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Education

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

Employment

2015-Present **Scientist** Environmental Genomics and Systems Biology Division, LBNL
2006-2015 **Scientist** Genomics Division, LBNL
2001-2006 **Bioinformatics Specialist** Howard Hughes Medical Institute, UC Berkeley
1999-2001 **Bioinformatics Scientist** Life Sciences Division, Lawrence Berkeley National Laboratory
1994-1999 **Bioinformatician** Roslin Institute, Edinburgh, UK

Publications

Google Scholar: [goo.gl/x2R5PC](https://scholar.google.com/citations?user=x2R5PC) h-index: 54
MyNCBI: [goo.gl/OFQ9k6](https://pubmed.ncbi.nlm.nih.gov/author/101111111/) i10-index: 95

Refereed Journal Articles

2016	Mungall, C.J. , McMurry, J. A., Köhler, S., Balhoff, J. P., Borromeo, C., Brush, M., Carbon, S., Conlin, T., Dunn, N., Engelstad, M., Foster, E., Gourdine, J., Jacobsen, J. O., Keith, D., Laraway, B., Lewis, S. E., NguyenXuan, J., Shefchek, K., Vasilevsky, N., Yuan, Z., Washington, N., Hochheiser, H., Groza, T., Smedley, D., Robinson, P. N., and Haendel, M. A. (2016b). The Monarch Initiative: an integrative data and analytic platform connecting phenotypes to genotypes across species. <i>Nucleic Acids Research</i> , page gkw1128
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- 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
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- 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., Vossell, L. B., Zhang, J., Zhao, Q., Zheng, X. H., and Lewis, S. (2000). Comparative genomics of the eukaryotes. *Science*, 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. *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

- 2016 Manda, P., **Mungall, C. J.**, Balhoff, J., Lapp, H., and Vision, T. (2016). Investigating the importance of anatomical homology for cross-species phenotype comparisons using semantic similarity. In *Pacific Symposium on Biocomputing 21*, pages 132–143. World Scientific Publishing Company
- 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)*

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| 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 | 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 |

Pre-prints

All pre-prints are on bioRxiv.

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| 2017 | Köhler, S., Robinson, P., and Mungall, C.J. (2017). Opposite-of information improves similarity calculations in phenotype ontologies |
| 2016 | Mungall, C.J. , Koehler, S., Robinson, P., Holmes, I., and Haendel, M. (2016a). k-BOOM: A Bayesian approach to ontology structure inference, with applications in disease ontology construction |
| | Holmes, I. H. and Mungall, C.J. (2016). BioMake: a GNU Make-compatible utility for declarative workflow management |
| 2014 | Mungall, C. J. (2014). Formalization of Genome Interval Relations |

Awards and Honors

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| 2017 | International Society for Biocuration, Exceptional Contributions to Biocuration Award |
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Awarded Proposals

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| 2016-2018 | NIH/NCATS OT3. co-PD. TransMed: A translational data integration machine for biomedical discovery. |
| 2016-2020 | NIH/OD. co-PD. The Monarch Initiative: Linking Diseases to Model Organism Resources. |
| 2016-2019 | NIH/BD2K. PI. An Intelligent Concept Agent for Assisting with the Application of Metadata |
| 2016-2017 | NIH/NHGRI. co-PI. The Alliance of Genomic Resources: towards integration of six model organism databases and the Gene Ontology Consortium. |

2016-2017	NIH/BD2K. co-PI. Supplement: Prefix-commons - BioCADDIE: Biomedical and healthCARE Data Discovery and Indexing Engine.
2016-2017	NIH/BD2K. co-PI. Supplement: BioCADDIE Harvester: Enhancing metadata using GitHub, YAML and Markdown.
2015-2016	NSF. co-PI. Ontology-enabled reasoning across phenotypes from evolution and model organisms.
2015-2017	NSF. co-PI. cROP: Common Reference Ontologies and Applications for Plant Biology.
2012-2016	NIH/OD. co-PI. Semantic LAMHDI: Linking Diseases to Model Organism Resources.

Invited Talks

2016	Incorporating the exposome into machine intelligence methods in biomedical research - Sanford Imagenetics, Sioux Falls, September 2016
2016	Panelist, Critical Assessment of Genome Interpretation, Open Challenges Conference, UCSF, March 2016
2016	Panelist, Data Integration Challenges, NSF Phenotype Research Coordination Network Meeting, BioSphere2, February 2016
2015	Computing on phenotypes across scale and species - Association for Molecular Pathology Annual Meeting, Austin, November 2015
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

2015	Tutorial Organizer. Introduction to ontologies, international plant trait curation workshop, Corvallis, OR, 2015
2014	Mentor. Harvey Mudd College, Industry Clinic Program
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, 2011
2009	Tutorial organizer. Developing ontologies in OBO and OWL, International Conference on Biomedical Ontologies, Buffalo, NY, 2009
2005	Undergraduate guest lecturer. Introduction to the Gene Ontology, Bio-Engineering, UC Berkeley
2001-2003	Instructor Programming for biology. Cold Spring Harbor Laboratory
2001	Module Organizer. World Health Organization International Training Course on Bioinformatics, FIOCRUZ, Rio de Janeiro, Brazil, May 21-June 15, 2001

Thesis Committees

2015	Master thesis Committee Bryan Laraway, Department of Biomedical Informatics, Oregon Health and Sciences University
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2013	PhD Thesis Committee Sebastian Koehler, Department of Mathematics and Computer Science, Charite - Universitätsmedizin Berlin
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Service

Program Committees

2016	Steering Committee 7th International Conference on Biological Ontology: Food, Nutrition, Health and Environment for the 9 billion, Corvalis, August 2016
2016	Program Committee 8th International Conference on Neural Computation Theory and Applications
2016	Program Committee ECCB 2016
2016	Program Committee Bio-Ontologies 2016
2016	Program Committee PhenoDay 2016
2016	Reviewer Pacific Symposium on Biocomputing 2016
2015	Program Committee Member 4th Workshop on Knowledge Discovery and Data Mining Meets Linked Open Data
2015	Program Committee Member Resources Program, ISWC 2016
2015	Program Committee Member Data Sets and Ontologies Program, ISWC 2015
2015	Program Committee Member Bio-Ontologies
2014	Program Committee Member 10th Workshop on Constraint-Based Methods for Bioinformatics, September 8 2014, Lyon, France
2014	Reviewer AMIA 2014
2014	Program Committee Member 6th Workshop on Formal Ontologies meet Industry
2014-Present	Program Committee Member PhenoDay ISMB 2014-2016
2013	Program Committee Member Declarative Logic Programming: Theory, Systems, and Applications
2009-2013	Program Committee Member Bio-Ontologies

2009-2013	Program Committee Member Semantic Web Applications in the Life Sciences
2009-2013	Program Committee Member / Track Chair International Conference on Biomedical Ontologies
2010	Program Committee Member OWL: Experience and Directions
2010-Present	Program Committee Member ISMB/ECCB
2010	Reviewer AMIA/TBI 2014
2007	Program Committee Member Bio-Ontologies
2007	Program Committee Member OWL: Experience and Directions
2007	Program Committee Member ISMB/ECCB

Journal Reviews

2016	Reviewing Editor eLife
2016	Reviewer International Journal of Approximate Reasoning
2016	Reviewer Systematic Biology
2016	Reviewer Nature Methods
2016	Reviewer Genome Research
2016	Reviewer Nucleic Acids Research
2016	Reviewer BioMed Research International
2015	Reviewer Nature Methods
2014-Present	Reviewer PLoS ONE
2014	Reviewer Peer/J
2014	Reviewer Gigascience
2014	Reviewer International Journal of Human-Computer Studies
2013	Reviewer PLoS Genetics

2013- Present	Reviewer Journal of Biomedical Semantics
2011- Present	Reviewer PLoS Computational Biology
2011- Present	Reviewer Human Mutation
2011- 2012	Reviewer Journal of Biomedical Informatics
2012- Present	Reviewer Nucleic Acids Research
2012	Reviewer International Journal on Semantic Web and Information Systems
2011- Present	Reviewer Database
2010- Present	Reviewer Bioinformatics
2010	Reviewer Genome Research

Working Groups and Advisory Boards

2016	Scientific Advisory Board Member NSF Phylotranscriptomics for the Tree of Life
2015	Working Group Member National Center for Ecological Analysis and Synthesis Ontology WG
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- Present	WG1 co-leader Transcription Factor TG Consortium
2010, 2011	Scientific Advisory Board Member Disease Ontology
2004- Present	Coordinator Open Biological Ontologies Library

Institutional Service

2016	Interview Committee Interviews for division head
2016	Working Group Member Neurosciences Interest Working Group
2016	Visioning Group Biosciences Strategic Plan

Review Panels

2017	NIH Proposal Review Panel Genomics, Computational Biology and Technology (GCAT) study panel
2017	SIB Proposal Review Swiss Institute of Bioinformatics, competitive proposal review
2014	DOE Proposal Review Department of Energy, Biological and Environmental Research, SBIR/STTR Program
2012	DOE Proposal Review Department of Energy, Biological and Environmental Research, SBIR/STTR Program

Last updated: March 2, 2017