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Education

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

Employment

2006-Present **Staff 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

2015

Mungall, C.J., Washington, N. L., Nguyen-Xuan, J., Condit, C., Smedley, D., Köhler, S., Groza, T., Shefchek, K., Hochheiser, H., Robinson, P. N., Lewis, S. E., and Haendel, M. A. (2015). Use of Model Organism and Disease Databases to Support Matchmaking for Human Disease Gene Discovery. *Human mutation*, 36(10):979–84

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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 *Anatomy Ontologies for Bioinformatics, Principles and Practice*, volume Albert Burger, Duncan Davidson and Richard Baldock (Eds.). Springer

Letters to the Editor

2013 Druzinsky, R., **Mungall, C.J.**, Haendel, M., Lapp, H., and Mabee, P. (2013). What is an anatomy ontology? Technical report

Conference Proceedings

2014 **Mungall, C. J.**, Dietze, H., and Osumi-Sutherland, D. (2014). Use of OWL within the Gene Ontology. In Keet, M. and Tamma, V., editors, *Proceedings of the 11th International Workshop on OWL: Experiences and Directions (OWLED 2014)*, pages 25–36, Riva del Garda, Italy, October 17-18, 2014

2013 Brush, M. H., **Mungall, C.J.**, Washington, N., and Haendel, M. A. (2013). What's in a Genotype ? An Ontological Characterization for Integration of Genetic Variation Data. In Dumontier, M., Hoehndorf, R., and Baker, C. J. O., editors, *Proceedings of the International Conference on Biomedical Ontology 2013, Montreal, Canada, July 7-12, 2013*, pages 105–108

2011 **Mungall, C.** (2011). POSH: The Prolog OWL Shell. In Dumontier, M. and Courtot, M., editors, *Proceedings of the 8th International Workshop on OWL: Experiences and Directions (OWLED2011), San Francisco, USA. June 5-6, 2011*

2009 **Mungall, C. J.** (2009). Experiences Using Logic Programming in Bioinformatics. In *Lecture notes in computer science*, 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 *6th OWL Experiences and Directions Workshop (OWLED 2009)*

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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 *5th OWL Experiences and Directions Workshop (OWLED 2008)*

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, *Proceedings of the OWLED 2007 Workshop on OWL: Experience and Directions*, Innsbruck, Austria

2003 Ashburner, M., **Mungall, C.J.**, and Lewis, S. (2003). Ontologies for biologists: a community model for the annotation of genomic data. In *Cold Spring Harbor symposia on quantitative biology*, volume 68, pages 227–235

Pre-prints

2014 **Mungall, C. J.** (2014). Formalization of Genome Interval Relations. *bioRxiv*

2014 Bolleman, J., **Mungall, C. J.**, Strozzi, F., Baran, J., Dumontier, M., Bonnal, R. J., Buels, R., Hoehndorf, R., Fujisawa, T., Katayama10, T., et al. (2014). Faldo: A semantic standard for describing the location of nucleotide and protein feature annotation. *bioRxiv*

Manuscripts in submission

Towards a computationally actionable phenotype data exchange (PDX). JAMIA. Role: middle author

Awards and Honors

2013 Encyclopedia of Life Rubenstein Fellowship award. Role: collaborator

Grants and Fellowships

Semantic LAMHDI (NIH) to develop a semantic infrastructure for linking human diseases to model systems. 2012-2016. Role: Site PI.

Invited Talks

2015 Crossing the Species Divide - NIH Symposium: Linking Disease Model Phenotypes to Human Conditions, NIH, September 2015

2015	From Phenotype Ontologies to Phenotype Networks, Stanford, May 2015
2015	Describing samples using the Uberon anatomy ontology - Genomics Standards Workshop JGI, May 2015
2015	Towards Common Peer Based Standards Development - NIH BD2K Data Standards Workshop, Bethesda, February 2015
2014	Computing on the environment - NIEHS Workshop, NC State, September 2014
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
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**. Module corganizer. WHO International Training Course on Bioinformatics, FIOCRUZ, Rio de Janeiro, Brazil, May 21-June 15, 2001

Service

2015	**Working Group Member** National Center for Ecological Analysis and Synthesis Ontology WG
2015	**Program Committee Member** 4th Workshop on Knowledge Discovery and Data Mining Meets Linked Open Data
2014-Present	**Working Group Member** Global Alliance for Genomics and Health, Clinical Working Group
2014-Present	**Working Group Member** International Rare Diseases Consortium, Ontologies and rare disease prioritization WG
2014	**Program Committee Member** 10th Workshop on Constraint-Based Methods for Bioinformatics, September 8 2014, Lyon, France
2014-Present	**WG1 co-leader** Transcription Factor TG Consortium
2014-Present	**Member** Orion Bionetworks Knowledge Engineering Working Group
2014	**Program Committee Member** 10th WCB- Workshop on Constraint-Based Methods for Bioinformatics at CP 2014 (Lyon, France, 8th Sept. 2014)
2014	**Program Committee Member, 6th Workshop on Formal Ontologies meet Industry**
2014	**Program Committee Member, PhenoDay** ISMB 2014
2012, 2014	**SBIR/STTR Reviewer**, Department of Energy
2004-Present	**Open Biological Ontologies Library Coordinator**
2009-2013	**Program Committee Member, Bio-Ontologies**
2011-2013	**Program Committee Member / Track Chair, International Conference on Biomedical Ontologies**
2011-2013	**Program Committee Member, Semantic Web Applications in the Life Sciences**
2011	**Program Committee Member, OWL: Experience and Directions**

2010-Present	**Program Committee Member, ISMB/ECCB**
2010, 2011	**Scientific Advisory Board Member, Disease Ontology**
2005-Present	**Reviewer** PLoS Genetics, PLoS Computational Biology, PLoS ONE, Nature Methods, Bioinformatics, Journal of Biomedical Informatics, Journal of Biomedical Semantics, Peer/J, Gigascience, Database, BMC Bioinformatics, Nucleic Acids Research

Last updated: September 26, 2015