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# CURRICULUM VITAE

*Last updated: 11/02/2021*

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## BIOGRAPHICAL

NAME: Michael Thomas Watkins  
ADDRESS: University of Chicago, 900 East 57th Street, Chicago, IL 60637  
EMAIL: michael.watkins.8@gmail.com  
BIRTHDATE: April 7, 1993  
HOMETOWN: Glendora, CA  
CITIZENSHIP: U.S.

## EDUCATION

Ph.D., BIOMEDICAL INFORMATICS, UNIVERSITY OF UTAH  
2017-2021

Concentrations: clinical genomics, variant representation, interoperable EHR app development  
Dissertation: *Addressing Barriers to the Practical Utility of Genomic Data in the Clinical Setting*  
Dissertation Advisors: Karen Eilbeck (Chair), Ph.D.; Guilherme Del Fiol, M.D., Ph.D.; Scott Narus, Ph.D., M.S.; Rong Mao, M.D., FACMG; Wendy Kohlmann, M.S.

B.S., BIOINFORMATICS, BRIGHAM YOUNG UNIVERSITY  
2011-2012, 2014-2017

## RESEARCH POSITIONS

POSTDOCTORAL SCHOLAR, PEDIATRIC CANCER DATA COMMONS, UNIVERSITY OF CHICAGO  
2021-PRESENT

Harmonizing several collections of pediatric cancer data (clinical, genomic, etc.) from national and international partners with the goal of maximizing the utility of the data and enhancing effective pediatric cancer research, cohort discovery, and proper enrollment in clinical trials.

NLM TRAINEE, DEPARTMENT OF BIOMEDICAL INFORMATICS, UNIVERSITY OF UTAH  
2018-2021

The department supports seven pre-doctoral researchers through a training grant from the National Library of Medicine. With my appointment, I expanded my research efforts to include the following: SMART on FHIR, CDS Hooks, CQL, Infobutton, social determinants of health, and FHIR Genomics.

RESEARCH ASSISTANT, DEPARTMENT OF BIOMEDICAL INFORMATICS, UNIVERSITY OF UTAH  
2017-2018

I spent this time supported by Dr. Karen Eilbeck, Ph.D., assisting in the maintenance of the Sequence Ontology, and developing tools to support our joint efforts on the GA4GH Variant Representation working group.

RESEARCH ASSISTANT, DEPARTMENT OF COMPUTER SCIENCE, BRIGHAM YOUNG UNIVERSITY  
2016-2017

I spent this time supported by Dr. Mark Clement, Ph.D., using multi-GPU computing libraries to optimize machine learning algorithms designed to synthesize novel protein structures.

## HONORS

2020 JOHN D. MORGAN AWARD - UNIVERSITY OF UTAH

This \$5000 cash award is given annually to a Ph.D. candidate who has made a significant contribution to the biomedical informatics community.

## SKILLS / INTERESTS

### BACK-END PROGRAMMING

Python, JavaScript, C++, Java, SQL/SQLite, GraphQL

### FRONT-END PROGRAMMING

HTML/CSS, D3

### APPLICATION ARCHITECTURE

ExpressJS, Flask

### CLINICAL DATA STANDARDS & TERMINOLOGIES

HL7 FHIR, FSH, HL7 V2, SNOMED-CT, RxNorm, LOINC, ICD-9/ICD-10

### CLINICAL INFORMATICS

HL7 Infobutton, CDS Hooks, SMART on FHIR, CQL

### GENOMICS

FHIR Genomics Reporting IG, HGVS, ISCN, GA4GH VRS, VCF, GFF3, ClinVar, PharmGKB

### DATA ANALYTICS

RStudio, TensorFlow

### EXTRACURRICULAR

Amateur cellist, member of The Church of Jesus Christ of Latter-day Saints

## CERTIFICATIONS



## INVITED PRESENTATIONS

### NATIONAL PEER-REVIEWED PRESENTATION

2021-03-21, American Medical Informatics Association, Virtual Summit, 'ResultsMyWay: combining Fast Healthcare Interoperability Resources (FHIR), Clinical Quality Language (CQL), and informational resources to create a newborn screening application'

2020-03-26, American Medical Informatics Association, Virtual Summit, 'FHIR Lab Reports: using SMART on FHIR and CDS Hooks to increase the clinical utility of pharmacogenomic laboratory test results.'

2019-11-20, American Medical Informatics Association, Washington, DC. 'Implementing the VMC specification to reduce ambiguity in genomic variant representation.'

#### NATIONAL INVITED PRESENTATION

2020-06-22, National Library of Medicine Informatics Training Conference, Indianapolis, ID, 'A SMART on FHIR and CDS-Hooks enabled approach to the exchange and review of genomic test results.'

2019-06-25, National Library of Medicine Informatics Training Conference, Indianapolis, ID, 'Use of Infobuttons to find answers to clinicians' questions in clinical genomics.'

2018-09-27, Brigham Young University Career Exploration, Provo, UT, 'Biomedical Informatics and Graduate Studies.'

#### LOCAL INVITED PRESENTATION (EXTRAMURAL)

2020-09-17, University of Utah Industry Advisory Board (IABTalks), Salt Lake City, UT. IAB Student Lightning Talk.

2018-05-04, University of Utah Industry Advisory Board (IABTalks), Salt Lake City, UT. 'Precision medicine and its emerging app development landscape.'

### PROFESSIONAL and SCIENTIFIC SOCIETY MEMBERSHIPS

2018-2021, American Medical Informatics Association

#### EDITORIAL EXPERIENCE

##### REVIEWER

2021, AMIA/HL7 FHIR App Competition

##### AD-HOC REVIEWER

2021, American Medical Informatics Association Annual Symposium

2020, BMC Med Informatics Dec Making

2019, American Medical Informatics Association Fall Symposium

#### WORKING GROUPS

2019-2021, AMIA Genomics and Translational Bioinformatics working group

2018-2021, HL7 FHIR Genomics Reporting working group

2018-2020, *Lead Investigator*, eMERGE EHRI working group

2017-2020, GA4GH Variant Representation working group

#### TEACHING

##### INTERNATIONAL INVITED TRAINING

2019-08-16, All-day technical training on FHIR, SMART, and social determinants of health for a group of 15-20 health informaticists in Lima, Peru—part of a four-day workshop sponsored by PAHO and the Peruvian Ministry of Health.

##### NATIONAL INVITED TRAINING

2021-04, 3 hour virtual training, 'HL7® FHIR® 101 for Developers ', for the MCG Health Organization. Given to 3 separate development teams of 20 employees each (9 total hours, 60 total participants).

2021-03 – 2021-02, a two-part 8 hour virtual training, 'HL7® FHIR® 101 for Developers ', for Walmart. Given to 4 separate development teams of 15 employees each (32 total hours, 60 total participants).

2020-07-20, 3 hour virtual technical training, 'Introduction to CQL hands-on training', for the MCG Health Organization. Given to a development team of 15-20 employees as part of a 6 week interoperability workshop.

2020-06-22, 3 hour virtual technical training, 'SMART on FHIR and CDS Hooks hands-on training', for the MCG Health Organization. Given to a development team of 15-20 employees as part of a 6 week interoperability workshop.

2020-06-02, 3 hour virtual technical training, 'SMART on FHIR and CDS Hooks hands-on training', for GigaTECH. Given to development team of 2 employees as part of a 3 week interoperability workshop.

2020-04-27, 5 hour virtual technical training, 'SMART on FHIR and CDS Hooks hands-on training', for the Leidos Corporation. Given to a development team of 15-20 employees as part of a 3 week interoperability workshop.

#### TEACHING ASSISTANT

2018-2020, FHIR Practicum, University of Utah, Dept. of Biomedical Informatics

2017-2020, Foundations of Bioinformatics, University of Utah, Dept. of Biomedical Informatics

#### LOCAL INVITED TRAINING

2017-2020, University of Utah, Department of Biomedical Informatics, Foundations of Bioinformatics, Salt Lake City, UT. 'Galaxy and Jupyter.'

2020-10-22, University of Utah, Department of Biomedical Informatics, Ph.D. Seminar, Salt Lake City, UT. 'Clinical Quality Language (CQL).'

2020-09-10, University of Utah, Department of Biomedical Informatics, Foundations of Bioinformatics, Salt Lake City, UT. 'Local and Global Sequence Alignment'

2020-03-04, University of Utah, Department of Biomedical Informatics, FHIR Practicum, Salt Lake City, UT. 'SMART on FHIR with an ExpressJS and Docker framework.'

2020-01-28, Huntsman Cancer Institute, Population Sciences Variant Data Team, Salt Lake City, UT. 'GA4GH VR-spec overview and implementation in HCL.'

2019-12-12, University of Utah, Molecular Data Warehouse (MDW) Group, Salt Lake City, UT. 'How using the GA4GH VR-Spec can improve & promote data sharing.'

2019-10-30, University of Utah, IT Exchange (ITX) Group, Salt Lake City, UT. 'Creating a SMART on FHIR application and deploying it with CDS Hooks.'

2019-04-17, University of Utah, Department of Biomedical Informatics, Translational Research Informatics Special Interest Group, Salt Lake City, UT. 'Genomic Infobuttons—Matching information needs to electronic knowledge resources.'

2019-03-28, University of Utah, Department of Biomedical Informatics, Ph.D. Seminar, Salt Lake City, UT. 'Addressing variant ambiguity—implementing the VMC specification.'

2019-03-05, University of Utah, Department of Biomedical Informatics, FHIR Practicum, Salt Lake City, UT. 'SMART on FHIR using Python/Flask or Javascript/Node.'

2018-07-18, University of Utah, School of Medicine, DeCART Summer Program, Salt Lake City, UT. 'FHIR queries and creating a FHIR-based medical calculator.'

2018-03-15, University of Utah, Department of Biomedical Informatics, Translational Research Informatics Special Interest Group, Salt Lake City, UT. 'Using genomic data in CDS via FHIR'

#### PUBLICATIONS

1. **Watkins M**, Rasmussen L, Williams M, Walton N, Johnson D, Overby Taylor C, Freimuth B, Connolly J, Heale B, Nielsen K, Del Fiol G. (2022) Classification of clinical genomic information needs with a taxonomy of clinical questions. Manuscript in preparation.
2. [Poster] **Watkins M**, Au A, Eilbeck K, Ruiz-Schultz N, Rohrwasser A, Hart K, Williams M. (2022) A comprehensive newborn screening data interface for Utah providers, parents, and guardians. *APHL*.
3. **Watkins M**, Au A, Vuong T, Wallis H, Hart K, Rohrwasser A, Eilbeck K. (2021) ResultsMyWay: combining FHIR, Clinical Quality Language (CQL), and informational resources to create a newborn screening application. *AMIA Annu Symp Proc.* ; 2021:615-623. [PMC8378617](#)
4. **Watkins M**, Viernes B, Nguyen V, Rojas Mezarina L, Silva Valencia J, Borbolla D. (2020) Translating social determinants of health into standardized clinical entities. *Stud Health Technol Inform.* 70:474-478. doi: 10.3233/SHTI200205. [PMC8083881](#)
5. **Watkins M**, Eilbeck K. (2020) FHIR Lab Reports: using SMART on FHIR and CDS Hooks to increase the clinical utility of pharmacogenomic laboratory test results. *AMIA Jt Summits Transl Sci Proc.* 2020:683-692. [PMC7233102](#)
6. **Watkins M**, Rynearson S, Henrie A, Eilbeck K. (2019) Implementing the VMC specification to reduce ambiguity in genomic variant representation. *AMIA Annu Symp Proc.* 2019:1226-1235. [PMC7153148](#)
7. [Poster] **Watkins M**, Fujimoto MS, Clement M. (2016) A Simplified Framework for Neural Networks. *BIOT*.