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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

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| 2015 | <p>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. <i>Human mutation</i>, 36(10):979–84</p> <p>Bone, W. P., Washington, N. L., Buske, O. J., Adams, D. R., Davis, J., Draper, D., Flynn, E. D., Girdea, M., Godfrey, R., Golas, G., Groden, C., Jacobsen, J., Köhler, S., Lee, E. M. J., Links, A. E., Markello, T. C., Mungall, C. J., Nehrebecky, M., Robinson, P. N., Sincan, M., Soldatos, A. G., Tifft, C. J., Toro, C., Trang, H., Valkanas, E., Vasilevsky, N., Wahl, C., Wolfe, L. A., Boerkoel, C. F., Brudno, M., Haendel, M. A., Gahl, W. A., and Smedley, D. (2015). Computational evaluation of exome sequence data using human and model organism phenotypes improves diagnostic efficiency. <i>Genetics in medicine : official journal of the American College of Medical Genetics</i></p> <p>Robinson, P. N., Mungall, C. J., and Haendel, M. (2015). Capturing phenotypes for precision medicine. <i>Molecular Case Studies</i>, 1(1):a000372</p> |
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- 1998 Hu, J., **Mungall, C. J.**, Nicholson, D., and Archibald, A. L. (1998). Design and implementation of a CORBA-based genome mapping system prototype. *Bioinformatics*, 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 *Anatomy Ontologies for Bioinformatics, Principles and Practice*, volume Albert Burger, Duncan Davidson and Richard Baldock (Eds.). Springer

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)*
- Gkoutos, G. V., **Mungall, C.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 *Proceedings of the 31st Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC 2009)*, 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 *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

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

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| 2015 | Manda, P., Mungall, C., Balhoff, J., Lapp, H., and Vision, T. (2015). Investigating the importance of anatomical homology for cross-species phenotype comparisons using semantic similarity. Technical report |
| 2014 | Mungall, C. J. (2014). Formalization of Genome Interval Relations. <i>bioRxiv</i> |
| 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. <i>bioRxiv</i> |

Awards and Honors

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| 2013 | Encyclopedia of Life Rubenstein Fellowship award. Role: collaborator |
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Awarded Proposals

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| 2012-2016 | Semantic LAMHDI: Linking Diseases to Model Organism Resources. NIH. Role: Site PI |
| 2016-2017 | BD2K BioCADDIE Harvester: Enhancing metadata using GitHub, YAML and Markdown. NIH. Role: PI |
| 2011-2016 | Ontology-enabled reasoning across phenotypes from evolution and model organisms. NSF. Role: Consortium PI |
| 2015-2017 | cROP: Common Reference Ontologies and Applications for Plant Biology . NSF. Role: Consortium PI |

Invited Talks

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| 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 organizer. 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

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