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Education

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

Appointments

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

Publications

Google Scholar: [goo.gl/x2R5PC](https://scholar.google.com/citations?user=x2R5PC) h-index: 87 i10-index: 172

Refereed Journal Articles

- 2023 Chan LE, Thessen AE, Duncan WD, Matentzoglou N, Schmitt C, Grondin CJ, Vasilevsky N, McMurry JA, Robinson PN, **Mungall CJ**, Haendel MA. The Environmental Conditions, Treatments, and Exposures Ontology (ECTO): connecting toxicology and exposure to human health and beyond. *J Biomed Semantics*. 2023 Feb 24;14(1):3. <http://dx.doi.org/10.1186/s13326-023-00283-x> PMID: PMC9951428
- Tan SZK, Kir H, Aevermann BD, Gillespie T, Harris N, Hawrylycz MJ, Jorstad NL, Lein ES, Matentzoglou N, Miller JA, Mollenkopf TS, **Mungall CJ**, Ray PL, Sanchez REA, Staats B, Vermillion J, Yadav A, Zhang Y, Scheuermann RH, Osumi-Sutherland D. Brain Data Standards - A method for building data-driven cell-type ontologies. *Sci Data*. 2023 Jan 24;10(1):50. <http://dx.doi.org/10.1038/s41597-022-01886-2> PMID: PMC9873614
- 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. Perspectives for self-driving labs in synthetic biology. *Curr Opin Biotechnol*. 2023 Jan 3;79:102881. <http://dx.doi.org/10.1016/j.copbio.2022.102881> PMID: 36603501
- 2022 Matentzoglou 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.

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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>

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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>

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/>

Awarded Proposals

ACTIVE

U41HG02273 Thomas 06/01/22-03/31/27 USC (NHGRI)
Gene Ontology Consortium

Launched in 1998, the Gene Ontology (GO) knowledgebase is the world's largest source of information on the functions of genes across the tree of life, and is among the most widely used resources for computational analysis

in biomedical research. With this renewal we will continue to expand the GO, broadening coverage, increasing precision for key pathways, and advancing the causal activity model.

Role: Co-Investigator

RM1HG010860 Chute, Mungall, Haendel 08/01/20 - 05/31/25 Univ. of Colorado
(NIH/NHGRI)

A phenomics-first resource for interpretation of variants

The Gene Ontology (of which Dr. Mungall is a PI) is the accepted standard for describing the functions of genes. We aim to develop a similarly universal ontology for representing the phenotypes of disease. The Human Phenotype Ontology (HPO) is used by many researchers who are studying rare diseases and the genetic variations associated with them. This project proposes to develop a framework that extends HPO to other species; develop an ontology of diseases that translates between biological research and clinical terminology; and design a way to share phenomics information between researchers working on different species and diseases. The demonstrated expertise of the LBNL project team in developing and utilizing biomedical ontologies make us particularly suitable for undertaking this ambitious project. Our hope is that these efforts will lead to a better understanding of the intricacies of human disease and, ultimately, improved treatment options for every individual.

Role: MPI

2R24OD011883 Haendel, Mungall, Robinson 04/01/21-03/31/25 Univ. of Colorado (NIH/NIA)

The Monarch Initiative: Linking Diseases to Model Organism Resources

The major goal of this renewal will be to extend Monarch's ontologies, linked data corpus (knowledge graph), and tools to optimize the precision and utility of model organism data—maximizing the investment made in research organisms for human disease research.

Role: PI

U24 HG011851 D'Eustachio 09/24/21-06/30/26 New York Univ. (NIH)

Reactome and the Gene Ontology: Digital pathway convergence for core data resources

The goal of the proposed work is to extend a collaboration between the GO and Reactome projects to better integrate content currently siloed in the two resources in order to provide a more fully interoperable open access resource for the biomedical research community.

Role: Co-Investigator

FP13680/TBD Green, Davis, Mangravite 04/01/22-03/31/26 Univ. of Colorado (NIH)

Integration, Dissemination, and Evaluation (BRIDGE) Center for the NIH Bridge to Artificial Intelligence (Bridge2AI) Program / Standards Module

The Bridge2AI project aims to generate new “flagship” data sets and best practices for machine learning analysis, in order to tackle complex biomedical challenges beyond human intuition. The purpose of the Standards Core in the BRIDGE Center is to coordinate the activities of the Standards Modules across all the Bridge2AI Data Generation Projects.

Role: Co-Investigator

U24GM143402 Musen 09/27/21-08/31/26 Stanford University (NIH)

BioPortal: An Expansive Knowledgebase of Biomedical Entities and Relations

Ontologies are a critical and widely-used biomedical informatics resource. They organize medical knowledge, enable data to be annotated in standardized ways, and help drive systems for natural language processing, data and knowledge integration, and information management. The currently unfunded BioPortal, which brings together over 800 biomedical ontologies, is accessed by over 75,000 unique users per month. With more funding, we will improve the BioPortal knowledge base and methods, making BioPortal an even more useful resource for the broader scientific community.

Role: Co-Investigator

U24HG010859 Sternberg 09/06/19-07/31/24 Caltech (NIH/NHGRI)
Alliance Central: A platform for sustainable development of next generation genome knowledgebases
A number of Model Organism Databases have been funded by the National Institutes of Health over the years, with each developing its own unique infrastructure. We have identified ways in which combining these resources into an "Alliance for Genomic Resources" can deliver cost savings and new ways of exploring disease. The teams at LBNL will devise the architecture and infrastructure for building this Alliance.

Role: Consortium PI

7OT2TR003449-02 Thessen, Bizon, Mungall (MPIs) 01/23/20-01/22/25 Univ. of Colorado (NIH/NCATS)

A Common Dialect for Infrastructure and Services in Translator

We will develop community-driven standards expanding Translator standards. They will define how Translator resources can be discovered, how they are invoked, and the format of data exchanged between them. It will define standards for capturing knowledge graphs, and ways to use metadata that facilitates data interpretation, integration and refinement into a response for a user's translational research question.

Role: Co-investigator/Sub PI

R01HD103805-01 Robinson, Mungall, Smedley 05/20/21-03/31/26 Jackson Laboratory (NIH)

Increasing the Yield and Utility of Pediatric Genomic Medicine with Exomiser

The goals of the Exomiser tool, which identifies potential disease-causing variants from whole-genome sequencing data, utilizes this type of information to help improve diagnostic accuracy. In this proposal, we aim to increase the yield and clinical utility of Exomiser. Our hope is that these efforts will ultimately lead to better diagnosis and more accurately targeted treatments for every individual.

Role: MPI

PENDING

DE-AC02-05CH11231 Mouncey 10/01/22 – 09/30/25 DOE BER

National Microbiome Data Collaborative (NMDC)

The vision of the NMDC is to empower the research community to harness microbiome data exploration and discovery through a collaborative and integrative data science ecosystem. The NMDC will address fundamental roadblocks in microbiome data science through implementation of guiding principles to make data findable, accessible, interoperable and reusable (FAIR).

Role: Co-Investigator (Renewal pending)

RC2 Iyengar 07/01/23-06/30/28 Mt. Sinai (NIDDK)

H2KG: Human Kidney Knowledge Graph

The kidney is a critical organ whose functions include excretion of waste products and clearance of drugs and their metabolites. In the US, chronic kidney disease affects around 15% of US adults, with an even higher rate among African Americans. Research into kidney disease is producing large amounts of data from different fields, but these data must be integrated in order to fully leverage them to improve diagnosis and treatment. We propose to develop an integrated Human Kidney Knowledge Graph (H2KG) that maps relationships across different types and sources of information, similar to what has been achieved in the KG-COVID-19 project, which united an assortment of data related to COVID-19 to help accelerate research into possible mechanisms and treatments. This knowledge graph will provide a resource that can be used for purposes such as characterizing biological pathways that are important in kidney dysfunction, and identifying proteins that can be targeted to better treat kidney diseases.

Role: Co-Investigator (pending)

RECENTLY COMPLETED

U41HG02273 Thomas 03/01/12-02/28/22 USC (NIH/NHGRI)

The Gene Ontology Consortium

The major goal is to provide a complete and integrated picture of what every single gene in a human being does, thus allowing us to better understand the genetic and cellular workings of human health and disease. We do this by developing the Gene Ontology, a computational resource that collects biological knowledge into a large network structure; connecting genes with the roles they play. Researchers, clinicians, and sophisticated computer programs use this network to interpret the massive amounts of biomedical and genomic data being generated in experiments and in studies designed to gain key insights into human health.

Role: Co-Investigator

U01CA239108 Robinson 04/01/19-02/28/22 (NCE) Jackson Laboratory (NIH)

Illuminating the Druggable Genome by Knowledge Graphs

Prioritizing novel drug targets is a slow, high-risk process. This proposal leverages two knowledge sources – the Monarch Initiative which aggregates gene-disease-phenotype knowledge plus the Illuminating the Druggable Genome (IDG) project knowledge base which collects information on drug characteristics. The end product is a combined database linking genes, diseases, phenotypes, and drugs, together with a system for predicting new disease targets.

Role: Consortium PI

DE-AC02-05CH11231 Bouchard 08/14/20 - 02/28/22 DOE

ENDURABLE: Benchmark datasets for AI with queryable metadata

Our goal is to provide the scientific and DL communities robust, scalable, and extensible tools to share and rigorously aggregate diverse scientific data sets for training state-of-the-art DL models, as well as the means to evaluate the models with respect to the details of the data. The creation of standard description languages and scalable interfaces enables querying the data and models, both individually and with respect to one another, greatly enhancing the FAIRness of the data and models.

Role: Co-Investigator

1RF1MH123220-01 Hawrylycz 12/21/20-09/03/22 Allen Institute (NIH)

A Community Framework for Data-driven Brain Transcriptomic Cell Type Definition, Ontology, and Nomenclature

Understanding how our brains work (and why they sometimes don't) is one of the key challenges of modern biology. A fundamental prerequisite for this is developing a detailed census of the different cell types in the mammalian brain, and the many facets of brain cell phenotype (observable characteristics). New techniques such as single-cell transcriptomics (which examines the level of expression of particular genes at the level of individual cells) are providing detailed new insights into neuronal phenotypes. However, this wealth of data is encoded in a variety of incompatible ways, limiting its reusability by other scientists and computational tools. This incompatibility can be addressed by using ontologies: standardized, computer-friendly encodings that allow data from a wide range of sources to be combined in a unified way. Dr. Mungall, who is recognized as one of the leading experts on biomedical ontologies, will lead the effort to develop a data-driven neuron type ontology. The end result of this project will be a practical cell type nomenclature that can be used by a wide community of researchers to access and contribute to single-cell transcriptomic data and other relevant information sources, such as the BRAIN Initiative. The classification will be structured so that it can be extended by the community to cover additional cell types (beyond neuronal), facilitating a range of research that will increase our understanding of brain organization and neurological disorders.

Role: Co Investigator/Sub-PI

ACO21007-001-0000 Mungall 04/11/21-01/07/22 NIH/NCI
Center for Cancer Data Harmonization (CCDH)

The Center for Cancer Data Harmonization (CCDH) will create a national Cancer Data Ecosystem that will enable participants across the cancer research and care spectrum to contribute, access, combine and analyze diverse data that will enable new discoveries and ultimately reduce the personal and public health burden of cancer. To support this, the CCDH will enable data collection, deposition, harmonization, quality assurance, query, integration, and analytics across an initial set of Cancer Research Data Commons (CRDC) nodes. The project team includes some of the world's most talented semantic engineers who will develop tools and processes for aligning and harmonizing data dictionaries, leveraging modern ontologies and data models.

Role: PI

DE-AC02-05CH11231

05/01/20 - 09/30/21

LBNL LDRD

Leveraging knowledge graphs and machine learning to produce actionable knowledge for COVID-19 response
We propose to 1) produce a COVID-19 knowledge graph (KG) to support both DOE and international COVID-19 efforts; 2) incorporate data from COVID-19 biomedical literature from sources as the Berkeley Lab covidscholar.com project in the form of natural language processing (NLP)-derived terms and deep learning embeddings ; 3) apply machine learning (ML) techniques to discover new links (for example, identifying existing drugs that could be repurposed to treat COVID-19) and generate actionable knowledge.

Role: PI

U01HG009453 Mungall (PI)

09/23/16-08/31/21 (NCE)

NIH/NCI

An Intelligent Concept Agent for Assisting with the Application of Metadata

The major goal is to develop an intelligent concept assistant that will allow researchers to generate and share sets of metadata elements relevant to their project, and will use machine learning techniques to automatically apply this to data.

Role: PI

R24ES028518 Peters, Mungall (MPIs)
Immunology/NIH

09/21/17-06/30/21 (NCE)

La Jolla Institute for Allergy &

Services to support the OBO foundry standards

The Open Biomedical Ontologies (OBO) Foundry is an established community resource, with a broad spectrum of contributing members, that promotes and facilitates the development, application, harmonization, and sharing of special digital objects known as 'ontologies'. Ontologies are multiple aspects of modern data-driven biomedical research, and the OBO Foundry provides a vital service in coordinating these resources. The work of this project will be to provide catalytic support to migrate the technical services of the OBO Foundry to modern cloud-based computing.

Role: PI

DE-AC02-05CH11231 Adams

05/01/20 - 03/31/21

DOE

Molecular design and analysis to inform therapeutics related to COVID-19

This multi-laboratory (ANL, BNL, LANL, LBNL, LLNL, ORNL, PNNL, SNL, SLAC) project will apply DOE capabilities to complement resources available in the public and private sector and thereby accelerate discovery of medical therapeutics targeting SARS-COV-2. The team will apply integrated computational, modeling, and AI expertise with structural biology and other analytical capabilities available in the national laboratories to accelerate the critical path for discovery of small molecules, vaccines, and antibodies that interact with key viral and human targets.

Role: Co-Investigator

Invited Talks and Panels

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.

- 2023 Panelist, Ontology Summit 2023, “Helping scientific researchers make better use of ontologies”, March 1, 2023.
- 2022 Panelist, US2TS, the 4th U.S. Semantic Technologies Symposium, “Towards FAIR, Trustworthy and Harmonized Semantic Resources”, September 30, 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
- 2020 Pistoia Alliance Seminar Series: Systematic curation of disease concept mappings in Mondo. Virtual seminar series. July 2020
- 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/npfUaGn-lQQ>

- 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
- 2018 Gene Ontology Program at Berkeley Lab - Triennial Biosciences Review, LBNL, January 2018
- 2018 Introduction to the Relation Ontology, University of Colorado, Denver, October 2018
- 2018 Use of Uberon in Kidney Precision Medicine, Kidney Precision Medicine Project project, Seattle, July 2018
- 2017 Ontology Learning for Biosciences, Energy, and the Environment - Environmental Knowledgebase Workshop - Berkeley Institute for Data Science, January 2017
- 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

- 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, 2018.2
- 2021 WSBO-2021: Workshop on Synergizing Biomedical Ontologies, “Synergizing Biomedical Ontologies with Genomics Databases”. July 15, 2021

Teaching Experience

- 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 - Universitätsmedizin Berlin

Service

Program Committees

- 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
BMC Bioinformatics
BioMed Research International
Bioinformatics
Cancer Research
Database
Environmental Health Perspectives
Genome Research
GigaScience
Human Mutation
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 Diseases
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

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 Phylotranscriptomics 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-Present Global Alliance for Genomics and Health, 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

Institutional Service

2022-present Enrolled as mentor in Biosciences Area Mentorship program

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

2018-present Member: Computational Biology Group

2016 Interview Committee, Interviews for division head
Working Group Member, Neurosciences Interest Working Group
Visioning Group, Biosciences Strategic Plan

Review Panels

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