John Didion | PhD

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Education

2008.08 to 2014.05	**Doctor of Philosophy, Bioinformatics and Computational Biology** *University of North Carolina, Chapel Hill, NC*
1996.09 to 2001.06	**Bachelor of Science, Computer Science** *Northwestern University, Evanston, IL*

Research Experience

2014.09 to Present	**National Human Genome Research Institute** Bethesda, MD

Postdoctoral Fellow, Laboratory of Dr. Francis S Collins

- Leveraging a large, multi-'omics dataset to investigate epigenetic mechanisms underlying regulatory variants implicated in type 2 diabetes.
- Developing machine-learning approaches for imputation of multi-'omics data.
- Designed a novel sequencing assay for single-molecule resolution transcriptome analysis.
- Using single-cell gene expression and chromatin accessibility data to understand cell-to-cell variability in pancreatic islets, including responses to glucose perturbation.
- Developed user-friendly software tools for QC and pre-processing of NGS reads.
- Awarded six grants, including an American Diabetes Association fellowship and an NIH K22.

2009.05 to 2014.08	**University of North Carolina at Chapel Hill** Chapel Hill, NC

Research Assistant, Laboratory of Dr. Fernando Pardo-Manuel de Villena

- Characterized the genetic determinants of two meiotic drive systems in the mouse. First, conducted a GWAS of wild mice to identify genes associated with the accumulation of Robertsonian translocations. Second, mapped a novel meiotic drive locus, *R2d2*, and multiple modifier loci responsible for extreme transmission distortion in interspecific crosses.
- Developed CLASP, a software tool for validation of cell lines used in research.

2007.08 to 2008.08	**Institute for Systems Biology** Seattle, WA

Computational Biology Software Engineer, Laboratory of Dr. Ruedi Aebersold
Created TIQAM, a work flow management system to support Multiple Reaction Monitoring (MRM) proteomics experiments.

Industry Experience

2004.09 to 2007.08	**Muze, Inc.** Seattle, WA *Software Development Engineer*
2003.09 to 2004.09	**Encyclopaedia Britannica, Online Services** Chicago, IL *Software Developer*
2001.05 to 2003.08	**ThoughtWorks, LLC** Chicago, IL *Software Developer/Consultant*

Publications

Journal Articles

[19]   **Didion JP**, Martin M, and Collins FS, "Atropos: specific, sensitive, and speedy trimming of sequencing reads," *Preprint, submitted*, 2017. DOI: 10.7287/peerj.preprints.2452v3.

[18]   Varshneya A, Scott LJ, Welch R, Erdos MR, Chines PS, Narisu N, D'Oliveira RA, Orchard P, Wolford BN, Kursawee R, Vadlamudi S, Cannon ME, **Didion JP**, et al. "Genetic regulatory signatures underlying islet gene expression and type 2 diabetes," *Proc Nat Acad Sci USA*, 2017. DOI: 10.1073/pnas.1621192114.

[17]   Morgan AP, **Didion JP**, et al. "Genome report: whole genome sequence of two wild-derived *Mus musculus domesticus* inbred strains, LEWES/EiJ and ZALENDE/EiJ, with different diploid numbers," *G3*, 2016. DOI: 10.1534/g3.116.034751.

[16]   **Didion JP**, Morgan AP, et al. "*R2d2* drives selfish sweeps in the house mouse," *Molecular Biology and Evolution*, vol. 33, no. 6, pp. 1381–1395, 2016. DOI: 10.1093/molbev/msw036.

[15]   Morgan AP, Holt JM, McMullan RC, Bell TA, Clayshulte AM-F, **Didion JP**, et al. "The many evolutionary fates of a large segmental duplication in mouse," *Genetics*, 2016. DOI: 10.1534/genetics.116.191007.

[14]   Scott LJ, Erdos MR, Huyghe JR, Welch RP, Beck AT, Wolford BN, Chines PS, **Didion JP**, et al. "The genetic regulatory signature of type 2 diabetes in human skeletal muscle," *Nature Communications*, vol. 7, p. 11 764, 2016. DOI: 10.1038/ncomms11764.

[13]   Chandler RL, Damrauer JS, Raab JR, Schisler JC, Wilkerson MD, **Didion JP**, et al. "Coexistent ARID1A–PIK3CA mutations promote ovarian clear-cell tumorigenesis through pro-tumorigenic inflammatory cytokine signaling," *Nature Communications*, vol. 6, p. 6118, 2015. DOI: 10.1038/ncomms7118.

[12]   Crowley JJ, ...13 others..., **Didion JP**, et al. "Analyses of allele-specific gene expression in highly divergent mouse crosses identifies pervasive allelic imbalance," *Nature Genetics*, vol. 47, no. 4, pp. 353–360, 2015. DOI: 10.1038/ng.3222.

[11]   **Didion JP**, Morgan AP, Clayshulte AMF, et al. "A Multi-Megabase Copy Number Gain Causes Maternal Transmission Ratio Distortion on Mouse Chromosome 2," *PLoS Genetics*, vol. 11, no. 2, e1004850, 2015. DOI: 10.1371/journal.pgen.1004850.

[10]   Morgan AP, Fu C-P, Kao C-Y, Welsh CE, **Didion JP**, et al. "The Mouse Universal Genotyping Array: from substrains to subspecies," *G3*, vol. 6, no. 2, pp. 263–279, 2015. DOI: 10.1534/g3.115.022087.

[9]   **Didion JP**, Buus RJ, Naghashfar Z, et al. "SNP array profiling of mouse cell lines identifies their strains of origin and reveals cross-contamination and widespread aneuploidy," *BMC Genomics*, vol. 15, p. 847, 2014. DOI: 10.1186/1471-2164-15-847.

[8]   **Didion JP** and Pardo-Manuel de Villena F, "Deconstructing *Mus gemischus*: advances in understanding ancestry, structure, and variation in the genome of the laboratory mouse," *Mammalian Genome*, vol. 24, no. 1–2, pp. 1–20, 2013. DOI: 10.1007/s00335-012-9441-z.

[7]   Calaway JD, Lenarcic AB, **Didion JP**, et al. "Genetic architecture of skewed X inactivation in the laboratory mouse," *PLoS Genetics*, vol. 9, no. 10, e1003853, 2013. DOI: 10.1371/journal.pgen.1003853.

[6]   Collaborative Cross Consortium, "The genome architecture of the Collaborative Cross mouse genetic reference population," *Genetics*, vol. 190, no. 2, pp. 389–401, 2012. DOI: 10.1534/genetics.111.132639.

[5]   **Didion JP**, Yang H, Sheppard K, et al. "Discovery of novel variants in genotyping arrays improves genotype retention and reduces ascertainment bias," *BMC Genomics*, vol. 13, p. 34, 2012. DOI: 10.1186/1471-2164-13-34.

[4]   Aylor DL, ...11 others..., **Didion JP**, et al. "Genetic analysis of complex traits in the emerging Collaborative Cross," *Genome Research*, vol. 21, no. 8, pp. 1213–1222, 2011. DOI: 10.1101/gr.111310.110.

[3]   Yang H, Wang JR, **Didion JP**, et al. "Subspecific origin and haplotype diversity in the laboratory mouse," *Nature Genetics*, vol. 43, no. 7, pp. 648–655, 2011. DOI: 10.1038/ng.847.

[2]   Eisener-Dorman AF, **Didion JP**, Santos C, Calaway JD, "The 23rd International Mammalian Genome Conference meeting report," *Mammalian Genome*, vol. 21, no. 5–6, pp. 217–223, 2010. DOI: 10.1007/s00335-010-9265-7.

[1]   Lange V, Malmstrom JA, **Didion JP**, et al. "Targeted quantitative analysis of Streptococcus pyogenes virulence factors by multiple reaction monitoring," *Molecular and Cellular Proteomics*, vol. 7, no. 8, pp. 1489–1500, 2008. DOI: 10.1074/mcp.M800032-MCP200.

Funding

2017.04 to 2021.04	**NIH 1 K22 ES028024-01 BD2K Career Transition Award** *A Big Data Approach to Learning the Type 2 Diabetes Regulome* Career transition award with 3 years tenure-track funding
2017.01 to 2019.12	**American Diabetes Association Postdoctoral Fellowship** *A Multi-Tissue and Multi-Omics Investigaton Type 2 Diabetes* Postdoctoral fellowship with up to 3 years salary and research support
2016.09	**NIH Intramural Sequencing Center Pilot Grant** *Transcriptome analysis at single-molecule resolution* Institutional award with funding for sequencing services
2015.11	**NIH Intramural Sequencing Center Pilot Grant** *Extending ATAC-Seq to archival frozen and fixed tissue samples* Institutional award with funding for sequencing services
2015.05	**NIH Intramural Sequencing Center Pilot Grant** *Identifying functional variants in T2D GWAS loci using CATCh-PET* Institutional award with funding for sequencing services
2014.12	**NIH Intramural Sequencing Center Pilot Grant** *Epigenomic regulation of glucose response in a human pancreatic Beta cell line* Institutional award with funding for sequencing services
2014.12 to 2015.04	**Department of Health and Human Services Ignite** *LabGenius: The Smart Lab Notebook for Scientists* Incubator program to fund innovative projects within HHS
2009.09 to 2010.08	**Bioinformatics and Computational Biology Training Grant** *NIH GM067553-04* Institution-awarded fellowship
2009.09	**International Mammalian Genome Society Fellowship** *Travel grant*

Teaching Experience

2016.10 to present	**NIH** *Software Carpentry, Instructor*
2016.10 to present	**FAES (NIH)** *American Academy of Bioinformatics, Instructor (paid)*
2015.06 to present	**NHGRI** *Graduate and undergraduate students, Mentor*
2013.09 to 2014.05	**University of North Carolina at Chapel Hill** *Undergraduate (senior research project), Mentor*
2013.09 to 2013.12	**University of North Carolina at Chapel Hill** *Genetic Analysis 2, Teaching Assistant*

Oral Presentations

2017.04	**NIAID Genomics and Immunology Speaker Series**	Bethesda, MD
2017.01	**NIH Data Science Interest Group**	Bethesda, MD
2015.10	**NIH Digital Summit**	Bethesda, MD
2013.09	**27th Intl. Mammalian Genome Conference**	Salamanca, Spain
2013.05	**12th Annual Meeting of the Complex Traits Community**	Madison, WI
2012.09	**16th EBM Conference**	Marseille, France
2012.09	**UNC Genetics Department Retreat**	Myrtle Beach, SC
2010.10	**24th Intl. Mammalian Genome Conference**	Heraklion, Greece
2010.05	**9th Annual Meeting of the Complex Traits Community**	Chicago, IL
2009.09	**23rd Intl. Mammalian Genome Conference**	San Diego, CA

Poster Presentations

2015.10	**American Society of Human Genetics Conference**	Baltimore, MD
2015.05	**Biology of Genomes Conference**	Cold Spring Harbor, NY
2014.10	**28th Intl. Mammalian Genome Conference**	Bar Harbor, ME
2011.09	**UNC Genetics Department Retreat**	Myrtle Beach, SC
2011.06	**Genetics Society of America Mouse Genetics**	Washington D.C.
2011.06	**National Centers for Systems Biology Annual Meeting**	Duke University
2010.09	**UNC Genetics Department Retreat**	Myrtle Beach, SC
2009.09	**UNC Genetics Department Retreat**	Asheville, NC

Honors & Awards

2014.12	**Dean's Distinguished Dissertation Award (Nominee)**
	University of North Carolina at Chapel Hill
	Nominee from the Bioinformatics and Computational Biology program
2013.09	**Verne Chapman Young Scientist Award**
	International Mammalian Genome Society
	Best trainee talk at the International Mammalian Genome Conference
2013.05	**Chicago Prize**
	Complex Traits Consortium
	Best graduate student talk at the Complex Traits Consortium meeting
2010.10	**Genome Research Award for Outstanding Poster**
	International Mammalian Genome Society
	Outstanding poster at the International Mammalian Genome Conference

Professional Memberships & Service

2016.08 to present	**Software Carpentry**
	Certified Instructor
2016.01 to present	**NHGRI Preprint Journal Club**
	Organizer
2016.01, 2016.08, 2016.10	**NCBI Hackathons**
	Team Lead
2013.09 to 2015.09	**International Mammalian Genome Society**
	Secretariat member (honorary)
2013.08	**UNC Genetics Department Retreat**
	Abstract Review Committee