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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>Oellrich, A., Koehler, S., Washington, N., <b>Mungall, C.J.</b>, 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

Kohler, S., Doelken, S. C., **Mungall, C. J.**, Bauer, S., Firth, H. V., Bailleul-Forestier, I., Black, G. C. M., Brown, D. L., Brudno, M., Campbell, J., FitzPatrick, D. R., Eppig, J. T., Jackson, A. P., Freson, K., Girdea, M., Helbig, I., Hurst, J. A., Jahn, J., Jackson, L. G., Kelly, A. M., Ledbetter, D. H., Mansour, S., Martin, C. L., Moss, C., Mumford, A., Ouwehand, W. H., Park, S.-M., Riggs, E. R., Scott, R. H., Sisodiya, S., Vooren, S. V., Wapner, R. J., Wilkie, A. O. M., Wright, C. F., Vulto-van Silfhout, A. T., de Leeuw, N., de Vries, B. B. A., Washington, N. L., Smith, C. L., Westerfield, M., Schofield, P., Ruef, B. J., Gkoutos, G. V., Haendel, M., Smedley, D., Lewis, S. E., and Robinson, P. N. (2014). The Human Phenotype Ontology project: linking molecular biology and disease through phenotype data. *Nucleic Acids Res.*, 42(D1):D966–D974

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Alam-Faruque, Y., Hill, D. P., Dimmer, E. C., Harris, M. A., Foulger, R. E., Tweedie, S., Attrill, H., Howe, D. G., Thomas, S. R., Davidson, D., Woolf, A. S., Blake, J. A., **Mungall, C. J.**, O'Donovan, C., Apweiler, R., and Huntley, R. P. (2014). Representing Kidney Development Using the Gene Ontology. *PloS one*, 9(6):e99864

Chibucos, M. C., **Mungall, C. J.**, Balakrishnan, R., Christie, K. R., Huntley, R. P., White, O., Blake, J. A., Lewis, S. E., and Giglio, M. (2014). Standardized description of scientific evidence using the Evidence Ontology ( ECO ). *Database*, 2014(0):1–11

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- 2012 **Mungall, C. J.**, Torniai, C., Gkoutos, G. V., Lewis, S. E., and Haendel, M. A. (2012). Uberon, an integrative multi-species anatomy ontology. *Genome Biology*, 13(1):R5
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| 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
- 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). In press, Journal of Biomedical Semantics. Role: senior author
- Global Biotic Interactions: An Open Infrastructure To Share, Discover and Analyze Species Interaction Datasets. Submitted to Eco-Informatics. Role: senior author

Deletions of Chromosomal Regulatory Boundaries are Associated with Congenital Disease. Accepted by Genome Biology. Role: middle author

Gateways to the FANTOM5 promoter level mammalian expression atlas. Genome Biology. Role: middle author

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

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

Clinical Interpretation of Copy-Number Variants with Cross-Species Phenotype Data. Submitted to Journal of Medical Genetics. Role: middle author

## Awards and Honors

2013	Encyclopedia of Life Rubenstein Fellowship award. Role: collaborator
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## 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
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## 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> International Rare Diseases Consortium, Ontologies and rare disease prioritization WG
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2014	<b>Program Committee Member</b> 10th Workshop on Constraint-Based Methods for Bioinformatics, September 8 2014, Lyon, France
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2014- Present	<b>WG1 co-leader</b> Transcription Factor TG Consortium
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2014- Present	<b>Member</b> Orion Bionetworks Knowledge Engineering Working Group
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2014	<b>Program Committee Member</b> 10th WCB- Workshop on Constraint-Based Methods for Bioinformatics at CP 2014 (Lyon, France, 8th Sept. 2014)
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2014	<b>Program Committee Member, 6th Workshop on Formal Ontologies meet Industry</b>
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2014	<b>Program Committee Member, PhenoDay</b> ISMB 2014
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2012, 2014	<b>SBIR/STTR Reviewer</b> , Department of Energy
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2004- Present	<b>Open Biological Ontologies Library Coordinator</b>
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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, Database, BMC Bioinformatics, Nucleic Acids Research

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