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Education

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

Appointments

2024-Present	**Senior Computational Scientist,** Environmental Genomics and Systems Biology Division, Lawrence Berkeley National Laboratory
2018-Present	**Dept. Head, Biosystems Data Science Dept**., Environmental Genomics and Systems Biology Division, Lawrence Berkeley National Laboratory
2021-Present	**Research Affiliate**, Berkeley Institute for Data Science (BIDS)
2018-2024	**Staff Scientist**, Environmental Genomics and Systems Biology Division, LBNL
2015-2018	**Research Scientist**, Environmental Genomics and Systems Biology Division, LBNL
2006-2015	**Research 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

Awards and Honors

2020	Lawrence Berkeley National Laboratory Director's Award for Exceptional Achievement Early Scientific Career https://recognition.lbl.gov/2020-laureates/
2017	International Society for Biocuration Exceptional Contributions to Biocuration Award https://www.biocuration.org/2017-biocuration-awards/

Publications

Google Scholar: goo.gl/x2R5PC   h-index: 92   i10-index: 202

Refereed Journal Articles

2024 Caufield JH, Hegde H, Emonet V, Harris NL, Joachimiak MP, Matentzoglu N, Kim H, Moxon S, Reese JT, Haendel MA, Robinson PN, **Mungall CJ** (2024). Structured Prompt Interrogation and Recursive Extraction of Semantics (SPIRES): a method for populating knowledge bases using zero-shot learning. In Bioinformatics doi:10.1093/bioinformatics/btae104 PMCID:PMC10924283 Role: senior

Wright A, Wilkinson MD, **Mungall C**, Cain S, Richards S, Sternberg P, Provin E, Jacobs JL, Geib S,

Raciti D, Yook K, Stein L, Molik DC (2024). FAIR Header Reference genome: a TRUSTworthy standard. In Brief. Bioinform. doi:10.1093/bib/bbae122 PMCID:PMC10981671 Role: contributor

Chan LE, Casiraghi E, Reese J, Harmon QE, Schaper K, Hegde H, Valentini G, Schmitt C, Motsinger-Reif A, Hall JE, **Mungall CJ**, Robinson PN, Haendel MA (2024). Predicting nutrition and environmental factors associated with female reproductive disorders using a knowledge graph and random forests. In Int. J. Med. Inform. doi:10.1016/j.ijmedinf.2024.105461 PMCID: PMC11188727 Role: contributor

Cappelletti L, Rekerle L, Fontana T, Hansen P, Casiraghi E, Ravanmehr V, **Mungall CJ**, Yang JJ, Spranger L, Karlebach G, Caufield JH, Carmody L, Coleman B, Oprea TI, Reese J, Valentini G, Robinson PN (2024). Node-degree aware edge sampling mitigates inflated classification performance in biomedical random walk-based graph representation learning. In Bioinform Adv, 4(1):vbae036 doi:10.1093/bioadv/vbae036 PMCID:PMC10994718 Role: contributor

Schadt C, Martin S, Carrell A, Fortner A, Hopp D, Jacobson D, Klingeman D, Kristy B, Phillips J, Piatkowski B, Miller MA, Smith M, Patil S, Flynn M, Canon S, Clum A, **Mungall CJ**, Pennacchio C, Bowen B, Louie K, Northen T, Eloe-Fadrosh EA, Mayes MA, Muchero W, Weston DJ, Mitchell J, Doktycz M (2024). An integrated metagenomic, metabolomic and transcriptomic survey of Populus across genotypes and environments. In Sci Data, 11(1):339 doi:10.1038/s41597-024-03069-7 PMCID:PMC10997577 Role: contributor

Callahan TJ, Tripodi IJ, Stefanski AL, Cappelletti L, Taneja SB, Wyrwa JM, Casiraghi E, Matentzoglu NA, Reese J, Silverstein JC, Hoyt CT, Boyce RD, Malec SA, Unni DR, Joachimiak MP, Robinson PN, **Mungall CJ**, Cavalleri E, Fontana T, Valentini G, Mesiti M, Gillenwater LA, Santangelo B, Vasilevsky NA, Hoehndorf R, Bennett TD, Ryan PB, Hripcsak G, Kahn MG, Bada M, Baumgartner Jr WA, Hunter LE (2024). An open source knowledge graph ecosystem for the life sciences. In Sci Data, 11(1):363 doi:10.1038/s41597-024-03171-w PMCID:PMC11009265 Role: contributor

2023 Gargano MA, Matentzoglu N, Coleman B, Addo-Lartey EB, … Zvolský M, Toro S, Carmody LC, Harris NL, Munoz-Torres MC, Danis D, **Mungall CJ**, Köhler S, Haendel MA, Robinson PN (2023). The Human Phenotype Ontology in 2024: phenotypes around the world. In Nucleic Acids Res. doi:10.1093/nar/gkad1005 Role: co_senior

Caufield JH, Putman T, Schaper K, Unni DR, Hegde H, Callahan TJ, Cappelletti L, Moxon SAT, Ravanmehr V, Carbon S, Chan LE, Cortes K, Shefchek KA, Elsarboukh G, Balhoff J, Fontana T, Matentzoglu N, Bruskiewich RM, Thessen AE, Harris NL, Munoz-Torres MC, Haendel MA, Robinson PN, Joachimiak MP, **Mungall CJ**, Reese JT (2023). KG-Hub-building and exchanging biological knowledge graphs. In Bioinformatics doi:10.1093/bioinformatics/btad418 PMCID:PMC10336030 Role: co_senior

Putman TE, Schaper K, Matentzoglu N, Rubinetti VP, Alquaddoomi FS, Cox C, Caufield JH, Elsarboukh G, Gehrke S, Hegde H, Reese JT, Braun I, Bruskiewich RM, Cappelletti L, Carbon S, Caron AR, Chan LE, Chute CG, Cortes KG, De Souza V, Fontana T, Harris NL, Hartley EL, Hurwitz E, Jacobsen JOB, Krishnamurthy M, Laraway BJ, McLaughlin JA, McMurry JA, Moxon SAT, Mullen KR, O'Neil ST, Shefchek KA, Stefancsik R, Toro S, Vasilevsky NA, Walls RL, Whetzel PL, Osumi-Sutherland D, Smedley D, Robinson PN, **Mungall CJ**, Haendel MA, Munoz-Torres MC (2023). The Monarch Initiative in 2024: an analytic platform integrating phenotypes, genes and diseases across species. In Nucleic Acids Res. doi:10.1093/nar/gkad1082 PMID: 38000386 Role: co_senior

Carmody LC, Gargano MA, Toro S, Vasilevsky NA, Adam MP, Blau H, Chan LE, Gomez-Andres D, Horvath R, Kraus ML, Ladewig MS, Lewis-Smith D, Lochmüller H, Matentzoglu NA, Munoz-Torres MC, Schuetz C, Seitz B, Similuk MN, Sparks TN, Strauss T, Swietlik EM, Thompson R, Zhang XA, **Mungall CJ**, Haendel MA, Robinson PN (2023). The Medical Action Ontology: A tool for annotating and analyzing

treatments and clinical management of human disease. In Med, 4(12):913-927.e3 doi:10.1016/j.medj.2023.10.003 PMCID:PMC10842845 Role: co_senior

Gene Ontology Consortium, Aleksander SA, Balhoff J, Carbon S, Cherry JM, Drabkin HJ, Ebert D, Feuermann M, Gaudet P, Harris NL, Hill DP, Lee R, Mi H, Moxon S, **Mungall CJ**, … (2023). The Gene Ontology knowledgebase in 2023. In Genetics doi:10.1093/genetics/iyad031 PMCID:PMC10158837 Role: co_senior

Chan LE, Thessen AE, Duncan WD, Matentzoglu N, Schmitt C, Grondin CJ, Vasilevsky N, McMurry JA, Robinson PN, **Mungall CJ,** Haendel MA (2023). The Environmental Conditions, Treatments, and Exposures Ontology (ECTO): connecting toxicology and exposure to human health and beyond. In J. Biomed. Semantics, 14(1):3 doi:10.1186/s13326-023-00283-x PMCID:PMC9951428 Role: co_senior

Danis D, Jacobsen JOB, Wagner AH, Groza T, Beckwith MA, Rekerle L, Carmody LC, Reese J, Hegde H, Ladewig MS, Seitz B, Munoz-Torres M, Harris NL, Rambla J, Baudis M, **Mungall CJ**, Haendel MA, Robinson PN (2023). Phenopacket-tools: Building and validating GA4GH Phenopackets. In PLoS One, 18(5):e0285433 doi:10.1371/journal.pone.0285433 PMCID:PMC10191354 Role: contributor

Hawrylycz M, Martone ME, Ascoli GA, … Mufti S, **Mungall CJ**, …, Zingg B (2023). A guide to the BRAIN Initiative Cell Census Network data ecosystem. In PLoS Biol., 21(6):e3002133 doi:10.1371/journal.pbio.3002133 PMCID:PMC10313015 Role: contributor

Karlebach G, Carmody L, Sundaramurthi JC, Casiraghi E, Hansen P, Reese J, **Mungall CJ,** Valentini G, Robinson PN (2023). An expectation-maximization framework for comprehensive prediction of isoform-specific functions. In Bioinformatics doi:10.1093/bioinformatics/btad132 PMCID:PMC10079350 Role: contributor

Meyer R, Appeltans W, Duncan WD, Dimitrova M, Gan YM, Stjernegaard Jeppesen T, **Mungall C**, Paul DL, Provoost P, Robertson T, Schriml L, Suominen S, Walls R, Sweetlove M, Ung V, Van de Putte A, Wallis E, Wieczorek J, Buttigieg PL (2023). Aligning Standards Communities for Omics Biodiversity Data: Sustainable Darwin Core-MIxS Interoperability. In Biodivers Data J doi:10.3897/BDJ.11.e112420 PMCID:PMC10565567 Role: contributor

Stefancsik R, Balhoff JP, Balk MA, Ball RL, Bello SM, Caron AR, Chesler EJ, de Souza V, Gehrke S, Haendel M, Harris LW, Harris NL, Ibrahim A, Koehler S, Matentzoglu N, McMurry JA, **Mungall CJ**, Munoz-Torres MC, Putman T, Robinson P, Smedley D, Sollis E, Thessen AE, Vasilevsky N, Walton DO, Osumi-Sutherland D (2023). The Ontology of Biological Attributes (OBA)-computational traits for the life sciences. In Mamm. Genome, 34(3):364-378 doi:10.1007/s00335-023-09992-1 PMCID:PMC10382347 Role: contributor

Fecho K, Bizon C, Issabekova T, Moxon S, Thessen AE, Abdollahi S, Baranzini SE, Belhu B, Byrd WE, Chung L, Crouse A, Duby MP, Ferguson S, Foksinska A, Forero L, Friedman J, Gardner V, Glusman G, Hadlock J, Hanspers K, Hinderer E, Hobbs C, Hyde G, Huang S, Koslicki D, Mease P, Muller S, **Mungall CJ**, Ramsey SA, Roach J, Rubin I, Schurman SH, Shalev A, Smith B, Soman K, Stemann S, Su AI, Ta C, Watkins PB, Williams MD, Wu C, Xu CH, Biomedical Data Translator Consortium (2023). An approach for collaborative development of a federated biomedical knowledge graph-based question-answering system: Question-of-the-Month challenges. In J Clin Transl Sci, 7(1):e214 doi:10.1017/cts.2023.619 PMCID:PMC10603356 Role: contributor

Ladewig MS, Jacobsen JOB, Wagner AH, Danis D, El Kassaby B, Gargano M, Groza T, Baudis M, Steinhaus R, Seelow D, Bechrakis NE, **Mungall CJ**, Schofield PN, Elemento O, Smith L, McMurry JA, Munoz-Torres M, Haendel MA, Robinson PN (2023). GA4GH Phenopackets: A Practical Introduction. In

Adv. Genet., 4(1):2200016 doi:10.1002/ggn2.202200016 PMCID:PMC10000265 Role: contributor

Tan SZK, Kir H, Aevermann BD, Gillespie T, Harris N, Hawrylycz MJ, Jorstad NL, Lein ES, Matentzoglu N, Miller JA, Mollenkopf TS, **Mungall CJ**, Ray PL, Sanchez REA, Staats B, Vermillion J, Yadav A, Zhang Y, Scheuermann RH, Osumi-Sutherland D (2023). Brain Data Standards - A method for building data-driven cell-type ontologies. In Sci Data, 10(1):246 doi:10.1038/s41597-023-02165-4 PMCID:PMC10147694 Role: contributor

Martin HG, Radivojevic T, Zucker J, Bouchard K, Sustarich J, Peisert S, Arnold D, Hillson N, Babnigg G, Marti JM, **Mungall CJ**, Beckham GT, Waldburger L, Carothers J, Sundaram S, Agarwal D, Simmons BA, Backman T, Banerjee D, Tanjore D, Ramakrishnan L, Singh A (2023). Perspectives for self-driving labs in synthetic biology. In Curr. Opin. Biotechnol. doi:10.1016/j.copbio.2022.102881 Role: contributor

2022   Matentzoglu, N., Balhoff, J. P., Bello, S. M., Bizon, C., Brush, M., Callahan, T. J., Chute, C. G., Duncan, W. D., Evelo, C. T., Gabriel, D., Graybeal, J., Gray, A., Gyori, B. M., Haendel, M., Harmse, H., Harris, N. L., Harrow, I., Hegde, H. B., Hoyt, A. L., … **Mungall, C. J.** (2022). A Simple Standard for Sharing Ontological Mappings (SSSOM). *Database: The Journal of Biological Databases and Curation*, *2022*. https://doi.org/10.1093/database/baac035

Matentzoglu N, Goutte-Gattat D, Tan SZK, Balhoff JP, Carbon S, Caron AR, Duncan WD, Flack JE, Haendel M, Harris NL, Hogan WR, Hoyt CT, Jackson RC, Kim H, Kir H, Larralde M, McMurry JA, Overton JA, Peters B, Pilgrim C, Stefancsik R, Robb SM, Toro S, Vasilevsky NA, Walls R, **Mungall CJ**, Osumi-Sutherland D (2022). Ontology Development Kit: a toolkit for building, maintaining and standardizing biomedical ontologies. Database. 2022 Oct 8;2022. http://dx.doi.org/10.1093/database/baac087 PMID: 36208225

Ladewig MS, Jacobsen JOB, Wagner AH, Danis D, El Kassaby B, Gargano M, Groza T, Baudis M, Steinhaus R, Seelow D, Bechrakis NE, **Mungall CJ,** Schofield PN, Elemento O, Smith L, McMurry JA, Munoz-Torres M, Haendel MA, Robinson PN (2022). GA4GH phenopackets: A practical introduction. Advanced Genetics. Wiley; 2022 Aug 25;2200016. https://onlinelibrary.wiley.com/doi/10.1002/ggn2.202200016

de Crécy-Lagard V, Amorin de Hegedus R, Arighi C, Babor J, Bateman A, Blaby I, Blaby-Haas C, Bridge AJ, Burley SK, Cleveland S, Colwell LJ, Conesa A, Dallago C, Danchin A, de Waard A, Deutschbauer A, Dias R, Ding Y, Fang G, Friedberg I, Gerlt J, Goldford J, Gorelik M, Gyori BM, Henry C, Hutinet G, Jaroch M, Karp PD, Kondratova L, Lu Z, Marchler-Bauer A, Martin M-J, McWhite C, Moghe GD, Monaghan P, Morgat A, **Mungall CJ**, Natale DA, Nelson WC, O'Donoghue S, Orengo C, O'Toole KH, Radivojac P, Reed C, Roberts RJ, Rodionov D, Rodionova IA, Rudolf JD, Saleh L, Sheynkman G, Thibaud-Nissen F, Thomas PD, Uetz P, Vallenet D, Carter EW, Weigele PR, Wood V, Wood-Charlson EM, Xu J (2022). A roadmap for the functional annotation of protein families: a community perspective. Database. academic.oup.com; 2022 Aug 12;2022. http://dx.doi.org/10.1093/database/baac062 PMID: 35961013

Unni, D. R., Moxon, S. A. T., Bada, M., & Brush, M, …, **Mungall, C.J**., The Biomedical Data Translator Consortium (2022). Biolink Model: A universal schema for knowledge graphs in clinical, biomedical, and translational science. *Clinical and Translational Science*. https://ascpt.onlinelibrary.wiley.com/doi/abs/10.1111/cts.13302

Fecho, K., Thessen, A. T., Baranzini, S. E., Bizon, C., Hadlock, J. J., Huang, S., Roper, R. T., Southall, N., Ta, C., Watkins, P. B., Williams, M. D., Xu, H., Byrd, W., Dančík, V., Duby, M. P., Dumontier, M., Glusman, G., Harris, N. L., Hinderer, E. W., … Biomedical Data Translator Consortium. (2022). Progress Toward a Universal Biomedical Data Translator. Clinical and Translational Science.

https://doi.org/10.1111/cts.13301

Jacobsen, J. O. B., Baudis, M., Baynam, G. S., Beckmann, J. S., Beltran, S., Buske, O. J., Callahan, T. J., Chute, C. G., Courtot, M., Danis, D., Elemento, O., Essenwanger, A., Freimuth, R. R., Gargano, M. A., Groza, T., Hamosh, A., Harris, N. L., Kaliyaperumal, R., Lloyd, K. C. K., **Mungall C.J,** … Robinson, P. N. (2022). The GA4GH Phenopacket schema defines a computable representation of clinical data. Nature Biotechnology, 40(6), 817–820.

Danis D, Jacobsen JOB, Balachandran P, Zhu Q, Yilmaz F, Reese J, Haimel M, Lyon GJ, Helbig I, **Mungall CJ**, Beck CR, Lee C, Smedley D, Robinson PN. SvAnna: efficient and accurate pathogenicity prediction of coding and regulatory structural variants in long-read genome sequencing. Genome Med. 2022 Apr 28;14(1):44. http://dx.doi.org/10.1186/s13073-022-01046-6 PMID: 35484572

Ravanmehr V, Blau H, Cappelletti L, Fontana T, Carmody L, Coleman B, George J, Reese J, Joachimiak M, Bocci G, Hansen P, Bult C, Rueter J, Casiraghi E, Valentini G, **Mungall C,** Oprea TI, Robinson PN. Supervised learning with word embeddings derived from PubMed captures latent knowledge about protein kinases and cancer. NAR Genom Bioinform. 2021 Dec;3(4):lqab113. http://dx.doi.org/10.1093/nargab/lqab113 PMCID: PMC8652379

Jacobsen JO, Kelly C, Cipriani V, Consortium GER, **Mungall CJ**, Reese J, Danis D, Robinson PN, Smedley D. Phenotype-driven approaches to enhance variant prioritization and diagnosis of rare disease. Hum Mutat. Wiley; 2022 Apr 7; https://onlinelibrary.wiley.com/doi/10.1002/humu.24380 PMID: 35391505

Reese, J. T., Coleman, B., Chan, L., Blau, H., Callahan, T. J., Cappelletti, L., Fontana, T., Bradwell, K. R., Harris, N. L., Casiraghi, E., Valentini, G., Karlebach, G., Deer, R., McMurry, J. A., Haendel, M. A., Chute, C. G., Pfaff, E., Moffitt, R., Spratt, H., … **Mungall, C.J**, Williams, A.E., Robinson, P. N. (2022). NSAID use and clinical outcomes in COVID-19 patients: a 38-center retrospective cohort study. Virology Journal, 19(1), 84. http://dx.doi.org/10.1186/s12985-022-01813-2 PMCID: PMC9107579

Sternberg PW, Agapite J, …, **Mungall CJ**, …, Zhou P, Zytkovicz M, The Alliance of Genome Resources Consortium. Harmonizing model organism data in the Alliance of Genome Resources. Genetics. Oxford University Press (OUP); 2022 Feb 25; https://academic.oup.com/genetics/advance-article/doi/10.1093/genetics/iyac022/6537086

Hu, B., Canon, S., Eloe-Fadrosh, E. A., Anubhav, Babinski, M., Corilo, Y., Davenport, K., Duncan, W. D., Fagnan, K., Flynn, M., Foster, B., Hays, D., …, Mouncey, N., **Mungall, C.J.**, … Chain, P. S. G. (2022). Challenges in Bioinformatics Workflows for Processing Microbiome Omics Data at Scale. Frontiers in Bioinformatics, 1. https://doi.org/10.3389/fbinf.2021.826370

Nadendla S, Jackson R, Munro J, Quaglia F, Mészáros B, Olley D, Hobbs ET, Goralski SM, Chibucos M, **Mungall CJ**, Tosatto SCE, Erill I, Giglio MG. ECO: the Evidence and Conclusion Ontology, an update for 2022. Nucleic Acids Res. Oxford University Press; 2021 Nov 19; https://academic.oup.com/nar/advance-article-abstract/doi/10.1093/nar/gkab1025/6431816

Eloe-Fadrosh, E.A., Ahmed, F., Anubhav, Babinski, M., Baumes, J., Borkum, M., Bramer, L., Canon, S., Christianson, D.S., Corilo, Y.E. Davenport, K.W., Davis, B., Drake, M., Duncan, W.D., … Chain, P.S.G., McCue, L.A., Mans, D., **Mungall, C.J.**, Mouncey, N.J., Fagnan, K.T. (2022). The National Microbiome Data Collaborative Data Portal: an integrated multi-omics microbiome data resource, Nucleic Acids Research, Volume 50, Issue D1, 7 January 2022, Pages D828–D836, https://doi.org/10.1093/nar/gkab990

2021 Sant DW, Sinclair M, **Mungall CJ**, Schulz S, Zerbino D, Lovering RC, Logie C, Eilbeck K. Sequence ontology terminology for gene regulation. Biochim Biophys Acta Gene Regul Mech. Elsevier BV; 2021 Aug;(194745):194745. https://linkinghub.elsevier.com/retrieve/pii/S1874939921000638

Kuiper M, Bonello J, Fernández-Breis JT, Bucher P, Futschik ME, Gaudet P, … Lovering R, **Mungall C**, Thomas P, Eibeck K. The Gene Regulation Knowledge Commons: The action area of GREEKC. Biochimica et Biophysica Acta (BBA) - Gene Regulatory Mechanisms. 2021 Oct 30;194768. https://www.sciencedirect.com/science/article/pii/S1874939921000869

Vangay P, Burgin J, Johnston A, ..., **Mungall C**, ..., Wood-Charlson EM, Eloe-Fadrosh EA. Microbiome metadata standards: Report of the national microbiome data collaborative's workshop and follow-on activities. mSystems. American Society for Microbiology; 2021 Feb 23;6(1). https://msystems.asm.org/content/6/1/e01194-20 PMID: 33622857

Good, B. M., Van Auken, K., Hill, D. P., Mi, H., Carbon, S., Balhoff, J. P., Albou, L.-P., Thomas, P. D., **Mungall, C. J**., Blake, J. A., & D'Eustachio, P. (2021). Reactome and the Gene Ontology: Digital convergence of data resources. *Bioinformatics* . https://doi.org/10.1093/bioinformatics/btab325

Gene Ontology Consortium. The Gene Ontology resource: enriching a GOld mine. Nucleic Acids Res. 2020 Dec 8; http://dx.doi.org/10.1093/nar/gkaa1113 PMID: 33290552

Köhler S, Gargano M, Matentzoglu N, ... Helbig I, **Mungall CJ,** Haendel MA, Robinson PN. The Human Phenotype Ontology in 2021. Nucleic Acids Res. 2021 Jan 8;49(D1):D1207–D1217. http://dx.doi.org/10.1093/nar/gkaa1043 PMCID: PMC7778952

Hannestad, L. M., Dančík, V., Godden, M., Suen, I. W., Huellas-Bruskiewicz, K. C., Good, B. M., **Mungall, C. J.**, & Bruskiewich, R. M. (2021). Knowledge Beacons: Web services for data harvesting of distributed biomedical knowledge. *PloS One*, *16*(3), e0231916.

Singer E, Vogel JP, Northen T, **Mungall CJ**, Juenger TE. Novel and emerging capabilities that can provide a holistic understanding of the plant root microbiome. Phytobiomes J. Scientific Societies; 2021 Jan 18;PBIOMES–05–20–0. https://apsjournals.apsnet.org/doi/10.1094/PBIOMES-05-20-0042-RVW

2020 Wood, V., Carbon, S., Harris, M.A., Lock, A., Engel, S.R., Hill, D.P., Van Auken, K., Attrill, H., Feuermann, M., Gaudet, P.,..., **Mungall, C.J**.. (2020) Term Matrix: a novel Gene Ontology annotation quality control system based on ontology term co-annotation patterns. *Open Biology* 10, 200149. https://doi.org/10.1098/rsob.200149

Touré, Vasundra, Steven Vercruysse, Marcio Luis Acencio, Ruth C. Lovering, Sandra Orchard, Glyn Bradley, Cristina Casals-Casas, …, **Mungall, C.J**., ...et al. (2020). The Minimum Information about a Molecular Interaction Causal Statement (MI2CAST). *Bioinformatics*, July 2020. https://doi.org/10.1093/bioinformatics/btaa622

Wood-Charlson, E.M., Anubhav, Auberry, D., …, **Mungall, C.J**., Mouncey, N.J., Maxon, M.E., Eloe-Fadrosh, E.A. (2020). The National Microbiome Data Collaborative: enabling microbiome science. *Nature Reviews Microbiology 18*, 313–314.

Ong E, Wang LL, Schaub J, ... **Mungall CJ**, Haendel M, Robinson PN, Himmelfarb J, Iyengar R, Kretzler M, Mooney S, He Y, (2020). Modelling kidney disease using ontology: insights from the Kidney Precision Medicine Project. Nat Rev Nephrol 2020 Sep 16; http://dx.doi.org/10.1038/s41581-020-00335-w PMID: 32939051

Arnaud, E., Laporte, M.-A., Kim, S., Aubert, C., Leonelli, S., Miro, B., Cooper, L., Jaiswal, P., Kruseman, G., Shrestha, R., … **Mungall CJ**, …, King, B (2020). The Ontologies Community of Practice: A CGIAR Initiative for Big Data in Agrifood Systems. *Patterns* 100105.

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Joachimiak MP, **Mungall CJ**. KG-COVID-19: a framework to produce customized knowledge graphs for COVID-19 response. *Patterns* (NY). 2020 Nov 9;100155. http://dx.doi.org/10.1016/j.patter.2020.100155 PMCID: PMC7649624

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Preprints

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Danis D, Bamshad MJ, Bridges Y, Cacheiro P, Carmody LC, Chong JX, Coleman B, Dalgleish R, Freeman PJ, Graefe ASL, Groza T, Jacobsen JOB, Klocperk A, Kusters M, Ladewig MS, Marcello AJ, Mattina T, **Mungall CJ**, Munoz-Torres MC, Reese JT, Rehburg F, Reis BCS, Schuetz C, Smedley D, Strauss T, Sundaramurthi JC, Thun S, Wissink K, Wagstaff JF, Zocche D, Haendel MA, Robinson PN (2024). A corpus of GA4GH Phenopackets: case-level phenotyping for genomic diagnostics and discovery. In medRxiv doi:10.1101/2024.05.29.24308104 PMCID:PMC11160806 Role: contributor

Mullen KR, Tammen I, Matentzoglu NA, Mather M, **Mungall CJ**, Haendel MA, Nicholas FW, Toro S, Consortium TVBO (2024). The Vertebrate Breed Ontology: Towards Effective Breed Data Standardization.

In ArXiv PMCID:PMC11177956 Role: contributor

2023 Joachimiak, M.P., Caufield, J.H., Harris, N. and **Mungall, C.J.**, 2023. Gene Set Summarization using Large Language Models. arXiv preprint arXiv:2305.13338. PMC10246080

Reese, J., Danis, D., Harry Caufield, J., Casiraghi, E., Valentini, G., **Mungall, C. J.,** & Robinson, P. N. (2023). On the limitations of large language models in clinical diagnosis. In medRxiv (p. 2023.07.13.23292613). https://doi.org/10.1101/2023.07.13.23292613

Callahan, T. J., Tripodi, I. J., Stefanski, A. L., Cappelletti, L., Taneja, S. B., Wyrwa, J. M., Casiraghi, E., Matentzoglu, N. A., Reese, J., Silverstein, J. C., Hoyt, C. T., Boyce, R. D., Malec, S. A., Unni, D. R., Joachimiak, M. P., Robinson, P. N., **Mungall, C. J**., Cavalleri, E., Fontana, T., … Hunter, L. E. (2023). An Open-Source Knowledge Graph Ecosystem for the Life Sciences. In arXiv [cs.AI]. arXiv. http://arxiv.org/abs/2307.05727

Carmody, L. C., Gargano, M. A., Toro, S., Vasilevsky, N. A., Adam, M. P., Blau, H., Chan, L. E., Gomez-Andres, D., Horvath, R., Ladewig, M. S., (2023). The Medical Action Ontology: A Tool for Annotating and Analyzing Treatments and Clinical Management of Human Disease. medRxiv, 2023–2007.

2022 Lubiana, T., Roncaglia, P., **Mungall, C. J.**, Quardokus, E. M., Fortriede, J. D., Osumi-Sutherland, D., & Diehl, A. D. (2022). Toward a minimal information reporting standard about new cell types. In *arXiv [q-bio.OT]*. arXiv. http://arxiv.org/abs/2204.09673

Toro S, Matentzoglu N, Mullen KR, Vasilevsky N, Rando HM, Haendel M, **Mungall CJ**, Hu Z-L, Leroy G, Tammen I, Nicholas FW (2022). Classifying animal breeds with the Vertebrate Breed Ontology (VBO). https://icbo-conference.github.io/icbo2022/papers/ICBO-2022_paper_1882.pdf

Niknejad, A., **Mungall, C. J.**, Osumi-Sutherland, D., Robinson-Rechavi, M., & Bastian, F. B. (2022). Creation and unification of development and life stage ontologies for animals. In arXiv [q-bio.QM]. arXiv. http://arxiv.org/abs/2206.12231

Saha, S., Cain, S., Cannon, E. K. S., Dunn, N., Farmer, A., Hu, Z.-L., Maslen, G., Moxon, S., **Mungall, C. J.**, Nelson, R., & Poelchau, M. F. (2022). Recommendations for extending the GFF3 specification for improved interoperability of genomic data. In arXiv [q-bio.OT]. arXiv. http://arxiv.org/abs/2202.07782

Cappelletti L, Fontana T, Casiraghi E, Ravanmehr V, Callahan TJ, Joachimiak MP, **Mungall CJ**, Robinson PN, Reese J, Valentini G. GraPE: fast and scalable Graph Processing and Embedding. arXiv. 2021. http://arxiv.org/abs/2110.06196

Vasilevsky, N. A., Matentzoglu, N. A., Toro, S., Flack, J. E., Hegde, H., Unni, D. R., Alyea, G., Amberger, J. S., Babb, L., Balhoff, J. P., …, **Mungall, C, J**, Hamosh, A, Haendel M.A. (2022). Mondo: Unifying diseases for the world, by the world. medRxiv.

Karlebach G, Carmody L, Sundaramurthi JC, Casiraghi E, Hansen P, Reese J, **Mungall CJ**, Valentini G, Robinson PN. An algorithmic framework for isoform-specific functional analysis. bioRxiv. 2022. p. 2022.05.13.491897. https://www.biorxiv.org/content/biorxiv/early/2022/05/15/2022.05.13.491897

2020 Hoyt, Charles Tapley; **Mungall, Christopher**; Vasilevsky, Nicole; Domingo-Fernández, Daniel; Healy, Matthew; Colluru, Viswa (2020: Extension of Roles in the ChEBI Ontology. ChemRxiv. Preprint. https://doi.org/10.26434/chemrxiv.12591221.v1

2019 **Mungall, C.J.**, Koehler, S., Robinson, P., Holmes, I., and Haendel, M. (2019). k-BOOM: A Bayesian approach to ontology structure inference, with applications in disease ontology construction. https://www.biorxiv.org/content/10.1101/048843v3

2017 Köhler, S., Robinson, P., and **Mungall, C.J.** (2017a). Opposite-of information improves similarity calculations in phenotype ontologies. https://www.biorxiv.org/content/10.1101/108977v1

Mungall, C.J. and Holmes, I. (2017). WTFgenes: What's The Function of these genes? Static sites for model-based gene set analysis.https://www.biorxiv.org/content/10.1101/114785v1

2014 **Mungall, C. J.** (2014a). Formalization of Genome Interval Relations. https://www.biorxiv.org/content/10.1101/006650v1

Book Chapters

2007 Haendel, M. A., Neuhaus, F., Osumi-Sutherland, D., Mabee, P. M., Mejino, J. L. J., **Mungall, C. 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.

Published 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)

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

Invited Talks and Panels

2024   Panelist, NSF "Microbiome Data Management in Action" workshop; Atlanta GA, June 12, 2024.

2024   Invited speaker at NIAID workshop on the application of AI to immunology and infectious disease (https://www.niaid.nih.gov/news-events/niaid-dait-ai-and-immunology-exploring-opportunities-and-chall enges-symposium), May 29, 2024. https://zenodo.org/records/12216212

2024   Panelist, AI and Biocuration, at NIH DRKB (Data Repositories and Knowledge Bases) meeting, March 2024. "The promise and perils of LLMs for AI driven ontology curation". https://zenodo.org/records/10866668

2024   Invited presentation on NMDC at a PAG interagency DOE/USDA/NSF Bioeconomy workshop, "Beyond the National Plant Genome Initiative" in January 2024, San Diego, CA

2023   Invited speaker, Ontology Summit 2023, https://ontologforum.org/index.php/OntologySummit. "COB: A Core Ontology for Biology". https://zenodo.org/records/7654926

2023   Invited Speaker, Pistoia series on Demystifying Ontologies for Life Science Leaders, October 2023. "pen Ontologies in the Biomedical Domain". https://zenodo.org/records/10344284

2023   Invited Speaker, Roche RAAN Insights series,"Generative AI tools from the Monarch Initiative; RAAN Insight Series", Sep 26, 2023. https://zenodo.org/records/10343298

2023   Keynote, DeclMed 2023, "Strange loops: journeys in declarative logic programming in genomics and beyond", Seattle, WA, Sep 9, 2023. https://zenodo.org/records/10343425

2023   Presentation: Airbus Semantic Technology Meetup, May 11, 2023. "OntoGPT: A framework for melding ontologies, knowledge bases, and large language models". https://zenodo.org/records/7995862

2023   Presentation: Global Soil Biodiversity Conference, March 2023, "Metadata and Ontologies for Soil Biodiversity Science". https://zenodo.org/records/10344471

2023   Panelist, Ontology Summit 2023, "Helping scientific researchers make better use of ontologies", March 1, 2023.

2023   Keynote, Conference on Semantic Web Applications in HealthCare and Life Sciences (SWAT4HCLS), Basel, Switzerland, "Scaling up semantics: lessons learned from across the life sciences", February 15, 2023. https://zenodo.org/records/7654899

2022   Panelist, US2TS, the 4th U.S. Semantic Technologies Symposium,"Towards FAIR, Trustworthy and Harmonized Semantic Resources", September 30, 2022.

2022   Invited talk: The Linked Data Modeling Language: A framework and toolkit for describing, integrating, and linking diverse datasets. NERSC Seminar Nov 2022

2022   Invited talk (with Justin Reese), "KG-COVID-19: Knowledge Graph for COVID-19 Response". "Ontolog" Ontology Summit 2022: Pandemics and other disasters. February 9, 2022.

2022   Panelist, Towards an Earth and Space Science Knowledge Commons, Earth Science Information Partnership (ESIP) virtual meeting, January 18, 2022

2022   Invited talk, LBNL Salon on Predictive Biomanufacturing

2021   Keynote, Disease Maps Community Meeting, "Biological Ontologies in the Systems Biology of Human Diseases." November 29, 2021.

2021   Panel Moderator, NMDC community webinar: "Making Ontologies Work for Microbiome Research". November 3, 2021.

2021   Keynote, International Conference on Biomedical Ontologies (ICBO 2022), "All Together Now: Piecing Together the Knowledge Graph of Life". September 17, 2021.

2021   Invited talk, Ontologies for Materials-Databases Interoperability (OMDI2021) conference, "Experiences in the biosciences with the Open Biological Ontologies Foundry and the Gene Ontology." October 7, 2021.

2021   Panelist, Data Reuse in Biomedical Research, LitCoin Stakeholder Feedback Workshop, June 18, 2021

2021   Invited talk, Gene Ontology: Causal Activity Modeling. Harvard DBMI, June 2021

2021   Yosemite Healthcare Information Interoperability Talk: LinkML, Linked Open Data Modeling Language, April 14, 2021. https://bids.berkeley.edu/resources/videos/linkml-linked-open-data-modeling-language

2021   Invited Speaker, J.P. Morgan Chase Knowledge Graph group, April 2021

2020   Keynote, "Aligning Design Patterns Across Multiple Ontologies in the Life Sciences." Workshop on Ontology Patterns, International Semantic Web Conference. Virtual, Nov 2020. https://zenodo.org/records/7655184

2020   Pistoia Alliance Seminar Series: Systematic curation of disease concept mappings in Mondo. Virtual seminar series. July 2020. https://zenodo.org/records/7657642

2019   Stanford Biomedical Informatics Research (BMIR) colloquium: Gene Ontology Causal Activity Modeling: Acquiring and reasoning over structured descriptions of biological systems. December 5, 2019

2019   Keynote, International Conference on Food Ontology Operability Data and Semantics, UC Davis, March 2019

2019   Reasoning across multiple open bio-ontologies. 2nd US Semantic Technologies Symposium Series, Duke University, March 2019

2019   Panelist, CGIAR webinar on reference ontologies for agriculture, March 2019, *https://youtu.be/nupfUaGn-lOQ*

2018   Ontologies and Knowledge Graphs for Microbiome Data Science, Microbiome Initiative Workshop on Data Sciences, UC Berkeley, Nov 2018

2018   Seminar presentation, "GO Causal Activity Models" (https://vimeo.com/307092087), BioOntologies Seminar Series, Iowa State University, December 2018. https://zenodo.org/records/7657694

2018   Gene Ontology Program at Berkeley Lab - Triennial Biosciences Review, LBNL, January 2018

2018   Seminar presentation, Introduction to the Relation Ontology, University of Colorado, Denver, October 2018

2018   Seminar presentation, Use of Uberon in Kidney Precision Medicine, Kidney Precision Medicine Project, Seattle, July 2018

2016   Incorporating the exposome into machine intelligence methods in biomedical research - Sanford Imagenetics, Sioux Falls, September 2016

Panelist, Critical Assessment of Genome Interpretation, Open Challenges Conference, UCSF, March 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

Crossing the Species Divide - NIH Symposium: Linking Disease Model Phenotypes to Human Conditions, NIH, September 2015

From Phenotype Ontologies to Phenotype Networks, Stanford, May 2015

Describing samples using the Uberon anatomy ontology - Genomics Standards Workshop JGI, May 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

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

Training/Workshops

2024   Presentation to OBO Academy (https://oboacademy.github.io/obook/courses/monarch-obo-training) on AI-driven Ontology Editing Workflow: "AI Guided Ontology Curation Workflows and the ROBOT Template GPT helper". March 2024. https://bit.ly/ai-ontology-workflows. https://zenodo.org/records/10901704

2024   Presentation: "Using Large Language Models to Build Ontologies". Systems Biology and Ontologies Workshop, Plant and Animal Genome Conference (PAG) 2024, January 2024. https://pag.confex.com/pag/31/meetingapp.cgi/Paper/53968, https://zenodo.org/records/10866680

2023   Presentation to OBO Academy: "Enhancing curation workflows with CurateGPT". November 11, 2023. https://zenodo.org/records/10343357

2023   Presentation to OBO Academy: "Ontology Access Kit (OAK)". March 7, 2023. https://zenodo.org/records/7708963

2023   Presentation at Mapping Commons Workshop (https://mapping-commons.github.io/sssom/workshops/) at ISB 2023. "Mapping Data Structures: Challenges and Approaches". Padua, Italy. April 23, 2023. https://zenodo.org/records/10343505

2022   LinkML workshop. International Conference for Bio Ontologies (ICBO), University of Michigan, September 2022. https://zenodo.org/records/7786606

2022   Ontology Access Kit (OAK) workshop, June 15, 2022. https://zenodo.org/records/7765089

2022   Presentation at INCF Assembly Workshop "Where was I? The problem of rigorously identifying placement of electrodes or other probes in the brain, for many species", https://neuroinformatics.incf.org/2022/program. Title: "Aligning multiple neuroanatomical reference resources across species with Uberon." September 14, 2022. https://zenodo.org/records/7657723

2021   WSBO-2021: Workshop on Synergizing Biomedical Ontologies, "Synergizing Biomedical Ontologies with Genomics Databases". July 15, 2021

2019   Randi Vita, Lynn Schriml, Rebecca Jackson, James A. Overton, Chris Mungall, Bjoern Peters. The OBO Foundry as a curation resource: Maintaining and improving OBO ontologies to provide an interoperable source of terms for biocuration. Biocuration 2019 April 7th - 10, 2019.

2018   Nicole Vasilevsky, James A. Overton, Melissa Haendel, Chris Mungall, Rebecca Tauber. A how-to guide to create, manage, and release an OBO ontology (Ontology 101). International Conference on Biological Ontology (ICBO) 2018 August 7-10, 2018.

2017   Ontology Learning for Biosciences, Energy, and the Environment - Environmental Knowledgebase Workshop - Berkeley Institute for Data Science, January 2017

Teaching and Mentorship Experience

2022-2024   Mentor, LBNL Biosciences Area Program

2023   Mentorship committee for University of Colorado F31 application

2019   Hosted and supervised international masters student internship

2018   Guest lecturer, Health Informatics Graduate Program, UC Davis, CA

2017   Tutorial Co-organizer. OBO Tutorial. International Conference on Biomedical Ontology, Newcastle upon Tyne, UK

2017   Tutorial Co-organizer, 2017 Berkeley GO Editors Workshop

2015   Tutorial Organizer, Introduction to ontologies, International Plant Trait Curation workshop, Corvallis, OR

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

2009   Tutorial organizer. Developing ontologies in OBO and OWL, International Conference on Biomedical Ontologies, Buffalo, NY

2005   Undergraduate guest lecturer, Introduction to the Gene Ontology, BioEngineering, UC Berkeley

2001-3 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

2013   Ph.D. Thesis Committee: Sebastian Koehler, Department of Mathematics and Computer Science, Charite - Universitatsmedizin Berlin

Service

Review Panels

2024   Reviewer for Swiss National Science Foundation

2024   NIH/NIAID special emphasis review panel ZAI1 RK-M for the Bioinformatics Resource Centers (BRCs)

2024   NIH/OD Office of Behavioral and Social Sciences Research special emphasis review panel

2023   Computing, Analytics, and Modeling (CAM) Panel, PNNL Environmental Molecular Sciences Laboratory (EMSL)

2022   NIH Common Fund Review Panel

2022   NIH Biomedical Knowledgebases and Data Repositories Panel

2022   NIAID SBIR reviewer

2021   UK Medical Research Council, ad-hoc reviewer

2021   NINDS ad-hoc panel member

2020   NIH COVID special emphasis panel

2020   ELIXIR Recommended Interoperability Resources, External Evaluation Committee

2020   NIH NCI ITCR ad-hoc panel member

2020   Invited reviewer, Ludwig Maximilian University of Munich, Research Fellowship Program

2019   NIH NCI ITCR ad-hoc panel member

2019   NIH BDMA ad-hoc panel member

2018   NLM ad-hoc reviewer, March 2018

2017   NIH ad-hoc Proposal Review Panel member, Genomics, Computational Biology and Technology (GCAT) study panel

NCI CBIIT Project Review

SIB Proposal Review Swiss Institute of Bioinformatics, competitive proposal review

2012, 2014   DOE Proposal Review Department of Energy, Biological and Environmental Research, SBIR/STTR Program

Institutional Service

2024-   Red team member for KBase review

2023-   LBNL Biosciences Area Representative for LBNL AI governance group

2023-   LBNL Biosciences Area representative for IDEA (Inclusion, Diversity, Equity, and Accountability) in Research Working Group

2023   LBNL Biosciences Area Deputy search committee

2023   LBNL Directors Award Labwide Recognition Committee

2018-present   Department Head, Biosystems Data Science (formerly Molecular Ecosystems Biology dept head)

2018-present   Member: Computational Biology Group

2016   Interview Committee, Interviews for division head

2016   Working Group Member, LBNL Neurosciences Interest Working Group

2016   Visioning Group, LBNL Biosciences Strategic Plan

Program Committees

2024 Program Committee, AAAI Fall symposium Large Language Models for Knowledge Graph and Ontology Engineering

2023 Program Committee, Semantic Web Applications in the Health and Life Sciences 2024

2023 Program Committee, Formal Ontology in Information Systems

2020-1 Scientific Organizing Committee, workshops on Plant single-cell solutions for energy and the environment, Jan 2020 and April 2021.

2019 International Scientific Committee, BioCuration 2019

Steering Committee, U.S. Semantic Technologies Symposium 2019

Co-organizer, Phenotype Ontologies Traversing All The Organisms (POTATO) workshop, International Conference on Biological Ontology, Corvallis, OR

Scientific Committee, Gene Ontology Workshop, Montreal, Canada, October 2018

2018 Program co-chair, International Conference on Biological Ontology, Corvallis, OR

2017 Review Committee, Internet of Food Conference, Davis, CA, November 2017

2016 Steering Committee, 7th International Conference on Biological Ontology: Food, Nutrition, Health and Environment for the 9 billion, Corvallis, OR, August 2016

Program Committee, 8th International Conference on Neural Computation Theory and Applications

Program Committee, ECCB 2016

Program Committee, Bio-Ontologies 2016

Reviewer, Pacific Symposium on Biocomputing 2016

2015 Program Committee, 4th Workshop on Knowledge Discovery and Data Mining Meets Linked Open Data

Program Committee, Resources Program, ISWC 2016

Program Committee, Data Sets and Ontologies Program, ISWC 2015

Program Committee, Bio-Ontologies

2014 Program Committee, 10th Workshop on Constraint-Based Methods for Bioinformatics, September 8, 2014, Lyon, France

Reviewer, AMIA 2014

Program Committee, 6th Workshop on Formal Ontologies meet Industry

Co-organizer Uberon workshop, Biocuration 2014, Toronto, Canada.

2014-2016 Program Committee, PhenoDay ISMB

2013 Program Committee, Declarative Logic Programming: Theory, Systems, and Applications

2009-2013 Program Committee, Bio-Ontologies

Program Committee, Semantic Web Applications in the Life Sciences

Program Committee / Track Chair, International Conference on Biomedical Ontologies

2010-2016 Program Committee, ISMB/ECCB

2010 Program Committee, OWL: Experience and Directions

Reviewer. AMIA/TBI 2014

2007 Program Committee, Bio-Ontologies

Program Committee, OWL: Experience and Directions

Program Committee, ISMB/ECCB

Journal Reviews

For complete record, see https://publons.com/researcher/1686250/chris-mungall/peer-review/

Editorial Boards: PeerJ, Nature Scientific Data

Academic Editor Role: eLife, PeerJ, Nature Scientific Data
ACS Synthetic Biology
Advanced Genetics
Applied Ontology
Bioinformatics
BMC Bioinformatics
BioMed Research International
Cancer Research
Database
Environmental Health Perspectives
Genome Research
GigaScience
Human Mutation
Infection and Immunity
International Journal of Approximate Reasoning
International Journal of Human-Computer Studies
International Journal on Semantic Web and Information Systems
Journal of Biomedical Informatics
Journal of Biomedical Semantics
Journal of Inherited Metabolic Disease
NAR Genomics and Bioinformatics
Nature Biotechnology
Nature Methods
Nucleic Acids Research
Open Biology
PLoS Computational Biology
PLoS Genetics
PLoS ONE
PeerJ (including serving as [Guest Editor in November 2019](#))
Review Editor eLife
Systematic Biology

Working Groups and Advisory Boards

2024	JGI Informatics Advisory Committee
2024	MICROBES-4-CLIMATE Scientific Advisory Board
2024	Member of RDA FAIR-Mapping Working Group
2020-present	GSC Compliance and Interoperability Working Group
2021-2022	Scientific Organizing Committee, LBNL [Plant single cell solutions for energy and the environment](#).
2019-2021	Earth Biogenome Project (EBP), Annotation Standards Committee
2016	Scientific Advisory Board Member, NSF Phyloreferences for the Tree of Life
	Subcommittee member, International Federation of Associations of Anatomists (IFAA)
2015	National Center for Ecological Analysis and Synthesis Ontology Working Group
2014-2019	Global Alliance for Genomics and Health (GA4GH), Clinical Working Group
	International Rare Diseases Consortium, Ontologies and rare disease prioritization Working Group

Working Group 1, co-leader Transcription Factor TG Consortium

2010, 2011 Scientific Advisory Board Member Disease Ontology

2004-Present Coordinator: Open Biological Ontologies Foundry