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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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| 2014 | <p>Huntley, R. P., Harris, M. A., Alam-Faruque, Y., Blake, J. A., Carbon, S., Dietze, H., Dimmer, E. C., Foulger, R. E., Hill, D. P., Khodiyar, V. K., Lock, A., Lomax, J., Lovering, R. C., Mutowo-Meullenet, P., Sawford, T., Van Auken, K., Wood, V., and <b>Mungall, C. J.</b> (2014). A method for increasing expressivity of Gene Ontology annotations using a compositional approach. <i>BMC Bioinformatics</i>, 15(1):155</p> <p>Haendel, M. A., Balhoff, J. P., Bastian, F. B., Blackburn, D. C., Blake, J. A., Bradford, Y., Comte, A., Dahdul, W. M., Dececchi, T. A., Druzinsky, R. E., Hayamizu, T. F., Ibrahim, N., Lewis, S. E., Mabee, P. M., Niknejad, A., Robinson-Rechavi, M., Sereno, P. C., and <b>Mungall, C. J.</b> (2014). Unification of multi-species vertebrate anatomy ontologies for comparative biology in Uberon. <i>Journal of Biomedical Semantics</i>, 5(1):21</p> <p>Poelen, J. H., Simons, J. D., and <b>Mungall, C. J.</b> (2014). Global Biotic Interactions: An open infrastructure to share and analyze species-interaction datasets. <i>Ecological Informatics</i>, 24:148–159</p> <p>Thacker, R. W., Díaz, M. C., Kerner, A., Vignes-Lebbe, R., Segerdell, E., Haendel, M. A., and <b>Mungall, C. J.</b> (2014). The Porifera Ontology (PORO): enhancing sponge systematics with an anatomy ontology. <i>Journal of Biomedical Semantics</i>, 5(1):39</p> |
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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., <b>Mungall, C. J.</b> , 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., <b>Mungall, C. J.</b> , 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

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| 2007 | Haendel, M. A., Neuhaus, F., Osumi-Sutherland, D., Mabee, P. M., Mejino, J. L. J., <b>Mungall, C. J. J.</b> , 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 |
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## Letters to the Editor

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

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| 2013 | Brush, M. H., <b>Mungall, C.J.</b> , 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, <i>Proceedings of the International Conference on Biomedical Ontology 2013, Montreal, Canada, July 7-12, 2013</i> , pages 105–108                                     |
| 2011 | <b>Mungall, C.</b> (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><br><br><b>Mungall, C.</b> , Torniai, C., Diehl, A., Haendel, M., Ireland, A., Manzoor, S., Meehan, T., and Osumi-Sutherland, D. (2011). Modularization for the Cell Ontology |

- 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
- 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

- 2014 Use of OWL in the GO. Accepted for OWLED 2014. Role: first author
- Clinical Interpretation of Copy-Number Variants with Cross-Species Phenotype Data. Accepted by Journal of Medical Genetics. Role: middle author
- Gateways to the FANTOM5 promoter level mammalian expression atlas. Accepted by Genome Biology. Role: middle author

Faldo: A semantic standard for describing the location of nucleotide and protein feature an- notation. Submitted to JBMS. Role: middle author

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

Disease Ontology 2015 update: an expanded and updated database of human diseases for linking biomedical knowledge through disease data. Submitted to NAR. Role: middle author

## 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

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

2014-Present	<b>Working Group Member</b> Global Alliance for Genomics and Health, Clinical Working Group
2014-Present	<b>Working Group Member</b> International Rare Diseases Consortium, Ontologies and rare disease prioritization WG
2014	<b>Program Committee Member</b> 10th Workshop on Constraint-Based Methods for Bioinformatics, September 8 2014, Lyon, France
2014-Present	<b>WG1 co-leader</b> Transcription Factor TG Consortium
2014-Present	<b>Member</b> Orion Bionetworks Knowledge Engineering Working Group
2014	<b>Program Committee Member</b> 10th WCB- Workshop on Constraint-Based Methods for Bioinformatics at CP 2014 (Lyon, France, 8th Sept. 2014)
2014	<b>Program Committee Member, 6th Workshop on Formal Ontologies meet Industry</b>
2014	<b>Program Committee Member, PhenoDay</b> ISMB 2014
2012, 2014	<b>SBIR/STTR Reviewer</b> , Department of Energy
2004-Present	<b>Open Biological Ontologies Library Coordinator</b>

2009- 2013	<b>Program Committee Member, Bio-Ontologies</b>
2011- 2013	<b>Program Committee Member / Track Chair, International Conference on Biomedical Ontologies</b>
2011- 2013	<b>Program Committee Member, Semantic Web Applications in the Life Sciences</b>
2011	<b>Program Committee Member, OWL: Experience and Directions</b>
2010- Present	<b>Program Committee Member, ISMB/ECCB</b>
2010, 2011	<b>Scientific Advisory Board Member, Disease Ontology</b>
2005- Present	<b>Reviewer</b> PLoS Genetics, PLoS Computational Biology, PLoS ONE, Bioinformatics, Journal of Biomedical Semantics, Gigascience, Database, BMC Bioinformatics, Nucleic Acids Research

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