






# Charles Tapley Hoyt, Ph.D.

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## Fields of Work

Bioinformatics, Pathway Analysis, Machine Learning, Natural Language Processing, Ontology, Knowledge Graph, Proteochemometrics, Drug Repositioning, Systems Biology, Cheminformatics

## Employment

I'm taking personal leave beginning May 2024 and will be considering new opportunities beginning in Fall 2024 (only remote from Germany).

- 2023–24 **Senior Scientist**, *Northeastern University*, Boston, MA, USA (remote).  
Moved with the Gyori Lab from Harvard Medical School
- 2021–23 **Research Fellow**, *Harvard Medical School, Laboratory of Systems Pharmacology*, Boston, MA, USA (remote).  
Biocuration, data standardization, natural language processing, data integration, and automated assembly of knowledge and models (Gyori/INDRA Lab)
- 2020 **Computational Biologist**, *Enveda Biosciences*, Boulder, CO, USA (remote).  
Biomedical data integration, knowledge graph construction, and analysis
- 2018–19 **Lecturer**, *University of Bonn*, Bonn, Germany.
- 2016–19 **Research Fellow**, *Fraunhofer SCAI, Dept. of Bioinformatics*, Sankt Augustin, Germany.  
Systems biology modeling and analysis with the Biological Expression Language
- 2012–15 **Teaching Assistant**, *Northeastern University*, Boston, MA, USA.
- 2014 **in Silico Lead Discovery Co-op**, *Novartis*, Cambridge, MA, USA.  
Mechanism of action deconvolution in high-throughput black-box phenotypic screens
- 2013–14 **Molecular Informatics Internship**, *Pfizer*, Cambridge, MA, USA.  
Software development and database development for cancer genomics data
- 2013 **Post-Selection Chemistry Co-op**, *GlaxoSmithKline*, Waltham, MA, USA.  
Lead optimization of antivirals identified by ultra-high-throughput screening
- 2012 **Research Assistant**, *Pollastri Laboratory, Northeastern University*, Boston, MA, USA.  
Medicinal synthetic chemistry for repurposing PDE4 inhibitors against *T. Brucei*

## Education

- 2018–19 **Doctor of Philosophy**, *Computational Life Sciences*, University of Bonn.  
Thesis: *Generation and Applications of Knowledge Graphs in Systems and Networks Biology*  
Research Advisor: Prof. Dr. Martin Hofmann-Apitius  
GPA: 1,3 (Magna Cum Laude)
- 2015–17 **Master of Science**, *Life Science Informatics*, University of Bonn.  
Thesis: *PyBEL: a Computational Framework for Biological Expression Language*  
Research Advisor: Prof. Dr. Martin Hofmann-Apitius  
GPA: 1,6
- 2011–15 **Bachelor of Science**, *Chemistry*, Northeastern University.  
GPA: 3.93/4.0 (Summa Cum Laude)  
Research Advisor: Prof. Dr. Michael P. Pollastri

## Awards

- 2023 **Excellence in Biocuration Early Career Award**, *International Society of Biocuration*.
- 2015 **Bernie Lemire Award**, *Department of Chemistry, Northeastern University*.
- 2011 **Presidential Scholarship**, *Northeastern University*.

# Research

## Publications

Author lists have been omitted to reduce visual clutter. The following are noted:

- † signifies first or co-first authorship
- ‡ signifies last or senior authorship

1. †**The O3 guidelines: open data, open code, and open infrastructure for sustainable curated scientific resources.** *Scientific Data*, 2024. doi:10.1038/s41597-024-03406-w
2. **An open source knowledge graph ecosystem for the life sciences.** *Scientific Data*, 2024. doi:10.1038/s41597-024-03171-w
3. **ptwt - The PyTorch Wavelet Toolbox.** *JMLR*, 2024
4. **The Human Phenotype Ontology in 2024: phenotypes around the world.** *NAR*, 2023. doi:10.1093/nar/gkad1005
5. †**Improving reproducibility and reusability in the Journal of Cheminformatics.** *J Cheminform*, 2023. doi:10.1186/s13321-023-00730-y
6. **Democratizing knowledge representation with BioCypher.** *Nature Biotechnology*, 2023. doi:10.1038/s41587-023-01848-y
7. **Optimal adjustment sets for causal query estimation in partially observed biomolecular networks.** *Bioinformatics*, 2023. doi:10.1093/bioinformatics/btad270
8. †**Prediction and curation of missing biomedical identifier mappings with Biomappings.** *Bioinformatics*, 2023. doi:10.1093/bioinformatics/btad130
9. (preprint) **Experimental design for causal query estimation in partially observed biomolecular networks.** *arXiv*, 2022. arxiv:2210.13423
10. †**Unifying the identification of biomedical entities with the Bioregistry.** *Scientific Data*, 2022. doi:10.1038/s41597-022-01807-3
11. **A Simple Standard for Ontological Mappings 2022: Updates of data model and outlook.** *OM 2022*
12. **A review of biomedical datasets relating to drug discovery: a knowledge graph perspective.** *Brief Bioinform*, 2022. doi:10.1093/bib/bbac404
13. **ChemicalX: A Deep Learning Library for Drug Pair Scoring.** *KDD*, 2022. doi:10.1145/3534678.3539023
14. **Integrating multi-omics data reveals function and therapeutic potential of deubiquitinating enzymes.** *eLife*, 2022. doi:10.7554/elife.72879
15. **Understanding the Performance of Knowledge Graph Embeddings in Drug Discovery.** *Artificial Intelligence in the Life Sciences*, 2022. doi:10.1016/j.ailsci.2022.100036
16. **A Simple Standard for Sharing Ontological Mappings (SSSOM).** *Database*, 2022. doi:10.1093/database/baac035
17. **Gilda: biomedical entity text normalization with machine-learned disambiguation as a service.** *Bioinformatics Advances*, 2022. doi:10.1093/bioadv/vbac034
18. **ProtSTonKGs: A Sophisticated Transformer Trained on Protein Sequences, Text, and Knowledge Graphs.** *SWAT4HCLS 2022*. ceur-ws:3127:13
19. (preprint) **Mondo: Unifying diseases for the world, by the world.** *medRxiv*, 2022. doi:10.1101/2022.04.13.22273750
20. **Do-calculus enables estimation of causal effects in partially observed biomolecular pathways.** *Bioinformatics*, 2022. doi:10.1093/bioinformatics/btac251
21. (preprint) †**A Unified Framework for Rank-based Evaluation Metrics for Link Prediction in Knowledge Graphs.** *arXiv*, 2022. arxiv:2203.07544
22. **PyBioPAX: biological pathway exchange in Python.** *JOSS*, 2022. doi:10.21105/joss.04136
23. (preprint) **An Open Challenge for Inductive Link Prediction on Knowledge Graphs.** *arXiv*, 2022. arxiv:2203.01520
24. **STonKGs: A Sophisticated Transformer Trained on Biomedical Text and Knowledge Graphs.** *Bioinform-*

*matics*, 2022. doi:10.1093/bioinformatics/btac001

25. **Ontology Development Kit: a toolkit for building, maintaining, and standardising biomedical ontologies.** *Database*, 2022. doi:10.1093/database/baac087
26. **Bringing Light Into the Dark: A Large-scale Evaluation of Knowledge Graph Embedding Models Under a Unified Framework.** *TPAMI*, 2021. doi:10.1109/tpami.2021.3124805
27. **The role of metadata in reproducible computational research.** *Patterns*, 2021. doi:10.1016/j.patter.2021.100322
28. **‡CLEP: a hybrid data- and knowledge-driven framework for generating patient representations.** *Bioinformatics*, 2021. doi:10.1093/bioinformatics/btab340
29. **A Systems Biology Approach for Hypothesizing the Effect of Genetic Variants on Neuroimaging Features in Alzheimer’s Disease.** *JAD*, 2021. doi:10.3233/jad-201397
30. **‡PyKEEN 1.0: A Python Library for Training and Evaluating Knowledge Graph Embeddings.** *JMLR*, 2021. arxiv:2007.14175
31. **Leveraging Structured Biological Knowledge for Counterfactual Inference: A Case Study of Viral Pathogenesis.** *IEEE TBDATA*, 2021. doi:10.1109/tbdata.2021.3050680
32. (preprint) **‡Extension of Roles in the ChEBI Ontology.** *ChemRxiv*, 2020. doi:10.26434/chemrxiv.12591221
33. **The Minimum Information about a Molecular Interaction Causal Statement (MI2CAST).** *Bioinformatics*, 2020. doi:10.1093/bioinformatics/btaa622
34. **GuiltyTargets: Prioritization of Novel Therapeutic Targets with Deep Network Representation Learning.** *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2020. doi:10.1109/tcbb.2020.3003830
35. **PS4DR: a multimodal workflow for identification and prioritization of drugs based on pathway signatures.** *BMC Bioinf.*, 2020. doi:10.1186/s12859-020-03568-5
36. **Identifying the parametric occurrence of multiple steady states for some biological networks.** *Journal of Symbolic Computation*, 2020. doi:10.1016/j.jsc.2019.07.008
37. **A Computational Approach for Mapping Heme Biology in the Context of Hemolytic Disorders.** *Frontiers in Bioengineering and Biotechnology*, 2020. doi:10.3389/fbioe.2020.00074
38. **The Impact of Pathway Database Choice on Statistical Enrichment Analysis and Predictive Modeling.** *Frontiers in Genetics*, 2019. doi:10.3389/fgene.2019.01203
39. **Quantifying mechanisms in neurodegenerative diseases (NDDs) using candidate mechanism perturbation amplitude (CMPA) algorithm.** *BMC Bioinf.*, 2019. doi:10.1186/s12859-019-3101-1
40. **The KEEN Universe.** *ISWC 2019*. doi:10.1007/978-3-030-30796-7\_1
41. **Predicting Missing Links Using PyKEEN.** *ISWC 2019*. ceur-ws:2456:64
42. **RatVec: A General Approach for Low-dimensional Distributed Vector Representations via Domain-specific Rational Kernels.** *LWDA 2019*
43. **BioKEEN: a library for learning and evaluating biological knowledge graph embeddings.** *Bioinformatics*, 2019. doi:10.1093/bioinformatics/btz117
44. **PathMe: merging and exploring mechanistic pathway knowledge.** *BMC Bioinf.*, 2019. doi:10.1186/s12859-019-2863-9
45. (preprint) **‡Integration of Structured Biological Data Sources using Biological Expression Language.** *bioRxiv*, 2019. doi:10.1101/631812 biorxiv:631812
46. **ComPath: an ecosystem for exploring, analyzing, and curating mappings across pathway databases.** *NPJ Syst Biol Appl.*, 2019. doi:10.1038/s41540-018-0078-8
47. **‡Re-curation and rational enrichment of knowledge graphs in Biological Expression Language.** *Database*, 2019. doi:10.1093/database/baz068
48. **Challenges of Integrative Disease Modeling in Alzheimer’s Disease.** *Frontiers in molecular biosciences*, 2019. doi:10.3389/fmolb.2019.00158
49. **‡BEL Commons: an environment for exploration and analysis of networks encoded in Biological Expression Language.** *Database*, 2018. doi:10.1093/database/bay126

50. **BEL2ABM: agent-based simulation of static models in Biological Expression Language.** *Bioinformatics*, 2018. doi:10.1093/bioinformatics/bty107
51. †**PyBEL: a Computational Framework for Biological Expression Language.** *Bioinformatics*, 2018. doi:10.1093/bioinformatics/btx660
52. †**A systematic approach for identifying shared mechanisms in epilepsy and its comorbidities.** *Database*, 2018. doi:10.1093/database/bay050
53. **A Case Study on the Parametric Occurrence of Multiple Steady States.** *ISSAC 2017*. doi:10.1145/3087604.3087622
54. **Repurposing human PDE4 inhibitors for neglected tropical diseases: design, synthesis and evaluation of cilomilast analogues as Trypanosoma brucei PDEB1 inhibitors.** *Bioorg Med Chem Lett*, 2014. doi:10.1016/j.bmcl.2014.07.063

## Invited Presentations (Selected)

1. **Assembly and inference over semantic mappings to support the NFDI Terminology Service.** *TS4NFDI Community Workshop* (April 9, 2024)
2. **Assembly of Domain Knowledge at Scale in Biomedicine and Beyond.** *Harvard Medical School - Laboratory of Systems Pharmacology Meeting* (January 19, 2024)
3. **Machine-assisted integration of data and knowledge at scale to support biomedical discovery.** *NIH BISTI Seminar* (December 7, 2023)
4. **Democratizing Biocuration, or, How I Learned to Love the Drive-by Curation.** *International Society of Biocuration Annual General Meeting* (October 18, 2023)
5. **Improving ontology interoperability with Biomappings.** *OBO Academy - Monarch Training Series* (September 19, 2023)
6. **Modern prefix management with the Bioregistry and ‘curies’.** *OBO Academy - Monarch Training Series* (September 5, 2023)
7. **Axiomatizing Chemical Roles.** *Ontologies4Chem Workshop 2022* (September 7, 2022)
8. **Knowledge Graph Embedding with PyKEEN in 2022.** *Knowledge Graph Conference (KGC 2022)* (May 5, 2022)
9. **The Biopragnatics Stack: Biomedical and Chemical Semantics for Humans.** *Machine-Actionable Data Interoperability for Chemical Sciences (MADICES)* (February 8, 2022)
10. **Current Issues in Theory, Reproducibility, and Utility of Graph Machine Learning in the Life Sciences.** *Graph Machine Learning in Industry* (September 23, 2021)
11. **Perspectives on Knowledge Graph Embedding Models in/out of Biomedicine.** *AstraZeneca* (April 6, 2021)
12. **Introduction to the Biological Expression Language and the Rational Enrichment Workflow.** *CoronaWhy* (May 6, 2020)
13. **Applications of Knowledge Graphs in Drug Discovery.** *Computational Drug Discovery Group, University of Leiden* (November 5, 2019)
14. **Generation and Application of Biomedical Knowledge Graphs.** *Harvard Medical School* (July 19, 2019)

## Talks and Posters (Selected)







1. **Assembly and Reasoning over Semantic Mappings at Scale.** *Biocuration 2024* (March 7, 2024)
2. **Introduction to WPCI 2023.** *Winter 2023 Workshop on Prefixes, CURIEs, and IRIs* (November 27, 2023)
3. **Standardization of chemical prefixes, CURIEs, URIs, and semantic mappings.** *Ontologies4Chem Workshop 2023* (October 12, 2023)
4. **Improving the reproducibility of cheminformatics workflows with chembl-downloader.** *RDKit User Group Meeting 2023* (September 21, 2023)
5. **Promoting the longevity of curated scientific resources through open code, open data, and public infrastructure.** *Biocuration 2023* (April 26, 2023)
6. **Using dashboards to monitor ontology standardisation and community activity.** *Ontology Summit 2023*

(February 15, 2023)



7. **Introduction to WPCI 2022.** *2022 Workshop on Prefixes, CURIEs, and IRIs* (December 5, 2022)
8. **The Bioregistry, CURIEs, and OBO Community Health.** *International Conference on Biomedical Ontology (ICBO)* (September 26, 2022)
9. **Closing the Semantic Gap: Identifying Missing Mappings and Merging Equivalent Concepts to Support Knowledge Graph Assembly.** *Harvard Medical School - Sorger Lab Meeting* (August 1, 2022)
10. **A Unified Framework for Rank-based Evaluation Metrics for Link Prediction in Knowledge Graphs.** *Graph Learning Benchmarks (GLB 2022)* (April 26, 2022)
11. **Introduction to WPCI 2021.** *2021 Workshop on Prefixes, CURIEs, and IRIs* (October 29, 2021)
12. **Biomappings: Community Curation of Mappings between Biomedical Entities.** *4th Session of the International Society of Biocuration 2021 Virtual Conference* (October 5, 2021; poster)
13. **The Bioregistry: A Metaregistry for Biomedical Entities.** *12th International Conference on Biomedical Ontologies* (September 17, 2021)
14. **Future Directions for WikiPathway Meta-curation.** *WikiPathways Developers Conference Call* (January 6, 2021)
15. **The Biological Expression Language and PyBEL in 2020.** *COVID-19 Disease Map Community Meeting* (July 10, 2020)
16. **Maintenance and Enrichment of Disease Maps in Biological Expression Language.** *4th Disease Maps Community Meeting* (October 4, 2019; poster)
17. **Identifying Drug Repositioning Candidates using Representation Learning on Heterogeneous Networks.** *The Eighth Joint Sheffield Conference on Chemoinformatics* (June 19, 2019; poster)
18. **The PyBEL Ecosystem in 2018.** *OpenBEL Community Meeting* (May 14, 2018)
19. **From Knowledge Assembly to Hypothesis Generation.** *Bio-IT World* (April 22, 2018)
20. **Knowledge Assembly in Systems and Networks Biology.** *Bio-IT World* (April 23, 2018; poster)
21. **The Human Brain Pharmacome: An Overview.** *3rd European Conference on Translational Bioinformatics* (April 17, 2018; poster)
22. **Gene Set Analysis using Phenotypic Screening Data.** *Research, Innovation and Scholarship Expo 2015* (April 9, 2015; poster)

## Research Software (Selected)







Achieving reproducibility and reusability in the computational sciences heavily depends on code that is developed, tested, documented, and distributed according to best software development practices. I aim to make as much of my research as possible available and reusable in the form of open source software. Accordingly, I have pushed tens of thousands of commits to GitHub across my own and external projects to which I have contributed. I have also written extensively on teaching best practices to scientists on my blog.

1. **PyBEL**  [pybel/pybel](#)  
A compiler for the Biological Expression Language (BEL)
2. **Bio2BEL**  [bio2bel/bio2bel](#)  
A framework for reproducible data integration in BEL and knowledge graph construction
3. **BEL Commons**  [bel-commons/bel-commons](#)  
A web application for the interactive exploration of networks encoded in BEL
4. **PyKEEN**  [pykeen/pykeen](#)  
The most expansive knowledge graph embedding framework to date
5. **SeMRA**  [biopragnatics/semra](#)  
Automated assembly and inference of semantic mappings
6. **Bioontologies**  [biopragnatics/bioontologies](#)




Access and processing of ontologies on top of ROBOT and OBO Graphs

7. **PyOBO**  pyobo/pyobo  
Harmonization of biological ontologies and controlled vocabularies
8. **curies**  cthoyt/curies  
Idiomatic conversion between URIs and compact URIs (CURIEs)
9. **GuiltyTargets**  guiltytargets/guiltytargets  
Target prioritization framework using gene expression and network representation learning
10. **RatVec**  ratvec/ratvec  
Sequence-based representation learning
11. **PS4DR**  ps4dr/ps4dr  
Drug repositioning based on bioactivity pattern matching and GWAS
12. **SeffNet**  seffnet/seffnet  
Drug repositioning framework based on network representation learning
13. **CLEP**  hybrid-kg/clep  
Patient stratification framework based on network representation learning
14. **BEL2SCM**  bel2scm/bel2scm  
Generation of structural causal models (SCMs) from BEL
15. **y0 Causal Inference Engine**  y0-causal-inference/y0  
Representation and manipulating probabilistic expressions
16. **STonKGs**  stonkgs/stonkgs  
Multimodal Transformers for biomedical text and Knowledge Graph data
17. **ChemicalX**  AstraZeneca/chemicalx  
A deep learning library for drug-drug interaction, polypharmacy side effect, and synergy prediction
18. **PathMe**  PathwayMerger/PathMe  
Web application for exploration of pathway databases
19. **INDRA**  sorgerlab/indra  
Automated knowledge assembly and modeling in biomedicine
20. **INDRA CoGEx**  bgyori/indra\_cogex  
A 10<sup>8</sup> relation-scale knowledge graph extending on causal knowledge from INDRA
21. **MIRA**  indralab/mira  
Machine-assisted scientific modeling using meta-model templates and domain knowledge graphs
22. **Gilda**  indralab/gilda  
Biomedical named entity recognition and grounding using machine-learned disambiguation

## Databases (Selected)

1. **Bioregistry**  bioregistry/bioregistry , <https://bioregistry.io>  
An integrative meta-registry of biological databases, ontologies, and nomenclatures
2. **Biomappings**  biopragnatics/biomappings , <https://biopragnatics.github.io/biomappings>  
Predicted and curated mappings between named biological entities
3. **Biolookup**  biopragnatics/biolookup , <http://biolookup.io>  
Comprehensive database of identifiers, names, synonyms, cross-references, properties, and relations for biomedical entities
4. **Bioversions**  biopragnatics/bioversions  
Automated tracking of the current version for each biological database?
5. **OBO Database Ingest**  biopragnatics/obo-db-ingest  
Conversion of biomedical databases into ontologies
6. **Chemical Roles Graph**  chemical-roles/chemical-roles

Connecting roles in the ChEBI ontology to their targets

7. **CONSO**  [pharmacome/conso](https://github.com/pharmacome/conso)  
Ontology of phenomena related to neurodegeneration
8. **CONIB**  [pharmacome/conib](https://github.com/pharmacome/conib)  
Curated knowledge graphs describing neurodegeneration in BEL
9. **ComPath**  [ComPath/ComPath](https://compath.scai.fraunhofer.de/), <https://compath.scai.fraunhofer.de/>  
A data integration pipeline, manually curated dataset of mappings between pathway databases, and web application for integrative analysis of pathways

### External Contributions

Manually and semi-automatically curated resources benefit greatly from open governance models that enable external contribution. Instead of creating siloed or single use improvements to resources I consume, I aim to make as many upstream contributions as possible. Accordingly, I have made hundreds of small contributions across 50+ ontologies in the OBO Foundry and other resources including:

SSSOM, EHDA2, BFO, GO, ECO, OMO, FYPO, COB, RO, HSAPDV, MMUSDV, MP, AGRO, CIDO, EUPATH, HANCESTRO, OBA, PDUMDV, GEO, HTN, TTO, MOD, CL, CDAO, AISM, HAO, ONS, PCL, SWO, TO, TAXRANK, WBBT, WBL, OLATDV, PECO, UPHENO, XCO, IAO, PO, OGMS, OHD, OBI, MIAPA, MONDO, LPAO, EXO, BSPO, DDPHENO, UBERON, FBBT, ENVO, SYMP, CHMO, OAE, HP, MAXO, COLAO

### Funding

1. **Advancing Data Integration and Discovery in Biomedicine with the Bioregistry**  
Chan Zuckerberg Initiative (CZI), (2023-329850), \$250K overall, 2023-2025 (24 months), Grant: 2023-329850  
PI: Benjamin M. Gyori  
Role: Key person. Co-wrote proposal, responsible for design and implementation of research plan.
2. **Rapid Assessment of Platform Technologies to Expedite Response**  
Defense Threat Reduction Agency (DTRA), (FP00012844), \$623K (subcontract) / \$15M overall, 2022-2024 (18 months), Grant: HDTRA1242031  
PI: Benjamin M. Gyori  
Role: Participant. Co-wrote proposal with PNNL collaborators. Responsible for design and implementation of research plan. Lead developer of semantic and analytical technologies.
3. **MIRA: Modeling with an Intelligent Reasoning Assistant**  
DARPA ASKEM Program, (HR00112220036), \$2.1M, 2022-2026 (42 months)  
PI: Benjamin M. Gyori  
Role: Participant
4. **Young Faculty Award / DARPA Director's Fellowship Award**  
DARPA, (W911NF2010255), \$750K, 2020-2023 (36 months)  
PI: Benjamin M. Gyori  
Role: Participant
5. (past) **Ecosystem of Machine-maintained Models with Automated Assembly**  
DARPA Automating Scientific Knowledge Extraction (ASKE) / Artificial Intelligence Exploration (AIE) program, (HR00111990009), \$2M, 2018-2020 (18 months + extension)  
PI: Benjamin M. Gyori  
Role: Participant
6. (past) **Interdisciplinary Research Award**  
Fraunhofer Center for Machine Learning, (Internal), \$40K 2019 (3 months)  
PI: Martin Hofmann-Apitius  
Role: Key person. Co-wrote proposal. Responsible for design and implementation of research plan including applications of PyKEEN in biomedicine.
7. (past) **PYBEL2NDEX**  
University of California, San Diego, (Contract), \$28K 2018 (6 months)



PI: Martin Hofmann-Apitius

Role: Key person. Wrote proposal. Responsible for design and implementation of research plan for implementing interoperability between PyBEL and NDEx.

## Community

### Professional Affiliations

- International Society of Biocuration (2021 -)
- CoronaWhy (2020 - 2021)
- OpenBEL Consortium (2017 -)
- Erasmus Student Network Bonn (2016 -)
- American Chemical Society (2011 - 2022)

### Service to the Community

#### Scholarly Journals

1. Scientific article reviewer (*ad hoc*) in:
  - Bioinformatics
  - Database
  - BMC Bioinformatics
  - Journal of Cheminformatics
  - Journal of Biomedical Semantics
  - eLife
  - MATCH Communications in Mathematical and in Computer Chemistry
  - PeerJ
2. Reproducibility Editor, Journal of Cheminformatics (pending)

#### Conference Organizing Committees

1. 2023 Workshop on Prefixes, CURIEs, and IRIs (Organizer)
2. Biocuration 2024 (Organizing Committee)
3. Biocuration 2023 (Co-chair)
4. 2022 Workshop on Prefixes, CURIEs, and IRIs (Organizer)
5. ICBO 2022 Workshop on Ontology Tools (Co-organizer)
6. ICBO 2022 (Program Committee)
7. ISMB 2022 (Bio-Ontologies/BOSC joint session) (Program Committee)
8. Biocuration 2022 (Organizing Committee)
9. 2021 Workshop on Prefixes, CURIEs, and IRIs (Organizer)

#### Other Service

1. International Society of Biocuration (Executive Committee)



# Teaching


## Courses Taught

### University of Bonn

1. Knowledge Assembly, Data Integration, and Modeling in Systems and Networks Biology (Seminar; Instructor; Winter 2018-2019)

## Supervision





### CoronaWhy

- o Aman Choudhri  Student Research Assistant (June - October 2020)

### Fraunhofer

- o Lauren Nicole DeLong  Student Research Assistant (September - December 2019)
- o Vinay Bharadhwaj  Student Research Assistant (July - December 2019)
- o Yojana Gadiya  Student Research Assistant (April - May 2019)
- o Trusha Adeshara  Student Research Assistant (April - May 2019)
- o Rana Aldisi  Student Research Assistant (July 2018 - March 2019)
- o Lingling Xu  Student Research Assistant (July 2018 - March 2019)
- o Kristian Kolpeja  Student Research Assistant (July - November 2018)
- o Esther Wollert  Student Research Assistant (July 2018 - August 2019)
- o Sandra Spalek  Student Research Assistant (July 2018 - August 2019)
- o Keerthika Lohanadan Student Research Assistant (July - September 2018)
- o Colin Birkenbihl  Student Research Assistant (July - October 2017)
- o Aram Grigoryan Student Research Assistant (July - December 2017)

### University of Bonn

- o Mauricio Pio de Lacerda  Master's Student (March - December 2019)
- o Rana Aldisi  Master's Student (March - December 2019)
- o Lingling Xu  Master's Student (March - December 2019)
- o Özlem Muslu  Master's Student (May - December 2018)