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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 Mungall, C. J. (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 Mungall, C. J. (2014). Unification of multi-species vertebrate anatomy ontologies for comparative biology in Uberon. <i>Journal of Biomedical Semantics</i>, 5(1):21</p> <p>Oellrich, A., Koehler, S., Washington, N., Mungall, C.J., Lewis, S., Haendel, M., Robinson, P. N., and Smedley, D. (2014). The influence of disease categories on gene candidate predictions from model organism phenotypes. <i>Journal of Biomedical Semantics</i>, 5(Suppl 1):S4</p> |
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Andersson, R., Gebhard, C., Miguel-Escalada, I., Hoof, I., Bornholdt, J., Boyd, M., Chen, Y., Zhao, X., Schmidl, C., Suzuki, T., Ntini, E., Arner, E., Valen, E., Li, K., Schwarzfischer, L., Glatz, D., Raithel, J., Lilje, B., Rapin, N., Bagger, F. O., Jørgensen, M., Andersen, P. R., Bertin, N., Rackham, O., Burroughs, A. M., Baillie, J. K., Ishizu, Y., Shimizu, Y., Furuhata, E., Maeda, S., Negishi, Y., **Mungall, C.J.**, Meehan, T. F., Lassmann, T., Itoh, M., Kawaji, H., Kondo, N., Kawai, J., Lennartsson, A., Daub, C. O., Heutink, P., Hume, D. A., Jensen, T. H., Suzuki, H., Hayashizaki, Y., Müller, F., Consortium, T. F., Forrest, A. R. R., Carninci, P., Rehli, M., and Sandelin, A. (2014). An atlas of active enhancers across human cell types and tissues. *Nature*, 507(7493):455–461

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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. <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., 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 |
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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., 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, <i>Proceedings of the International Conference on Biomedical Ontology 2013, Montreal, Canada, July 7-12, 2013</i> , pages 105–108 |
| 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>

Mungall, C. , 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 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 The Porifera Ontology (PORO). Submitted to Journal of Biomedical Semantics. Role: senior author
- Deletions of Chromosomal Regulatory Boundaries are Associated with Congenital Disease. Submitted to Genome Biology. Role: middle author
- The Biological Spatial Ontology. Accepted by Journal of Biomedical Semantics. Role: middle author

The Cell Line Ontology (CLO). Provisionally accepted by Journal of Biomedical Semantics. Role: middle author

Standardized description of scientific evidence using the Evidence Ontology (ECO). Accepted by Database. Role: middle author

Faldo: A semantic standard for describing the location of nucleotide and protein feature annotations. Submitted to JBMS. 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

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	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, Bioinformatics, Journal of Biomedical Semantics, Database, BMC Bioinformatics, Nucleic Acids Research

Last updated: June 19, 2014