralogous proteins. *PLoS Computational Biology*, 4:e1000218
- Pfeiffer, B. D., Jenett, A., Hammonds, A. S., Ngo, T.-T. B., Misra, S., Murphy, C., Scully, A., Carlson, J. W., Wan, K. H., Lavery, T. R., **Mungall, C. J.**, Svirskas, R., Kadonaga, J. T., Doe, C. Q., Eisen, M. B., Celniker, S. E., and Rubin, G. M. (2008). Tools for neuroanatomy and neurogenetics in *Drosophila*. *Proceedings of the National Academy of Sciences of the United States of America*, 105:9715–9720
- Carbon, S., Ireland, A., **Mungall, C. J.**, Shu, S., Marshall, B., Lewis, S., the AmiGO Hub, and the Web Presence Working Group (2008). AmiGO: online access to ontology and annotation data. *Bioinformatics*
- 2007 **Mungall, C. J.**, Emmert, D. B., and Consortium, T. F. (2007a). A Chado case study: an ontology-based modular schema for representing genome-associated biological information. *Bioinformatics*, 23(13):i337–346
- Smith, C. D., Shu, S., **Mungall, C. J.**, and Karpen, G. H. (2007b). The Release 5.1 annotation of *Drosophila melanogaster* heterochromatin. *Science*, 316:1586–1591
- Smith, B., Ashburner, M., Rosse, C., Bard, J., Bug, W., Ceusters, W., Goldberg, L. J., Eilbeck, K., Ireland, A., **Mungall, C. J.**, Consortium, T. O. B. I., Leontis, N., Rocca-Serra, P., Ruttenberg, A., Sansone, S.-A., Scheuermann, R. H., Shah, N., Whetzel, P. L., and Lewis, S. (2007a). The OBO Foundry: coordinated evolution of ontologies to support biomedical data integration. *Nat Biotechnol*, 25(11):1251–1255
- 2006 Yandell, M., **Mungall, C. J.**, Smith, C., Prochnik, S., Kaminker, J., Hartzell, G., Lewis, S., and Rubin, G. M. (2006). Large-scale trends in the evolution of gene structures within 11 animal genomes. *PLoS Computational Biology*, 2(3):e15

- Rubin, D. L., Lewis, S. E., **Mungall, C. J.**, Misra, S., Westerfield, M., Ashburner, M., Sim, I., Chute, C. G., Solbrig, H., Storey, M.-A., Smith, B., Day-Richter, J., Noy, N. F., and Musen, M. A. (2006). National Center for Biomedical Ontology: advancing biomedicine through structured organization of scientific knowledge. *OMICS: A Journal of Integrative Biology*, 10(2):185–198
- 2005 Smith, B., Ceusters, W., Kohler, J., Kumar, A., Lomax, J., **Mungall, C. J.**, Neuhaus, F., Rector, A., and Rosse, C. (2005). Relations in Biomedical Ontologies. *Genome Biology*, 6(5)
- Eilbeck, K., Lewis, S. E., **Mungall, C. J.**, Yandell, M. D., Stein, L. D., Durbin, R., and Ashburner, M. (2005). The Sequence Ontology: a tool for the unification of genome annotations. *Genome Biology*, 6(5)
- 2004 **Mungall, C. J.** (2004). Obol: Integrating Language and Meaning in Bio-Ontologies. *Comparative and Functional Genomics*, 5(7):509–520
- Harris, M. A., Clark, J., Ireland, A., Lomax, J., Ashburner, M., Foulger, R., Eilbeck, K., Lewis, S., Marshall, B., **Mungall, C. J.**, Richter, J., Rubin, G. M., Blake, J. A., Bult, C., Dolan, M., Drabkin, H., Eppig, J. T., Hill, D. P., Ni, L., Ringwald, M., Balakrishnan, R., Cherry, J. M., Christie, K. R., Costanzo, M. C., Dwight, S. S., Engel, S., Fisk, D. G., Hirschman, J. E., Hong, E. L., Nash, R. S., Sethuraman, A., Theesfeld, C. L., Botstein, D., Dolinski, K., Feierbach, B., Berardini, T., Mundodi, S., Rhee, S. Y., Apweiler, R., Barrell, D., Camon, E., Dimmer, E., Lee, V., Chisholm, R., Gaudet, P., Kibbe, W., Kishore, R., Schwarz, E. M., Sternberg, P., Gwinn, M., Hannick, L., Wortman, J., Berriman, M., Wood, V., de la Cruz, N., Tonellato, P., Jaiswal, P., Seigfried, T., White, R., and Consortium, G. O. (2004). The Gene Ontology (GO) database and informatics resource. *Nucleic Acids Res*, 32(Database issue):D258—D261
- 2002 **Mungall, C. J.**, Misra, S., Berman, B. P., Carlson, J., Frise, E., Harris, N., Marshall, B., Shu, S., Kaminker, J. S., Prochnik, S. E., Smith, C. D., Smith, E., Tupy, J. L., Wiel, C., Rubin, G. M., and Lewis, S. E. (2002). An integrated computational pipeline and database to support whole-genome sequence annotation. *Genome Biol*, 3(12):RESEARCH0081
- Stein, L. D., **Mungall, C. J.**, Shu, S., Caudy, M., Mangone, M., Day, A., Nickerson, E., Stajich, J. E., Harris, T. W., Arva, A., and Lewis, S. (2002). The generic genome browser: a building block for a model organism system database. *Genome Res*, 12(10):1599–1610
- Stajich, J. E., Block, D., Boulez, K., Brenner, S. E., Chervitz, S. A., Dagdigian, C., Fuellen, G., Gilbert, J. G., Korf, I., Lapp, H., Lehtvaslaiho, H., Matsalla, C., **Mungall, C. J.**, Osborne, B. I., Pocock, M. R., Schattner, P., Senger, M., Stein, L. D., Stupka, E., Wilkinson, M. D., and Birney, E. (2002). The Bioperl toolkit: Perl modules for the life sciences. *Genome Res*, 12(10):1611–1618

Misra, S., Crosby, M. A., **Mungall, C. J.**, Matthews, B. B., Campbell, K. S., Hradecky, P., Huang, Y., Kaminker, J. S., Millburn, G. H., Prochnik, S. E., Smith, C. D., Tupy, J. L., Whitfield, E. J., Bayraktaroglu, L., Berman, B. P., Bettencourt, B. R., Celniker, S. E., de Grey, A. D. N. J., Drysdale, R. A., Harris, N. L., Richter, J., Russo, S., Schroeder, A. J., Shu, S. Q., Stapleton, M., Yamada, C., Ashburner, M., Gelbart, W. M., Rubin, G. M., and Lewis, S. E. (2002). Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review. *Genome Biol*, 3(12)

Lewis, S. E., Searle, S. M., Harris, N., Gibson, M., Lyer, V., Richter, J., Wiel, C., Bayraktaroglu, L., Birney, E., Crosby, M. A., Kaminker, J. S., Matthews, B. B., Prochnik, S. E., Smith, C. D., Tupy, J. L., Rubin, G. M., Misra, S., **Mungall, C. J.**, and Clamp, M. E. (2002). Apollo: a sequence annotation editor. *Genome Biol*, 3(12):81–82

Gardner, M. J., Hall, N., Fung, E., White, O., Berriman, M., Hyman, R. W., Carlton, J. M., Pain, A., Nelson, K. E., Bowman, S., Paulsen, I. T., James, K., Eisen, J. A., Rutherford, K., Salzberg, S. L., Craig, A., Kyes, S., Chan, M. S., Nene, V., Shallom, S. J., Suh, B., Peterson, J., Angiuoli, S., Pertea, M., Allen, J., Selengut, J., Haft, D., Mather, M. W., Vaidya, A. B., Martin, D. M., Fairlamb, A. H., Fraunholz, M. J., Roos, D. S., Ralph, S. A., McFadden, G. I., Cummings, L. M., Subramanian, G. M., **Mungall, C. J.**, Venter, J. C., Carucci, D. J., Hoffman, S. L., Newbold, C., Davis, R. W., Fraser, C. M., and Barrell, B. (2002). Genome sequence of the human malaria parasite *Plasmodium falciparum*. *Nature*, 419(6906):498–511

Bergman, C. M., Pfeiffer, B. D., Rincón-Limas, D. E., Hoskins, R. A., Gnirke, A., **Mungall, C. J.**, Wang, A. M., Kronmiller, B., Pacle, J., Park, S., Stapleton, M., Wan, K., George, R. A., de Jong, P. J., Botas, J., Rubin, G. M., and Celniker, S. E. (2002). Assessing the impact of comparative genomic sequence data on the functional annotation of the *Drosophila* genome. *Genome Biol*, 3(12):RESEARCH0086

2001 Hu, J., **Mungall, C. J.**, Law, A., Papworth, R., Nelson, J. P., Brown, A., Simpson, I., Leckie, S., Burt, D. W., Hillyard, A. L., and Archibald, A. L. (2001). The ARKdb: genome databases for farmed and other animals. *Nucleic Acids Res*, 29(1):106–110

Ashburner, M., Ball, C. A., Blake, J. A., Butler, H., Cherry, J. M., Corradi, J., Dolinski, K., Eppig, J. T., Harris, M., Hill, D. P., Lewis, S., Marshall, B., **Mungall, C. J.**, Reiser, L., Rhee, S., Richardson, J. E., Richter, J., Ringwald, M., Rubin, G. M., Sherlock, G., and Yoon, J. (2001). Creating the gene ontology resource: design and implementation. *Genome Res*, 11(8):1425–1433

- | | |
|------|---|
| 2000 | Rubin, G. M., Yandell, M. D., Wortman, J. R., Miklos, G. L. G., Nelson, C. R., Hariharan, I. K., Fortini, M. E., Li, P. W., Apweiler, R., Fleischmann, W., Cherry, J. M., Henikoff, S., Skupski, M. P., Misra, S., Ashburner, M., Birney, E., Boguski, M. S., Brody, T., Brokstein, P., Celniker, S. E., Chervitz, S. A., Coates, D., Cravchik, A., Gabrielian, A., Galle, R. F., Gelbart, W. M., George, R. A., Goldstein, L. S., Gong, F., Guan, P., Harris, N. L., Hay, B. A., Hoskins, R. A., Li, J., Li, Z., Hynes, R. O., Jones, S. J., Kuehl, P. M., Lemaitre, B., Littleton, J. T., Morrison, D. K., Mungall, C. J. , O'Farrell, P. H., Pickeral, O. K., Shue, C., Voss hall, L. B., Zhang, J., Zhao, Q., Zheng, X. H., and Lewis, S. (2000). Comparative genomics of the eukaryotes. <i>Science</i> , 287(5461):2204–2215 |
| 1998 | Hu, J., Mungall, C. J. , Nicholson, D., and Archibald, A. L. (1998). Design and implementation of a CORBA-based genome mapping system prototype. <i>Bioinformatics</i> , 14(2):112–120 |

Book Chapters

- | | |
|------|---|
| 2007 | Haendel, M. A., Neuhaus, F., Osumi-Sutherland, D., Mabee, P. M., Mejino, J. L. J., Mungall, C. J. J. , and Smith, B. (2007). CARO - The Common Anatomy Reference Ontology. In <i>Anatomy Ontologies for Bioinformatics, Principles and Practice</i> , volume Albert Burger, Duncan Davidson and Richard Baldock (Eds.). Springer |
|------|---|

Conference Proceedings

- | | |
|------|--|
| 2013 | Brush, M. H., Mungall, C., Washington, N., and Haendel, M. A. (2013). What's in a Genotype?: An Ontological Characterization for Integration of Genetic Variation Data. In <i>Fourth International International Conference on Biomedical Ontology</i> , pages 1–4 |
| 2011 | Mungall, C. (2011). POSH: The Prolog OWL Shell. In Dumontier, M. and Courtot, M., editors, <i>Proceedings of the 8th International Workshop on OWL: Experiences and Directions (OWLED2011), San Francisco, USA. June 5-6, 2011</i> |
| 2009 | Mungall, C. J. (2009). Experiences Using Logic Programming in Bioinformatics. In <i>Lecture notes in computer science</i> , volume Volume 564, pages 1–21. Springer |
| | Vassiliadis, V., Wielemaker, J., and Mungall, C. J. (2009). Processing OWL2 ontologies using Thea: An application of logic programming. In <i>6th OWL Experiences and Directions Workshop (OWLED 2009)</i> |

- | | |
|------|---|
| | Gkoutos, G. V., Mungall, Chris J , Doelken, S., Ashburner, M., Lewis, S., Hancock, J., Schofield, P., Köhler, S., Robinson, P. N., Dolken, S., and Kohler, S. (2009). Entity/Quality-Based Logical Definitions for the Human Skeletal Phenome using PATO. In <i>Proceedings of the 31st Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC 2009)</i> , volume 2009, pages 7069–72 |
| 2008 | Bada, M., Mungall, C. J. , and Hunter, L. (2008). A Call for an Abductive Reasoning Feature in OWL-Reasoning Tools toward Ontology Quality Control. In <i>5th OWL Experiences and Directions Workshop (OWLED 2008)</i> |
| 2007 | Mungall, C. J. , Gkoutos, G., Washington, N., and Lewis, S. (2007b). Representing Phenotypes in OWL. In Golbreich, C., Kalyanpur, A., and Parsia, B., editors, <i>Proceedings of the OWLED 2007 Workshop on OWL: Experience and Directions</i> , Innsbruck, Austria |
| 2003 | |

Manuscripts in submission

- | | |
|------|---|
| 2013 | <p>A promoter level mammalian expression atlas. Submitted to Nature. Role: middle author</p> <p>An atlas of active enhancers across human cell types and tissues. Provisionally accepted by Nature. Role: middle author</p> <p>Improved exome prioritization of disease genes through cross species phenotype comparison. Submitted to Genome Research. Role: middle author</p> <p>The Porifera Ontology (PORO). Submitted to JBMS. Role: senior author</p> <p>Uberon in 2013. Submitted to JBMS. Role: senior author</p> <p>The Cell Ontology in 2013. Submitted to JBMS. Role: senior author</p> <p>The Environment Ontology. Accepted by JBMS pending revisions. Role: middle author</p> <p>The Biological Spatial Ontology. Submitted to JBMS. Role: middle author</p> <p>The Cell Line Ontology (CLO). Provisionally accepted by JBMS. Role: middle author</p> <p>The Human Phenotype Ontology Databases and Resource. Submitted to NAR. Role: middle author</p> |
|------|---|

Awards and Honors

2013	Encyclopedia of Life Rubenstein Fellowship award. Role: collaborator
------	--

Grants and Fellowships

Semantic LAMHDI to develop a semantic infrastructure for linking human diseases to model systems. 2012-2016. Role: Co-investigator.

Invited Talks

2013	Uberon : an integrative multi-species ontology - European Bioinformatics Institute Industry Workshop, Hinxton Genome Campus, April 2013
2013	Mapping Phenotype Ontologies for diabetes and obesity - European Bioinformatics Institute, Hinxton Genome Campus, April 2013
2012	Helping Machines to Help Us (Keynote) - Rocky Bioinformatics Summit, November 2012
2011	The Environment Ontology, Environmental Protection Agency offices, San Francisco, March 2011
Conference on Logic Pro- gram- ming, Pasadena, July 2009	
2009	Logic Programming in Bioinformatics (Keynote) - International Conference on Logic Programming, Pasadena, July 2009
2007	Overview of the Open Biomedical Ontologies Foundry - Clinical Trial Ontology Workshop, NIH, Bethesda, May 2007
2006	Ontologies for Evo-Devo, National Evolutionary Synthesis Center, Nov 2006

Teaching Experience

- 2012: **Course organizer**. Developing ontologies in Protege/OWL, Hinxton, UK, January 2012
- 2011: **Tutorial organizer**. Developing ontologies in OBO and OWL, International Conference on Biomedical Ontologies, Buffalo, NY, 2009
- 2009: **Tutorial co-organizer**. Developing ontologies in OBO and OWL, International Conference on Biomedical Ontologies, Buffalo, NY, 2009
- 2001, 2002, 2003: **Teaching assistant** Programming for biology. Cold Spring Harbor Laboratory
- 2001: **Module Organizer**. Taught perl scripting module as part of International Training Course on Bioinformatics, FIOCRUZ, Rio de Janeiro, Brazil, May 21-June 15, 2001

Service

- 2006-Present : **Open Biological Ontologies Library Coordinator**
- 2011, 2012, 2013: **Program Committee Member, International Conference on Biomedical Ontology**
- 2011, 2012, 2013: **Program Committee Member, Semantic Web Applications in the Life Sciences**
- 2011: **Program Committee Member, OWL: Experience and Directions**
- 2011: **Program Committee Member, ISMB/EECB**
- 2010, 2011: **Scientific Advisory Board Member, Disease Ontology**
- 2005-Present : **Reviewer** Bioinformatics, Journal of Biomedical Semantics, Database, BMC Bioinformatics, Nucleic Acids Research