# 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 Present Na

#### 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.
- o Developing machine-learning approaches for imputation of multi-omics data.
- Using single-cell gene expression and chromatin accessibility data to understand cellto-cell variability in pancreatic islets, including responses to glucose perturbation.
- o Designed a novel sequencing assay for single-molecule resolution transcriptome analysis.
- o 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

- o 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.
- o 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**

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...

[21] **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.

- [20] 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.
- [19] **Didion JP**, "xphyle: Extraordinarily simple file handling," *Journal of Open Source Software*, 2017. DOI: http://dx.doi.org/10.21105/joss.00255.
- [18] Zou LS, ..., Collins FS, **Didion JP**, "BoostMe accurately predicts DNA methylation values in whole-genome bisulfite sequencing of multiple human tissues," *Submitted*, 2017.
- [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. 11764, 2016. DOI: 10.1038/ncomms11764.
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- [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.
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- [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.
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- [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.
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# **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 Investigation 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, Tall	k 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, Poste	r 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* 

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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