Charles W. O'Donnell, Ph.D.

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SUMMARY

Data Scientist and Computational Biologist with over a decade experience in multi-disciplinary teams intent on solving big scientific problems to improve patient lives. Deep expertise in data analysis and integration, NGS, gene regulation, systems biology, genetics, gene therapy, molecular biophysics, inference, machine learning, HPC, and scalable algorithm design. Looking to grow my skills, contribute to strategic decision making, lead and teach others, and have impact.

EDUCATION

- Ph.D. EECS/Computational Biology, **Massachusetts Institute of Technology (MIT)**, 2011
- S.M. EECS, **Massachusetts Institute of Technology (MIT)**, 2005
- B.S. Computer Engineering, **Columbia University**, 2003

EXPERIENCE

Camp4 Therapeutics, Assoc. Director, *Head of Computational Biology & Data Science*   2017 – present

Established Camp4's bioinformatic functions and architect of data science strategy to derive cell-type-specific gene circuitry maps (employee #8). Managed PhD-level bioinformatician, external contributors and partnerships, and member of leadership team working intimately with Discovery and Translation groups to chart scientific course and make recommendation to C-level and Founders.

- Implemented robust, scalable data processing pipelines and infrastructure, along with human & technical processes for clear cross-team communication of results, tracking, and reproducible research.
- Helped set cell "mapping" strategy and built predictive models integrating pathways with gene regulation.
- Responsible for solutions to broad sets of statistical & computational needs across all facets of company.
- Engaged external partners to in-house state-of-the-art methods, datasets, and data integration practices.
- Helped develop novel NGS-based assays and analysis techniques for deciphering cell state dynamics.
- Set plan for use of genetics in functional genomics; integrated known variants to prioritize target ID.

Biogen, Senior Scientist, Research, *Epigenetics and Cell & Gene Therapy*   2016 – 2017
Biogen, Scientist II, Research, *Epigenetics and Cell & Gene Therapy*   2014 – 2016

Founding member of Biogen's Epigenetics group. Project head for a series of epigenomic association studies (EWASs) with team of computational & bench scientists. Computational lead for Epigenetics and Cell & Gene Therapy group, focusing on NGS analysis, target discovery/prioritization, novel therapeutic modalities, and multi-omics integration.

- Initiated and led EWAS programs in Parkinson's Disease & Down Syndrome, liaising with clinical partners.
- Managed EWAS team; 2 comp. biologists (myself+direct PhD report), 3 bench scientists (non-reporting).
- Teamed with Clinical and Digital Health on wearables integration within studies.
- Championed R&D's RNA-seq development and strategy; wrote first centralized pipelines.
- Introduced novel molecular seq-based assays and analyses.
- Provided domain expertise on NGS data interpretation throughout multiple therapeutic area partnerships.
- Piloted cloud compute efforts and internal standardization of multi-omics data analysis.
- Primary NGS analyst and assay designer for Biogen/Rodin Therapeutics partnership.
- Investigated CRISPR-based therapeutic platform for site-specific epigenomic modulation.
- Genome editing off-target analysis and assay development.
- People management training program completed (Biogen, 2016).

Harvard University, Postdoctoral Fellow, *Melton Lab, Harvard Stem Cell Institute*   2011 – 2014
MIT, Postdoctoral Fellow, *Gifford Lab, Computer Science & AI Laboratory*

Joint Postdoctoral Fellowship in labs of Douglas Melton (Harvard) and David Gifford (MIT). Applied diverse NGS-based assays to study chromatin dynamics and the epigenetic regulation of pluripotent cells during differentiation. Identified novel factors controlling cell state change and developed new methods for studying heterogeneous populations and single-cells.

- NIH Ruth L. Kirschstein NRSA Fellowship awardee.
- Managed group's involvement & contribution as an ENCODE consortium member group.
- Modeled NGS data to uncover determinants of cell state regulation.
- Discovery of novel class of directional pioneer transcription factors (TFs).
- Technique development for TF binding site identification and chromatin architecture analysis.
- Systems biological, multi-omics analysis for improvement of ES/iPS differentiation protocols.
- Design and use of massively parallel reporter assays (MPRAs) and capture technologies.
- Single-cell RNA-seq and cell-type heterogeneity analysis.
- Extensive experience with *-seq assays (RNA/DNA/DNase/ATAC/ChIP/WGBS/miR/ChIA-PET/Hi-C).
- Management/use of high-performance compute, NGS pipelines, and cloud compute within group.

MIT, Ph.D. Student, *Berger Group, Devadas Group, Computer Science & AI Laboratory*   2003 – 2011
Whitehead Institute, Ph.D. Student, *Lindquist Lab*
Ph.D. performed jointly in labs of Bonnie Berger and Srini Devadas (MIT) and Susan Lindquist (Whitehead Institute). Developed algorithms that characterized folding and misfolding of proteins and RNA across their sequence and structure landscapes. Methods enabled and suggested targeted experimental investigations of amyloid and transmembrane proteins, and the demonstrated inhibition of bacterial amyloid fibril formation.

- Algorithm development modeling amyloid structure and sequence-mutation landscape.
- Data-driven hypothesis generation, working closely with bench scientists on subsequent assay designs.
- Demonstrated inhibition of bacterial biofilms via amyloid capping (patented).
- Algorithm development modeling transmembrane transport protein structure/sequence.
- Novel molecular energy model development for RNA/protein interfaces.
- Introduced some of the earliest SAT-based optimization techniques for bioinformatics.

IBM Research, Summer Intern, *Biomolecular Dynamics and Scalable Modeling Group*   2006
- Applied concepts from relational databases to advance a massively parallel application.
- Contributed to BlueMatter Molecular Dynamics simulation package run on the BlueGene/L.

Columbia University, Research Assistant, *Nowick Group, Async. Circuits and Systems*   2001 – 2003
- Awarded Theodore R. Bashkow Award by CS Dept. as Senior who most excelled in independent research.
- Solved open theoretical question on existence of hazard-free logic circuits; proving minimal requirements.

PUBLIC SOFTWARE TOOLS CO/AUTHORED

- PIQ
- AmyloidMutants
- partiFold-Align
- partiFold-TMB
- MINIMALIST

PUBLICATIONS

1. L.M.R. Ferreira, T.B. Meissner, T.S. Mikkelsen, W. Mallard, **C.W. O'Donnell**, T. Tilburgs, H.A.B. Gomes, R. Camahort, R.I. Sherwood, D.K. Gifford, J.L. Rinn, C.A. Cowan, J.L. Strominger, A distant trophoblast-specific enhancer controls HLA-G expression at the maternal-fetal interface. *PNAS*, 113(15):5364-5369, 2016.
2. S. Hrvatin, **C.W. O'Donnell**, F. Deng, J.R. Millman, F.W. Pagliuca, P. DiIorio, A. Rezania, D.K. Gifford, D.A. Melton, Differentiated human stem cells resemble fetal, not adult β cells. *PNAS*, 111(8):3038-3043, 2014.
3. S. Hrvatin, F. Deng, **C.W. O'Donnell**, D.K. Gifford, D.A. Melton, MARIS: Method for Analyzing RNA following Intracellular Sorting. *PLoS ONE*, 9(3):e89459, 2014.
4. R.I. Sherwood*, T. Hashimoto*, **C.W. O'Donnell***, S. Lewis, A.A. Barkal, J.P. van Hoff, V. Karun, T. Jaakkola, D.K. Gifford (**equal contrib.**), Discovery of directional and nondirectional pioneer transcription factors by modeling DNase profile magnitude and shape, *Nature Biotech.*, 32:171-178, 2014.
5. J. Waldispühl*, **C.W. O'Donnell***, S. Will*, S. Devadas, R. Backofen, B. Berger (**equal contrib.**), Simultaneous Alignment and Folding of Multiple Protein Sequences. *J. Computational Biology*, Apr. 2014.
6. A. Levin, M. Lis, Y. Ponty, **C.W. O'Donnell**, S. Devadas, B. Berger, J. Waldispühl, A global sampling approach to designing and reengineering RNA secondary structures. *Nucleic Acids Research*, 40(20):10041-10052, 2012.

7. V. Ganesh, **C.W. O'Donnell**, A. Solar-Lezama, S. Devadas, M. Soos, M. Rinard Lynx: A Programmatic SAT Solver for the RNA-folding Problem, *SAT 2012*, Trento, Italy. *Lecture Notes in Computer Science* 7317, pp. 143-156 2012.
8. A.W. Bryan Jr., **C.W. O'Donnell**, M. Menke, L.J. Cowen, S. Lindquist, B. Berger STITCHER: Dynamic assembly of likely amyloid and prion β-structures from secondary structure predictions, *Proteins: Structure, Function, and Bioinformatics,* 80(2):410-420, 2012.
9. R. Halfmann, S. Alberti, R. Krishnan, N. Lyle, **C.W. O'Donnell**, O.D. King, B. Berger, R. Pappu, S. Lindquist, Opposing effects of glutamine and asparagine govern prion formation by instrinsically disordered proteins, *Molecular Cell*, 41(1):72–84, 2011.
10. **C.W. O'Donnell**, J. Waldispühl, M. Lis, R. Halfmann, S. Devadas, S. Lindquist, B. Berger, A method for probing the mutational landscape of amyloid structure. *ISMB/ECCB 2011*, Vienna, Austria. *Bioinformatics*, 27(13):i34-42, 2011.
11. S. Shenker, **C.W. O'Donnell**, S. Devadas, B. Berger, J. Waldispühl, Efficient traversal of protein folding pathways using ensemble models. *RECOMB 2011*, Vancouver, BC, Canada.
12. J. Waldispühl, **C.W. O'Donnell**, S. Will, S. Devadas, R. Backofen, B. Berger, Simultaneous Alignment and Folding of Protein Sequences, *RECOMB 2009*, Tucson, AZ.
13. J. Waldispühl*, **C.W. O'Donnell***, S. Devadas, P. Clote, B. Berger (***equal contrib.***), Modeling Ensembles of Transmembrane β-barrel Proteins, *Proteins: Structure, Function, and Bioinformatics*, 71(3):1097–1112, 2008.
14. B. Gassend, **C.W. O'Donnell**, W. Thies, A. Lee, M. van Dijk, S. Devadas, Learning Biophysically-Motivated Parameters for Alpha Helix Prediction, *BMC Bioinformatics*, 8(Suppl. 5):S3, 2007.
15. B. Gassend, **C.W. O'Donnell**, W. Thies, A. Lee, M. van Dijk, S. Devadas, Predicting Secondary Structure of All-Helical Proteins Using Hidden Markov Support Vector Machines*, PRIB 2006*, Hon Kong, China, Lecture Notes in Computer Science 4146, pp. 93-104 2006.
16. G.E. Suh, **C.W. O'Donnell**, S. Devadas, AEGIS: A Single-Chip Secure Processor, *IEEE Design & Test*, 24(6):570–580, 2007.
17. **C.W. O'Donnell**, G.E. Suh, M. van Dijk, S. Devadas, Memoization Attacks and Copy Protection in Partitioned Applications, *Proc. of the 2007 IEEE Workshop on Information Assurance (IAW 2007)*, West Point, NY.
18. L.F.G. Sarmenta, M. van Dijk, **C.W. O'Donnell**, J. Rhodes, S. Devadas, Virtual Monotonic Counters and Count-Limited Objects using a TPM without a Trusted OS, Proc. of *2006 Workshop on Scalable Trusted Comput.*, Fairfax, VA.
19. G.E. Suh, **C.W. O'Donnell**, S. Devadas, Design and Implementation of the AEGIS Single-Chip Secure Processor Using Physical Random Functions, *ISCA 2005*, Madison, WI.
20. **C.W. O'Donnell**, V. Vaikuntanathan, Information Leak in the Chord Lookup Protocol, *Proc. of the 4th Annual IEEE International Conference on Peer-to-Peer Computing (P2P 2004)*, Zurich, Switzerland.
21. S.M. Nowick, **C.W. O'Donnell**, On the Existence of Hazard-Free Multi-Level Logic, *Proc. of the 9th Annual IEEE International Conference on Advanced Research in Asynchronous Circuits and Systems (ASYNC 2003)*, Vancouver, Canada.

PATENTS

1. T.K. Lu, R. Krishnan, **C.W. O'Donnell**, S. Devadas, B. Berger, J. Collins, S. Lindquist, Bacteriophages Expressing Amyloid Peptides and Uses Thereof, Provisional applications 61/229,703 (filed July 29, 2009), 61/233,697 (filed August 13, 2009). International Serial Number: PCT/US2010/043770. Published February 3, 2011.
2. Camp4 Therapeutics omnibus patent. U.S. Provisional application 62/501,795 (filed May 5, 2017). Fully filed in PCT and to be made public Nov. 4, 2018.