DeannaMChurch

Genomics and Bioinformatics Leader

contact

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languages

english mother tongue

Genomics

Genome assembly, Genome annotation, variant analysis, & Single-cell 'omics

Bioinformatics

Python, R, HTML, XML/XSLT, Javascript, CSS3, SQL & Perl

focus

Leading interdisciplinary teams using genomics and computation to improve human health.

experience

2016–Present **10x Genomics** Pleasant, California
Senior Director of Applications
Lead an interdisciplinary team of top rate scientists in demonstrating the scientific value of the full 10x product suite. This work covered a variety of scientific areas including genome assembly, analysis, tumor microenvironment analysis, tumor heterogeneticy and immune profiling.

2014-2016 **Personalis, Inc** Menlo Park, CA
Senior Director of Genomics and Content
Lead a team developing novel genome analysis pipelines and building knowledge systems to support genome interpretation.

2001-2014 **National Center for Biotechnology Information, NIH** Bethesda, MA
Staff Scientist
Lead a team of biologists and software developers in developing databases and tools to make genomic data accessible to the scientific community. Participated in numerous international collaborations including helping to found the Genome Reference Consortium, the group tasked with maintaining the human reference assembly.

1990-1992 **MIT and MGH** Boston, MA
Laboratory Technician
Managed laboratory and performed experiments, including helping to develop the exon amplification protocol.

education

1999-2001 **National Center for Biotechnology Information, NIH** Bethesda, MD
Postdoctoral fellow Coordinated mouse genome resources.

1997-1999 **Laboratory of Janet Rossant, Mt. Sinai Hospital** Toronto, Ontario
Postdoctoral fellow Applying genomics methods to understanding mouse developmental biology

1992-1997 **PhD** of Biological Sciences The University of California, Irvine
Phenotype-genotype correlation in the Cri-du-Chat region of chromosome 5

1986-1990 **Bachelor** of Liberal Arts University of Virginia
Research project focused on cell cycle regulation using yeast

additional training

2010	**Client-Side Web Development**	University of Illinois (O'Reilly)
2009	**XSLT/XPATH: Introduction and Syntax**	Mulberry Technologies
2007	**Introduction to XML**	University of Illinois (O'Reilly)

advisory boards and professional service

2018-present	**Genome Quebec**	Scientific Advisory Board
2012-present	**Ensembl**	Scientific Advisory Board
2013-2016	**The Genome Analysis Center/Earlham Institute**	Scientific Advisory Board
2010-2014	**Database of Genomic Variants**	Scientific Advisory Board
2010-present	**American Society of Human Genetics**	Member
2008-2013	**Advances in Genome Biology and Technology**	Organizing Committee Member
2008-2013	**International Standards Cytogenomic Arrays**	Committee Member
2008-2012	**International Mammalian Genome Society**	Nomenclature Committee Member
2004-2012	**International Mammalian Genome Society**	Member
2006-2011	**European Conditional Mouse Mutagenesis Program**	Scientific Advisory Board
2006-2009	**Genome Canada-MORGEN project**	Scientific Advisory Board
2005	**Mouse Genome Finishing Meeting**	Organizer

awards

2012 **Special Service Award** — National Library of Medicine
For extraordinary effort in providing access to the 1000 genomes project data.

1997-1999 **Human Frontiers Postdoctoral Fellowship** — Mt. Sinai Hospital
Awarded to early career scientist to enable them to broaden their skills in a new country.

1986-1990 **Echols Scholar** — University of Virginia
Awarded to select undergraduates who exhibit academic independence.

presentations

2018-Feb **Beckman Symposium, Technology Innovation and Human Genomics** Palo Alto, CA
Invited Speaker, "The impact of technology on our view of biology"

2018-Jan **Polyploid Genome Workshop** San Diego, CA
Invited Speaker, "Linked-Reads for haplotype reconstruction and improved de novo assembly"

2017-Nov **Australasian Genomic Technologies Association Annual Meeting** Hobart, AUS
Keynote, "High resolution biology with 10x"

2017-Nov **Australasian Genomic Technologies Association Annual Meeting** Hobart, AUS
Keynote, "The impact of technology on biology"

2017-Apr **NGS Barcelona** Barcelona, SP
Keynote, "Advancing genomics drop by drop"

2017-Feb **Advance in Genomics and Biotechnology** Hollywood, FL
Abstract Selected, "More complete genome analysis"

2017-Jan **Personalized World Medicine Conference** Palo Alto, CA
Speaker, "Expanding the reach of genomic analysis"

2017-Jan **Plant and Animal Genome Conference** San Diego, CA
Invited Speaker, "Quantitative profiling of large and complex populations by single cell RNA-sequencing"

2017-Jan **Plant and Animal Genome Conference** San Diego, CA
Invited Speaker, "Using Linked-Reads to enable efficient de novo, diploid assembly"

2016-Oct **American Society of Human Genetics** Vancouver, CA
Abstract Selected, "De novo assembly of individual human haplotypes from diploid samples"

2016-Oct **Genome Reference Consortium Workshop** Vancouver, CA
Invited Speaker, "Everyday de novo assembly"

2016-Sep **Genome Informatics** Hinxton, UK
Abstract Selected, "Improving genome analysis using Linked-Reads"

2016-Aug **Cancer Genomics Consortium** Denver, CO
Invited Speaker, "Complete genome analysis"

2016-May **Sequencing and Finishing in the Future** Santa Fe, NM
Abstract Selected, "Improving genome analysis using Linked-Reads"

2016-May **Rady Symposium** San Diego, CA
Invited Speaker, "Advancing Precision Medicine with Linked-Reads"

2016-Feb **Stanford Big Data in Genomics** Palo Alto, CA
Invited Speaker, "Truly personalized genomics"

2015-Oct **Genome informatics** Cold Spring Harbor, NY
Invited Speaker, "The Rumsfeldian challenge of developing clinical sequencing tests"

2015-May **The 11th International Workshop on Advanced Genomics** Tokyo, JP
Speaker, "Dissecting the diagnostic yield in exome sequencing"

2015-Mar **American College of Medical Genetics Annual Meeting** Salt Lake City, UT
Invited Speaker, "Technical limitations of variant identification and annotation"

2015-Feb **Advance in Genomics and Biotechnology, Pacific Biosciences Workshop** Marco Island, FL
Invited Speaker, "Finishing genomes, why does it matter"

2014-Nov **Biological Data Sciences** Cold Spring Harbor, NY
Keynote Speaker, "Analog reporting in a digital age"

2014-Oct **American Society of Human Genetics** San Diego, CA
Abstract Selected, "The impact of GRCh38 on clinical sequencing"

2014-May **Sequencing and Finishing in the Future** Santa Fe, NM
Abstract Selected, "Dissecting the missing diagnostic yield in exome sequencing"

publications