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EDUCATION

Masters in Genetic Counseling, Medical College of Virginia, Aug. 1999 – May 2001.
Research project: Physician practices in identifying individuals at increased risk for colon cancer.
GPA: 4.0

Postdoctoral training Department of Molecular and Cell Biology, University of California, Berkeley. Jan 1997 – Mar 1999.
Research project: Analysis of motor proteins in the vertebrate retina.

PhD in Medical Genetics, University of Aberdeen, Scotland. Sept 1993 – Dec 1996.
Thesis: Molecular analysis of candidate genes in retinitis pigmentosa.

Bachelor of Science (Genetics), 1st class honors, University of Aberdeen, Scotland
Sep. 1989 – May 1993

PROFESSIONAL EXPERIENCE

Research Assistant Professor, ClinGen Biocuration Core
Department of Genetics, University of North Carolina at Chapel Hill
Sep. 2016 – present (80% FTE)

- Expertise in assessment of variant pathogenicity and gene-disease clinical validity with a focus on inborn errors of metabolism.
- Excellent knowledge of literature searching using tools such as PubMed and Google Scholar; relevant databases (e.g. OMIM, gnomAD, ClinVar, NCBI resources, Ensembl, UniProt); and use of disease and phenotype ontologies (Mondo, HPO).
- Chair, ClinGen Biocurator Working Group, which provides training on useful resources to all ClinGen gene and variant curators; membership >500 worldwide. I coordinate and host conference calls, twice per month, with presentations from experts on curation resources e.g. gnomAD, DECIPHER, NCBI, Ensembl, and I developed and update our Biocurator Educational resources webpage (https://clinicalgenome.org/tools/educational-resources/)
- Member of multiple ClinGen working groups including the Variant Curation Core team, Gene Curation Working Group, Lumping and Splitting Working Group, Education Coordination and Training Working Group, and Software Prioritization group.
- Stakeholder proxy for ClinGen Variant Curation Interface, providing input on the development of the Variant Curation Interface (used by all ClinGen Variant Curation Expert panels for curation of data to be submitted to ClinVar as part of ClinGen's FDA-approved human variant database)

Clinical Research Coordinator/Genetic Counselor
Division of Medical Genetics, Department of Pediatrics, Duke University Health System
July 2008 – Aug. 2016 (50-75% FTE)

- Clinical research coordinator for multiple research projects on metabolic disorders and neuropsychiatric conditions.
- Responsibilities included editing grants for submission to various funding organizations including the NIH, writing and coordinating IRB documentation, recruiting patients for research studies, coordinating sample and data collection, supervision of research personnel, variant interpretation, manuscript preparation, and writing genetic testing research reports.
- Provided genetic counseling support for the Duke Biochemical Genetics Laboratory and Metabolic clinic.

Research Assistant
Division of Medical Genetics, Department of Pediatrics, Duke University Health System
May 2005 – June 2008 30-50% FTE

- Coordinator for research studies on incidence of Cerebral Creatine Deficiency syndromes and laboratory diagnosis of Pompe disease.

Scientific writer
Online Mendelian Inheritance in Man
June 2005 – June 2008, Freelance (~5 hours per week)

- Summarized published scientific papers on genes (e.g. cloning, function, expression) in order to produce online content.

Editor
Cancer Control and Prevention Program, Department of Community and Family Medicine, Duke University Health System
Sep. 2006 – Aug 2007, Freelance (~5 hours per week)

- Edited grant applications and manuscripts, performed literature reviews, and helped with manuscript preparation.

Genetic Counselor
Division of Medical Genetics, Department of Pediatrics, Duke University Health System
Jul. 2001 – Aug. 2003 (100% FTE)

- Genetic counselor for pediatric and adult patients in the general genetics clinic with a wide range of reasons for referral including chromosome conditions, single gene disorders, metabolic disorders, hereditary cancer syndromes, and pre-symptomatic testing for adult onset diseases.

HONORS AND AWARDS

- Lang Kucera award for outstanding genetic counseling student (Virginia Commonwealth University, May 2001)
- Fight For Sight postdoctoral research grant (1998-1999)
- Wellcome Prize studentship for graduate work (1993-1996)
- Brenda Paige Memorial Prize for top undergraduate Genetics student (University of Aberdeen, 1992)

BIBLIOGRAPHY (for the last 12 years)

1. Thaxton CL, **Goldstein JL**, DiStefano M, Wallace KE, Witmer PD, Haendel M, Hamosh A, Rehm H, Berg JS. Lumping versus Splitting: How to approach defining a disease to enable accurate genomic curations. Cell Genomics (Accepted with revisions, April 2021)

2. Preston CG, Wright MW, Madhavrao R, Harrison SM, **Goldstein JL**, Luo X, Wand H, Wulf B, Cheung G, Mandell ME, Tong H, Cheng S, Iacocca MA, Pineda AL, Popejoy AB, Dalton K, Zhen J, Dwight SS, Babb L, DiStefano M, O'Daniel JM, Lee K. Riggs ER, Zastrow DB, Mester JL, Ritter DI, Patel RY, Subramanian SL, Milosavljevic A, Berg JS, Rehm HL, Plon SE, Cherry JM, Bustamante CD, Costa HA, on behalf of the Clinical Genome (ClinGen) Resource. ClinGen Variant Curation Interface: A Variant Classification Platform for the Application of Evidence Criteria from ACMG/AMP Guidelines. Genome Medicine (Accepted, April 2021)
medRxiv 2021.02.12.21251663; doi: https://doi.org/10.1101/2021.02.12.21251663

3. Wain KE, Azzariti DR, **Goldstein JL**, Johnson AK, Krautscheid P, Lepore B, O'Daniel JM, Ritter D, Savatt JM, Riggs ER, Martin CL, on behalf of the Clinical Genome Resource Education, Coordination, and Training Working Group. Variant Interpretation is a Component of Clinical Practice Among Genetic Counselors in Multiple Specialties. Genet Med. (2020) 22:785-792. doi: 10.1038/s41436-019-0705-9. Epub 2019 Nov 22.PMID: 31754268

4. Ingles J, **Goldstein J**, Thaxton C, Caleshu C, Corty EW, Crowley SB, Dougherty K, Harrison SM, McGlaughon J, Milko LV, Morales A, Seifert BA, Strande N, Thomson K, Peter van Tintelen J, Wallace K, Walsh R, Wells Q, Whiffin N, Witkowski L, Semsarian C, Ware JS, Hershberger RE, Funke B. Evaluating the Clinical Validity of Hypertrophic Cardiomyopathy Genes. *Circ Genom Precis Med.* (2019) 12:e002460. PubMed PMID: 30681346; PubMed Central PMCID: PMC6410971.

5. McGlaughon JL, **Goldstein JL**, Thaxton C, Hemphill SE, Berg JS. The progression of the ClinGen gene clinical validity classification over time. *Hum Mutat.* (2018) 39:1494-1504. PubMed PMID: 30311372; PubMed Central PMCID: PMC6190678.

6. Strande NT, Riggs ER, Buchanan AH, Ceyhan-Birsoy O, DiStefano M, Dwight SS, **Goldstein J**, Ghosh R, Seifert BA, Sneddon TP, Wright MW, Milko LV, Cherry JM, Giovanni MA, Murray MF, O'Daniel JM, Ramos EM, Santani AB, Scott AF, Plon SE, Rehm HL, Martin CL, Berg JS. Evaluating the Clinical Validity of Gene-Disease Associations: An Evidence-Based Framework Developed by the Clinical Genome Resource. *Am J Hum Genet.* (2017) 100:895-906. PubMed PMID: 28552198; PubMed Central PMCID: PMC5473734.

7. Kishnani PS, Gibson JB, Gambello MJ, Hillman R, Stockton DW, Kronn D, Leslie ND, Pena LDM, Tanpaiboon P, Day JW, Wang RY, **Goldstein JL**, An Haack K, Sparks SE, Zhao Y, Hahn SH; Pompe ADVANCE Study Consortium. Clinical characteristics and genotypes in the ADVANCE baseline data set, a comprehensive cohort of US children and adolescents with Pompe disease. Genet Med. (2019) May 14. doi:10.1038/s41436-019-0527-9. [Epub ahead of print] PubMed PMID: 31086307.

8. Kishnani PS, **Goldstein J**, Austin SL, Arn P, Bachrach B, Bali DS, Chung WK, El-Gharbawy A, Brown LM, Kahler S, Pendyal S, Ross KM, Tsilianidis L, Weinstein DA, Watson MS; ACMG Work Group on Diagnosis and Management of Glycogen Storage Diseases Type VI and IX. Diagnosis and management of glycogen storage diseases type VI and IX: a clinical practice resource of the American College of Medical Genetics and Genomics (ACMG). *Genet Med.* (2019) 21:772-789. PubMed PMID: 30659246.

9. Khaikin Y, Sidky S, Abdenur J, Anastasi A, Ballhausen D, Buoni S, Chan A, Cheillan D, Dorison N, Goldenberg A, **Goldstein J**, Hofstede FC, Jacquemont ML, Koeberl DD, Lion-Francois L, Lund AM, Mention K, Mundy H, O'Rourke D, Pitelet G, Raspall-Chaure M, Tassini M, Billette de Villemeur T, Williams M, Salomons GS, Mercimek-Andrews S. Treatment outcome of twenty-two patients with guanidinoacetate methyltransferase deficiency: An international retrospective cohort study. *Eur J Paediatr Neurol.* (2018) 22:369-379. PubMed PMID: 29506905.

10. Bruun TUJ, Sidky S, Bandeira AO, Debray FG, Ficicioglu C, **Goldstein J**, Joost K, Koeberl DD, Luísa D, Nassogne MC, O'Sullivan S, Õunap K, Schulze A, van Maldergem L, Salomons GS, Mercimek-Andrews S. Treatment outcome of creatine transporter deficiency: international retrospective cohort study. *Metab Brain Dis.* (2018) 33:875-884. PubMed PMID: 29435807.

11. Mori M, Haskell G, Kazi Z, Zhu X, DeArmey SM, **Goldstein JL**, Bali D, Rehder C, Cirulli ET, Kishnani PS. Sensitivity of whole exome sequencing in detecting infantile- and late-onset Pompe disease. *Mol Genet Metab.* (2017) 122:189-197. PubMed PMID: 29122469; PubMed Central PMCID: PMC5907499.

12. Bali DS, **Goldstein JL**, Fredrickson K, Austin S, Pendyal S, Rehder C, Kishnani PS. Clinical and Molecular Variability in Patients with PHKA2 Variants and Liver Phosphorylase b Kinase Deficiency. *JIMD Rep.* (2017) 37:63-72. PubMed PMID: 28283841; PubMed Central PMCID: PMC5740042.
CONTRIBUTION: ***Wrote original first draft; consented patients, collected samples, interpreted variants, reviewed all medical records and extracted relevant information; IRB renewal.***

13. Bali DS, Chen YT, Austin S, **Goldstein JL**. Glycogen Storage Disease Type I.2006 Apr 19 [updated 2016 Aug 25]. In: Adam MP, Ardinger HH, Pagon RA, Wallace SE, Bean LJH, Stephens K, Amemiya A, editors. GeneReviews® [Internet]. Seattle (WA): University of Washington, Seattle; 1993-2019. Available from http://www.ncbi.nlm.nih.gov/books/NBK1312/; PubMed PMID: 20301489.

14. Bali DS, **Goldstein JL**, Rehder C, Kazi ZB, Berrier KL, Dai J, Kishnani PS. Clinical Laboratory Experience of Blood CRIM Testing in Infantile Pompe Disease. *Mol Genet Metab Rep.* (2015) Dec 1;5:76-79. PubMed PMID: 26693141; PubMed Central PMCID: PMC4674832.

CONTRIBUTION: ***Wrote original first draft; collected and analyzed all data.***

15. Chien YH, **Goldstein JL**, Hwu WL, Smith PB, Lee NC, Chiang SC, Tolun AA, Zhang H, Vaisnins AE, Millington DS, Kishnani PS, Young SP. Baseline Urinary Glucose Tetrasaccharide Concentrations in Patients with Infantile- and Late-Onset Pompe Disease Identified by Newborn Screening. *JIMD Rep.* (2015) 19:67-73. PubMed PMID: 25681082; PubMed Central PMCID: PMC4501239.

16. Zhu X, Petrovski S, Xie P, Ruzzo EK, Lu YF, McSweeney KM, Ben-Zeev B, Nissenkorn A, Anikster Y, Oz-Levi D, Dhindsa RS, Hitomi Y, Schoch K, Spillmann RC, Heimer G, Marek-Yagel D, Tzadok M, Han Y, Worley G, **Goldstein J**, Jiang YH, Lancet D, Pras E, Shashi V, McHale D, Need AC, Goldstein DB. Whole-exome sequencing in undiagnosed genetic diseases: interpreting 119 trios. *Genet Med.* (2015) 17:774-81. PubMed PMID: 25590979; PubMed Central PMCID: PMC4791490.

17. Mori M, **Goldstein J**, Young SP, Bossen EH, Shoffner J, Koeberl DD. Complex III deficiency due to an in-frame MT-CYB deletion presenting as ketotic hypoglycemia and lactic acidosis. *Mol Genet Metab Rep.* (2015) 30:39-41. PubMed PMID: 26937408; PubMed Central PMCID: PMC4750615.

18. Berrier KL, Kazi ZB, Prater SN, Bali DS, **Goldstein J**, Stefanescu MC, Rehder CW, Botha EG, Ellaway C, Bhattacharya K, Tylki-Szymanska A, Karabul N, Rosenburg AS, Kishnani PS. CRIM-negative infantile Pompe disease: characterization of immune responses in patients treated with ERT monotherapy. *Genet Med.* (2015) 17:912-8. PubMed PMID: 25741864

19. Zhu L, Wang X, Li XL, Towers A, Cao X, Wang P, Bowman R, Yang H, **Goldstein J**, Li YJ, Jiang YH. Epigenetic dysregulation of SHANK3 in brain tissues from individuals with autism spectrum disorders. *Hum Mol Genet.* (2014) 23:1563-78, 2014. PubMed PMID: 24186872; PubMed Central PMCID: PMC3929093

20. Bali DS, **Goldstein JL**, Fredrickson K, Rehder C, Boney A, Austin S, Weinstein DA, Lutz R, Boneh A, Kishnani PS. Variability of disease spectrum in children with liver phosphorylase kinase deficiency caused by mutations in the *PHKG2* gene. *Mol Genet Metab.* (2014) 111:309-13. PubMed PMID: 24389071; PubMed Central PMCID: PMC3952947
CONTRIBUTION: ***Wrote original first draft; consented patients, collected samples, interpreted variants, reviewed all medical records and extracted relevant information; IRB renewal.***

21. **Goldstein JL**, Dickerson G, Kishnani PS, Rehder C, Bali DS. Blood-based diagnostic testing for Pompe disease: consistency between GAA enzyme activity in dried blood spots and GAA gene sequencing results. *Muscle Nerve* (2014) 49:775-6. PubMed PMID: 24338800

22. El-Gharbawy AH, **Goldstein JL**, Millington DS, Vaisnins AE, Schlune A, Barshop BA, Schulze A, Koeberl DD, Young SP. Elevation of guanidinoacetate in newborn dried blood spots and impact of early treatment in GAMT deficiency. *Mol Genet Metab.* (2013) 109:215-7. PubMed PMID: 23583224

23. Young SP, Piraud M, **Goldstein JL**, Zhang H, Rehder C, Laforet P, Kishnani PS, Millington DS, Bashir MR, Bali DS. Assessing disease severity in Pompe disease: the roles of a urinary glucose tetrasaccharide biomarker and imaging techniques. *Am J Med Genet C Semin Med Genet.* (2012) 60:50-8. PubMed PMID: 22252961

24. Bali DS, **Goldstein JL**, Banugaria S, Dai J, Mackey J, Rehder C, Kishnani PS. Predicting cross-reactive immunological material (CRIM) status in Pompe disease using GAA mutations: lessons learned from 10 years of clinical laboratory testing experience. *Am J Med Genet C Semin Med Genet.* (2012) 160:40-9. PubMed PMID: 22252923; PubMed Central PMCID: PMC3278076
CONTRIBUTION: *Wrote original first draft; collected and analyzed all data.*

25. Johnson AO, **Goldstein JL**, Bali D. Glycogen storage disease type IX: novel *PHKA2* missense mutation and cirrhosis. *J Pediatr Gastroenterol Nutr.* (2012) 55:90-2, 2012. PubMed PMID: 21857251

26. **Goldstein J**, Austin S, Kishnani P, Bali D. Phosphorylase Kinase Deficiency. 2011 May 31. In: Pagon RA, Bird TD, Dolan CR, Stephens K, Adam MP, editors. GeneReviews, Seattle (WA): University of Washington, Seattle; 1993-2010. PubMed PMID: 21634085 (Updated in 2018)

27. Achouitar S, **Goldstein JL**, Mohamed M, Austin S, Boyette K, Blanpain FM, Rehder CW, Kishnani PS, Wortmann SB, den Heijer M, Lefeber DJ, Wevers RA, Bali DS, Morava E. Common mutation in the PHKA2 gene with variable phenotype in patients with liver phosphorylase b kinase deficiency. *Mol Genet Metab.* (2011) 104:691-4. PubMed PMID: 21911307.

28. Bali DS, Tolun AA, **Goldstein JL**, Dai J, Kishnani PS. Molecular analysis and protein processing in late-onset Pompe disease patients with low levels of acid alpha-glucosidase activity. Muscle Nerve. (2011) 43:665-70. PubMed PMID: 21484825

29. **Goldstein JL**, Austin SL, Boyette K, Kanaly A, Veerapandiyan A, Rehder C, Kishnani PS, Bali DS. Molecular analysis of the *AGL* gene: identification of 25 novel mutations and evidence of genetic heterogeneity in patients with Glycogen Storage Disease Type III. *Genet Med.* (2010) 2:424-30. PubMed PMID: 20648714

30. Li SC, Chen CM, **Goldstein JL**, Wu JY, Lemyre E, Burrow TA, Kang PB, Chen YT, Bali DS. Glycogen storage disease type IV: novel mutations and molecular characterization of a heterogeneous disorder. *J Inherit Metab Dis.* (2010) 33 Suppl 3:S83-90. PubMed PMID: 20058079

31. **Goldstein JL**, Young SP, Changela M, Dickerson GH, Zhang H, Dai J, Peterson D, Millington DS, Kishnani PS, Bali DS. Screening for Pompe disease using a rapid dried blood spot method: experience of a clinical diagnostic laboratory. Muscle Nerve. (2009) 40:32-6. PubMed PMID: 19533645

Platform presentations (Since June 2017)

- "Tools for Single Nucleotide Variant Interpretation" as part of the "Variant Analysis Workshop featuring the UCSC Genome Browser and other tools", at the National Society of Genetic Counselors (NSGC) Annual Education Conference, November 2020. 1 hour lecture - + 0.5 hours Q and A).

- Curating the Clinical Genome conference, Hinxton, UK, May 2018
  "The ClinGen Storage Disorders Expert Panel's Guidelines for *GAA* Variant Interpretation".
  On behalf of the ClinGen Lysosomal Storage Disorders Variant Curation Expert Panel.

- Curating the Clinical Genome conference, Washington DC, June 2017
  "Use of the ClinGen clinical validity framework to evaluate the strength of evidence for genes implicated in hypertrophic cardiomyopathy."
  On behalf of the ClinGen Hypertrophic Cardiomyopathy Gene Curation Expert Panel.

Poster presentations (Since June 2017)

- "Genetic Counseling Student Remote Rotation in ClinGen Variant Interpretation: Expanding Training Options"; Diane B. Zastrow, Meredith Weaver, Jenny Goldstein, Sharon Chan, Emily Quinn, Ashley Mills.
  Poster presentation, National Society of Genetic Counselors, Virtual meeting, Nov 2020.

- Curating the Clinical Genome conference, Washington DC, May 2019
  "Assessing the Strength of Evidence for Genes Implicated in Aminoacidopathies Using the ClinGen Clinical Validity Framework"
  On behalf of the ClinGen Aminoacidopathy Gene Curation Expert Panel.

- Curating the Clinical Genome conference, Washington DC, May 2019
  "Opinions of ClinGen Members on the Use of ClinGen Clinical Validity Classifications in Genetic Testing" Jennifer L Goldstein, Julianne O'Daniel, Marina DiStefano, Adam Buchanan, Kelly Ormond, Laura Milko, Heidi Rehm, Jonathan S Berg

- American College of Medical Genetics and Genomics, Seattle, WA, April 2019
  "Opinions of ClinGen Members on the Use of ClinGen Clinical Validity Classifications in Genetic Testing" Jennifer L Goldstein, Julianne O'Daniel, Marina DiStefano, Adam Buchanan, Kelly Ormond, Laura Milko, Heidi Rehm, Jonathan S Berg

- American College of Medical Genetics and Genomics, Charlotte, NC, April 2018
  "ClinGen Storage Disorders Expert Panel specifications to the ACMG/AMP criteria for *GAA* variant interpretation".
  On behalf of the ClinGen Lysosomal Storage Disorders Variant Curation Expert Panel.

- American Society of Human Genetics, Orlando, FL, Oct 2017
  "Use of the ClinGen clinical validity framework to evaluate the strength of evidence for genes implicated in hypertrophic cardiomyopathy."
  On behalf of the ClinGen Hypertrophic Cardiomyopathy Gene Curation Expert Panel.

TEACHING RECORD

In the last 4 years:

- UNC Program in Precision Medicine and Health Care “Explorations in Genomic Medicine Research” undergraduate summer program, taught a class on “ClinGen and annotation”.
  June 2021.
  Contact hours: 3 hours (1 hour presentation, 2 in breakout rooms supervising annotation activity)
  Course organizers: Dr. Sabrina Powell and Dr. Grace Byfield

- Class on “Tools for Variant Interpretation” as part of the Exome course for UNC-Greensboro Masters in Genetic Counseling students, held at UNC-Chapel Hill,
  Nov 2018, Oct 2019, Nov 2020 (virtual)
  Contact hours: 1 hour per class + 1 hour for breakout rooms facilitating variant interpretation activity for students (2020)
  Course organizer: Kristy Lee, MS, CGC

- UNC Program for Precision Medicine in Health Care, undergraduate Summer program, “A Day in the Life of Biocurator”
  Contact hours: 1 (talk, and Q and A), July 2020
  Subsequently did an interview with the course director wich was made into an Apple Podcast.
  Course director: Dr. Sabrina Powell

- UNC Summer of Learning and Research (SOLAR) program,
  Contact hours: 0.25 (talk - “The Clinical Genome resource”) July 2020.
  Course director: Dr. Sabrina Powell

- Prairie View A & M University, class on “Biocuration” given to undergraduate upperclassmen as part of a course on Genomics
  Oct 2017, Nov 2018, Nov 2019
  Contact hours: 1.25 hours per class
  Course organizer: Gloria Regisford. PhD

- Prairie View A & M University, presentation on “Genetic Counseling as a career”, as part of a course on careers in science.
  Oct 2017
  Contact hours: 1.0

GRANTS

I have not been Principal Investigator or Co-Principal Investigator for any contracts or grants.

PROFESSIONAL SERVICE

Association for Creatine Deficiencies (patient advocacy organization)
Member of the Corporate Alliance for Research and Education Advisory Committee (Jan 2019 – present) which facilitates communication between key industry partners and families in order to promote research.
Member of the Ambassador team (Nov 2020 – present), working on efforts to promote the awareness and education of healthcare providers on these disorders.

Member of the American College of Medical Genetics Work Group on Diagnosis and Management of Glycogen Storage Diseases Type VI and IX (2010 – 2018);
This group published peer-reviewed guidelines in 2019 (PMID 34659246)

PROFESSIONAL MEMBERSHIPS

National Society of Genetic Counselors
Certified by the American Board of Genetic Counseling, 2002; recertification in December 2022

RESEARCH STATEMENT

With the advent of next-generation DNA sequencing techniques, the ability to detect genetic variation has greatly surpassed our ability to understand the impact of this genetic variation on the health of an individual. While some genes are well-known to cause specific diseases when they are altered, other genes may have only a tenuous relationship with disease. Even for genes with a well-known gene-disease relationship (BRCA1 with breast-ovarian cancer, for example), identifying which variant within the gene are disease-causing and which are benign can be challenging.

As a genetic counselor who worked for several years with pediatric and adult patients and who later focused on research on rare metabolic disorders, I have a deep appreciation for accurate, comprehensive sources of knowledge that pull information together in a transparent manner to help to us to understand the impact of genetic variation on the health of an individual. This includes the provision of information that supports the understanding of gene-disease relationships and variant pathogenicity and therefore facilitates the accurate interpretation of genetic testing results for patients and families, and supports research. My role as a senior biocurator in the ClinGen Biocuration and Coordination Core at UNC, allows me to be part of such an effort, ClinGen (the Clinical Genome Resource), an NIH-funded initiative which is creating a publicly available database of the clinical relevance of gene and variants. My work is funded by an NIH grant awarded to Dr. Jonathan Berg.

ClinGen is composed of various working groups which work synergistically towards ClinGen's goals. These groups include expert panels (groups of curators and experts that work on the assessment of gene-disease clinical validity and variant classification in different clinical domains) as well as other groups that help to support and organize the expert panels, including informatics development, development of frameworks, guidance, coordination, and education.

As part of my work, I train and oversee curators in our UNC core, as well as curators and experts across the world in the various curation groups that I work with. Effective training of curators is essential to the goals of ClinGen in order to maintain the dissemination of high quality information. Throughout my work with various expert panels (groups of curators and

experts that work on the assessment of gene-disease clinical validity and variant classification), I look for areas that may raise questions for curators, in the assessment of published data, application of ClinGen's curation frameworks, and use of ClinGen's online interfaces. Only after recognizing the challenges that curators may encounter, can we initiate the development of resources and additional training which will be helpful for curators working on different genes and disease areas. I enjoy working towards solving these challenges by collaborating with other members of the consortium. For example, I recently led a small group effort to create a document with standardized text which acts as a starting point for input of data into the ClinGen Variant Curation Interface.

My involvement as lead curator in various expert panels under the umbrella of the Inborn Errors of Metabolism Working Group and Retina Gene Curation Expert Panel allows me both to build on and utilize my previous clinical and research experience, and thus take a deeper dive into various curation challenges. An area of interest and active research for me is the issue of circularity in variant classification. Circularity, the use of circular logic and double-counting of evidence, can falsely elevate the final pathogenicity classification of a genetic variant. While this is known to occur, the extent of this issue has not been studied. Circularity warrants a detailed analysis, which will include the ability to effectively track which pieces of evidence, including which other variants, are used to support variant classification. Work in this area will involve developing informatics approaches to track the use of evidence and analyze the impact of circularity. In addition to research on circularity, I am also interested in providing guidance on the use of other types of evidence for variant classification, including the functional evidence and defining phenotype. This work will be useful to ClinGen's Variant Curation Expert Panels, and will be generalizable to the wider genetics community.

In addition, as a member of the core group of the Variant Curation Working Group, I provide input to guide the development of informatics resources, such as the Variant Curation Interface, and lead and worn on various projects to facilitate the work of ClinGen's Variant Curation Expert panels.

In summary my interests involve the development of methods and guidance for the accurate, efficient, and consistent collection and interpretation of data on gene-disease relationships and variant classification for translation into a publicly available, expert-approved assertion that is transparent and understandable by the user. I have been excited to see the consortium gain momentum and grow into an internationally recognized genetic resource. With the growth of the ClinGen, new challenges arise as well as opportunities to research and develop solution to those challenges. I look forward to being a part of this consortium moving forward due to the great opportunities to work with world experts in different genetic disorders, and to continuously expand my knowledge and experience in the human genetics field.

TEACHING STATEMENT

My current position does not include any formal teaching responsibilities. However, I am delighted to teach classes whenever asked, if I feel comfortable that I have sufficient knowledge to give the students a positive experience. I draw on my own experience as a learner and try to provide practical examples. I like to maintain an informal atmosphere, where possible, to encourage discussion.