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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 **Staff Scientist** Environmental Genomics and Systems Biology Division, LBNL

2006-2015 **Staff Scientist** Genomics Division, LBNL

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><b>Mungall, C.J.</b>, 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., <b>Mungall, C. J.</b>, 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</i></p> <p>Robinson, P. N., <b>Mungall, C. J.</b>, and Haendel, M. (2015). Capturing phenotypes for precision medicine. <i>Molecular Case Studies</i>, 1(1):a000372</p> |
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Thessen, A. E., Bunker, D. E., Buttigieg, P. L., Cooper, L. D., Dahdul, W. M., Domisch, S., Franz, N. M., Jaiswal, P., Lawrence-Dill, C. J., Midford, P. E., **Mungall, C. J.**, Ramírez, M. J., Specht, C. D., Vogt, L., Vos, R. A., Walls, R. L., White, J. W., Zhang, G., Deans, A. R., Huala, E., Lewis, S. E., and Mabee, P. M. (2015). Emerging semantics to link phenotype and environment. *PeerJ*, 3:e1470

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Lizio, M., Harshbarger, J., Shimoji, H., Severin, J., Kasukawa, T., Sahin, S., Abuges-saisa, I., Fukuda, S., Hori, F., Ishikawa-Kato, S., **Mungall, C. J.**, Arner, E., Baillie, J. K., Bertin, N., Bono, H., de Hoon, M., Diehl, A. D., Dimont, E., Freeman, T. C., Fujieda, K., Hide, W., Kaliyaperumal, R., Katayama, T., Lassmann, T., Meehan, T. F., Nishikata, K., Ono, H., Rehli, M., Sandelin, A., Schultes, E. A., t Hoen, P. A., Tatum, Z., Thompson, M., Toyoda, T., Wright, D. W., Daub, C. O., Itoh, M., Carninci, P., Hayashizaki, Y., Forrest, A. R., and Kawaji, H. (2015). Gateways to the FANTOM5 promoter level mammalian expression atlas. *Genome Biology*, 16(1):22

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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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## 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., <b>Mungall, C.J.</b> , 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

- |      |  |
|------|--|
| 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 | <b>Mungall, C. J.</b> (2014). Formalization of Genome Interval Relations. <i>bioRxiv</i>   |
| 2014 | Bolleman, J., <b>Mungall, C. J.</b> , 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 | Computing on phenotypes across scale and species - Association for Molecular Pathology Annual Meeting, Austin, November 2015 |
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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

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| 2012      | <b>Course organizer.</b> Developing ontologies in Protege/OWL, Hinxton, UK, January 2012   |
| 2011      | <b>Tutorial organizer.</b> Developing ontologies in OBO and OWL, International Conference on Biomedical Ontologies, Buffalo, NY, 2009    |
| 2009      | <b>Tutorial co-organizer.</b> Developing ontologies in OBO and OWL, International Conference on Biomedical Ontologies, Buffalo, NY, 2009 |
| 2001-2003 | <b>Teaching assistant</b> Programming for biology. Cold Spring Harbor Laboratory   |

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| 2001 | <b>Module Organizer.</b> Module organizer. WHO International Training Course on Bioinformatics, FIOCRUZ, Rio de Janeiro, Brazil, May 21-June 15, 2001 |
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## Service

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| 2015         | <b>Working Group Member</b> National Center for Ecological Analysis and Synthesis Ontology WG   |
| 2015         | <b>Program Committee Member</b> 4th Workshop on Knowledge Discovery and Data Mining Meets Linked Open Data                                  |
| 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         | <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 ISMB 2014</b>   |
| 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>   |



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| 2010-<br>Present | <b>Program Committee Member, ISMB/ECCB</b>  |
| 2010,<br>2011    | <b>Scientific Advisory Board Member, Disease Ontology</b>   |
| 2005-<br>Present | <b>Reviewer</b> PLoS Genetics, PLoS Computational Biology, eLife, 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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