

John Didion | PhD

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Education

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

Research Experience

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| 2014 to Present | National Human Genome Research Institute <i>Postdoctoral Fellow, Laboratory of Dr. Francis S Collins</i> Bethesda, MD <ul style="list-style-type: none">○ 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 <i>Research Assistant, Laboratory of Dr. Fernando Pardo-Manuel de Villena</i> Chapel Hill, NC <ul style="list-style-type: none">○ Characterized a novel meiotic drive locus, <i>R2d2</i>, 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 <i>Computational Biology Software Engineer, Laboratory of Dr. Ruedi Aebersold</i> Seattle, WA Created TIQAM, a work flow management system to support Multiple Reaction Monitoring (MRM) proteomics experiments. |

Industry Experience

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| 2004 to 2007 | Muze, Inc. <i>Software Development Engineer</i> Seattle, WA |
| 2003 to 2004 | Encyclopaedia Britannica, Online Services <i>Software Developer</i> Chicago, IL |
| 2001 to 2003 | ThoughtWorks, LLC <i>Software Developer/Consultant</i> Chicago, IL |

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 ZALLENDE/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.
- [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

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| 2017 | NIH 1 K22 ES028024-01 BD2K Career Transition Award <i>A Big Data Approach to Learning the Type 2 Diabetes Regulome</i> Career transition award with 3 years tenure-track funding |
| 2017 | American Diabetes Association Postdoctoral Fellowship <i>A Multi-Tissue and Multi-Omics Investigaton of Type 2 Diabetes</i> Postdoctoral fellowship with up to 3 years salary and research support |
| 2016 | NIH Intramural Sequencing Center Pilot Grant <i>Transcriptome analysis at single-molecule resolution</i> Institutional award with funding for sequencing services |
| 2015 | NIH Intramural Sequencing Center Pilot Grant <i>Extending ATAC-Seq to archival frozen and fixed tissue samples</i> Institutional award with funding for sequencing services |
| 2015 | NIH Intramural Sequencing Center Pilot Grant <i>Identifying functional variants in T2D GWAS loci using CATCh-PET</i> Institutional award with funding for sequencing services |
| 2014 | NIH Intramural Sequencing Center Pilot Grant <i>Epigenomic regulation of glucose response in a human pancreatic Beta cell line</i> Institutional award with funding for sequencing services |
| 2014 | Department of Health and Human Services Ignite <i>LabGenius: The Smart Lab Notebook for Scientists</i> 3-month incubator program to fund innovative projects within HHS |
| 2009 | Bioinformatics and Computational Biology Training Grant <i>NIH GM067553-04</i> Institution-awarded fellowship, 1 year stipend support |
| 2009 | International Mammalian Genome Society Fellowship <i>Travel grant</i> |

Honors & Awards

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

Conference Participation

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| 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

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| 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

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

Professional Memberships & Service

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