John Didion | PhD

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Education

2008 to 2014	**Doctor of Philosophy, Bioinformatics and Computational Biology** *University of North Carolina, Chapel Hill, NC*
1996 to 2001	**Bachelor of Science, Computer Science** *Northwestern University, Evanston, IL*

Research Experience

2014 to 2017 — 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.
- Using single-cell gene expression and chromatin accessibility data to understand cell-to-cell variability in pancreatic islets, including responses to glucose perturbation.
- Designed a novel sequencing assay for single-molecule resolution transcriptome analysis.
- Developed Atropos, user-friendly software for QC and pre-processing of NGS reads.
- Awarded six grants, including an American Diabetes Association fellowship and an NIH K22.

2009 to 2014 — University of North Carolina at Chapel Hill — Chapel Hill, NC
Research Assistant, Laboratory of Dr. Fernando Pardo-Manuel de Villena
- Characterized a novel meiotic drive locus, *R2d2,* and multiple modifier loci responsible for extreme transmission distortion in interspecific crosses.
- Conducted a GWAS of wild mice to identify genes associated with the accumulation of Robertsonian translocations.
- Developed CLASP, a software tool for validation of cell lines used in research.

2007 to 2008 — 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

2018 to present	**DNAnexus** *Principal Scientist - FDA Specialist*	Rockville, MD (remote)
2017 to 2018	**Personal Genome Diagnostics** *Principal Bioinformatics Scientist*	Baltimore, MD
2004 to 2007	**Muze, Inc.** *Software Development Engineer*	Seattle, WA
2003 to 2004	**Encyclopaedia Britannica, Online Services** *Software Developer*	Chicago, IL
2001 to 2003	**ThoughtWorks, LLC** *Software Developer/Consultant*	Chicago, IL

Publications

Journal Articles...

[23]   Morgan AP, **Didion JP**, . . . , Pardo-Manuel de Villena F, "Genetic characterization of invasive house mouse populations on small islands," *Submitted*, 2018. DOI: https://www.biorxiv.org/content/early/2018/05/28/332064.

[22]   Taylor DL, Scott LJ, Jackson AU, Narisu N, Hemani G, Erdos MR, Chines PS, Swift A, Idol J, **Didion JP**, . . . , Birney E, Collins FS, "Integrative analysis of molecular traits, clinical traits, and genetic variation in human skeletal muscle," *Submitted*, 2018.

[21]   Zou LS, . . . , Collins FS, **Didion JP**, "BoostMe accurately predicts DNA methylation values in whole-genome bisulfite sequencing of multiple human tissues," *BMC Bioinformatics*, 2018. DOI: 10.1186/s12864-018-4766-y.

[20]   **Didion JP**, Martin M, and Collins FS, "Atropos: specific, sensitive, and speedy trimming of sequencing reads," *PeerJ*, 2017. DOI: 10.7717/peerj.3720.

[19]   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.

[18]   **Didion JP**, "xphyle: Extraordinarily simple file handling," *Journal of Open Source Software*, 2017. DOI: http://dx.doi.org/10.21105/joss.00255.

[17]   **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.

[16]   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.

[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]   **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.

[12]   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.

[11]   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.

[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]   **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.

[5]   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.

[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	**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	**American Diabetes Association Postdoctoral Fellowship**
	A Multi-Tissue and Multi-Omics Investigaton of Type 2 Diabetes
	Postdoctoral fellowship with up to 3 years salary and research support
2016	**NIH Intramural Sequencing Center Pilot Grant**
	Transcriptome analysis at single-molecule resolution
	Institutional award with funding for sequencing services
2015	**NIH Intramural Sequencing Center Pilot Grant**
	Extending ATAC-Seq to archival frozen and fixed tissue samples
	Institutional award with funding for sequencing services
2015	**NIH Intramural Sequencing Center Pilot Grant**
	Identifying functional variants in T2D GWAS loci using CATCh-PET
	Institutional award with funding for sequencing services
2014	**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	**Department of Health and Human Services Ignite**
	LabGenius: The Smart Lab Notebook for Scientists
	3-month incubator program to fund innovative projects within HHS
2009	**Bioinformatics and Computational Biology Training Grant**
	NIH GM067553-04
	Institution-awarded fellowship; 1 year stipend support
2009	**International Mammalian Genome Society Fellowship**
	Travel grant

Honors & Awards

2014.12	**Dean's Distinguished Dissertation Award (Department 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

Conference Participation

2016.10	**Biological Data Science Meeting**	Cold Spring Harbor, NY
2015.10	**American Society of Human Genetics Conference**, Poster	Baltimore, MD
2015.05	**Biology of Genomes Conference**, Poster	Cold Spring Harbor, NY
2014.10	**28th Intl. Mammalian Genome Conference**, Poster	Bar Harbor, ME
2013.09	**27th Intl. Mammalian Genome Conference**, Talk	Salamanca, Spain
2013.05	**12th Annual Meeting of the Complex Traits Community**, Talk	Madison, WI
2012.09	**16th Evolutionary Biology Meeting**, Talk, Poster	Marseille, France
2011.06	**Genetics Society of America Mouse Genetics**, Poster	Washington D.C.
2011.06	**National Centers for Systems Biology Annual Meeting**, Poster	Duke University
2010.10	**24th Intl. Mammalian Genome Conference**, Talk	Heraklion, Greece
2010.05	**9th Annual Meeting of the Complex Traits Community**, Talk	Chicago, IL
2009.09	**23rd Intl. Mammalian Genome Conference**, Talk	San Diego, CA

Other Invited Talks

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
2012.09	**UNC Genetics Department Retreat**	Myrtle Beach, SC

Teaching Experience

2016 to Present	**NIH**
	Software Carpentry, Instructor
2016 to Present	**FAES (NIH)**
	American Academy of Bioinformatics, Instructor (paid)
2015 to Present	**NHGRI**
	Graduate and undergraduate students, Mentor
2013 to 2014	**University of North Carolina at Chapel Hill**
	Undergraduate (senior research project), Mentor
2013 Fall	**University of North Carolina at Chapel Hill**
	Genetic Analysis 2, Teaching Assistant

Professional Memberships & Service

2016 to Present	**Software Carpentry**
	Certified Instructor
2016 to Present	**NHGRI Preprint Journal Club**
	Organizer
2016	**NCBI Hackathons (multiple dates)**
	Team Lead
2013 to 2015	**International Mammalian Genome Society**
	Secretariat member (honorary)
2013	**UNC Genetics Department Retreat**
	Abstract Review Committee