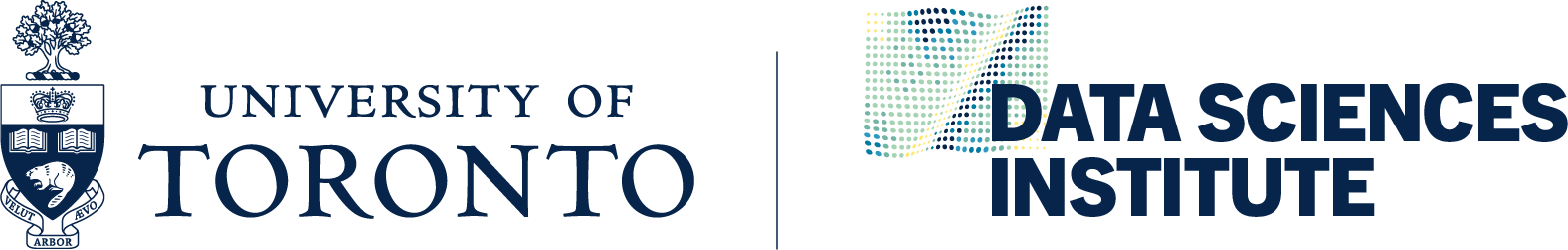
/

**Abbreviated 3-Page CV template**

Your CV should not exceed three pages and should be presented according to the following specifications: single-spaced, body text in Arial, 11pt font, and 1” margins.

|  |  |
| --- | --- |
| **Name** | Michael M. Hoffman |
| **Institution** | University Health Network |
| **Division\*** | Princess Margaret Cancer Centre |
| **Unit\*** | Computational Biology and Medicine Program |

**\*if applicable**

**Education**

Instructions: Reverse Chronological. Add/delete rows as necessary.

|  |  |  |
| --- | --- | --- |
| **Institution, Location** | **Degree** | **Completion Date\*** |
| University of Cambridge (Trinity College), UK | PhD | Jul 2008 |
| University of Texas at Austin, USA | B.S./B.A. | May 2003 |

**\*mmm yyyy**

**Research**

Instructions: For non-academic team members, it is not strictly necessary to follow the below categories.

### 1. Brief Personal Statement

Michael Hoffman creates predictive computational models to understand interactions between the genome, epigenome, and phenotype in human cancers. His influential machine learning approaches have reshaped researchers’ analysis of gene regulation. These approaches include the genome annotation method Segway, which enables simple interpretation of multivariate genomic data. It was a linchpin of the ENCODE Project analysis, which transformed our thinking about the role of noncoding DNA in the human genome.

### 2. Main Affiliation(s), Positions and Honors

**Chair**, Computational Biology and Medicine Program, Princess Margaret Cancer Centre, University Health Network, 2023–2026. **Senior Scientist**, 2020–.  
**Assoc. Professor**, Depts of Medical Biophysics & Computer Science, U. of Toronto, 2020–.

* Canadian Institutes of Health Research New Investigator, 2017–2022
* Ontario Early Researcher Award, 2016–2021.
* *Genome Technology* Young Investigator, 2011.
* NIH K99/R00 Pathway to Independence Award, 2011–2013.
* National Science Foundation Graduate Research Fellow, 2003–2008.
* Marshall Scholar, 2003–2005.

### 3. Relevant Contributions to Research

Dr. Hoffman is an international leader in the field of computational biology, for which he has developed several widely used methods for analyzing epigenomics data. Specifically, Dr. Hoffman’s research program focuses on creating and validating predictive models of how genetic variants cause epigenomic changes and how these epigenomic changes affect gene regulation and phenotype. Dr. Hoffman’s commitment to openly sharing his research methods, software, and genome annotations have enabled scientists around the world to address fundamental questions in biological and biomedical research.

### 4. Publications (including Working Papers and Forthcoming Work) (selected)

J39. **Viner C**, *(12 authors)*, **Hoffman MM**. [“Modeling methyl-sensitive transcription factor motifs with an expanded epigenetic alphabet.”](https://genomebiology.biomedcentral.com/articles/10.1186/s13059-023-03070-0) *Genome Biol* 2024; 25:11.

J36. **Karimzadeh M**, *(4 authors)*, **Hoffman MM**. [“Human papillomavirus integration transforms chromatin to drive oncogenesis.”](https://genomebiology.biomedcentral.com/articles/10.1186/s13059-023-02926-9) *Genome Biol* 2023; 24:142.

J35. **Denisko D**\*, **Viner C**\*, **Hoffman MM**. [“Motif elucidation in ChIP-seq datasets with a knockout control.”](https://doi.org/10.1093/bioadv/vbad031) *Bioinf Adv* 2023; 3(1): vbad031.

J32. **Wilson SL**, *(6 authors)*, **Hoffman MM**. [“Sensitive and reproducible cell-free methylome quantification with synthetic spike-in controls.”](https://www.cell.com/cell-reports-methods/fulltext/S2667-2375(22)00176-X) *Cell Rep Methods* 2022; 2(9):100294.

J31. **Karimzadeh M**, **Hoffman MM**. [“Virtual ChIP-seq: predicting transcription factor binding by learning from the transcriptome.”](https://genomebiology.biomedcentral.com/articles/10.1186/s13059-022-02690-2) *Genome Biology* 2022; 23:126.

J30. **Niu J**, **Denisko D**, **Roberts EG**, **Hoffman MM**. [“Assessing and assuring interoperability of a genomics file format.”](https://academic.oup.com/bioinformatics/advance-article-abstract/doi/10.1093/bioinformatics/btac327/6586286) *Bioinformatics* 2022; 38(13):3327.

J29. Libbrecht MW\*, **Chan RCW**\*, **Hoffman MM**. [“Segmentation and genome annotation algorithms for identifying chromatin state and other genomic patterns.”](https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1009423) *PLOS Comput Biol* 2021; 17(10):e1009423.

J23. **Sood AJ**\*, **Viner C**\*, **Hoffman MM**. [“DNAmod: the DNA modification database.”](https://jcheminf.biomedcentral.com/articles/10.1186/s13321-019-0349-4) *J Cheminform* 2019; 11:30.

J22. Zitnik M, **Nguyen F**, *(3 authors)*, **Hoffman MM**. [“Machine learning for integrating data in biology and medicine: principles, practice, and opportunities.”](https://www.sciencedirect.com/science/article/pii/S1566253518304482) *Inf Fusion* 2019; 50:71.

J20. **Karimzadeh M**, Ernst C, Kundaje A, **Hoffman MM**. [“Umap and Bismap: quantifying genome and methylome mappability.”](https://academic.oup.com/nar/article/46/20/e120/5086676) *Nucleic Acids Res* 2018; 46:e120.

J18. **Chan RCW**\*, Libbrecht MW\*, **Roberts EG**, Bilmes JA, Noble WS, **Hoffman MM**. [“Segway 2.0: Gaussian mixture models and minibatch training.”](https://doi.org/10.1093/bioinformatics/btx603) *Bioinformatics* 2018; 34(4):669.

J17. **Karimzadeh M**, **Hoffman MM**. [“Top considerations for creating bioinformatics software documentation.”](https://academic.oup.com/bib/article/doi/10.1093/bib/bbw134/2907814/Top-considerations-for-creating-bioinformatics) *Brief Bioinform* 2018; 19(4):693.

J12. **Hoffman MM**\*, Ernst J\*, *(5 authors)*, **Ellenbogen PM**, *(6 authors)*. [“Integrative annotation of chromatin elements from ENCODE data.”](https://academic.oup.com/nar/article/41/2/827/1071531) *Nucleic Acids Res* 2013; 41(2):827.

J9. **Hoffman MM**, **Buske OJ**, *(3 authors)*. [“Unsupervised pattern discovery in human chromatin structure through genomic segmentation.”](http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3340533/) *Nat Methods* 2012; 9(5):473.

J6. **Hoffman MM**, **Buske OJ**, Noble WS. [“The Genomedata format for storing large-scale functional genomics data.”](http://doi.org/10.1093/bioinformatics/btq164) *Bioinformatics* 2010; 26(11):1458.

N5. **Wilson SL**, Way GP, Bittremieux W, Armache J-P, Haendel MA, **Hoffman MM**. [“Sharing biological data: why, when, and how.”](https://doi.org/10.1002/1873-3468.14067) *FEBS Lett* 2021; 595(7):847–863.

N4. **Denisko D**, **Hoffman MM**. [“Classification and interaction in random forests.”](https://doi.org/10.1073/pnas.1800256115) *Proc Natl Acad Sci U S A* 2018; 115(8):1690.

N3. **Chicco D**, **Hoffman MM**. [“Genome Informatics 2016.”](https://doi.org/10.1186/s13059-016-1135-5) *Genome Biol* 2017; 18(1):5.

N2. **Viner C**, **Hoffman MM**. [“Determining the epigenome using DNA alone.”](http://pubmed.gov/25719827) *Nat Methods* 2015; 12(3):191.

S13. **Mendez M**, **Liu Y**, Ponce de León MA, **Hoffman MM**. [“Segzoo: a turnkey system that summarizes genome annotations.”](https://doi.org/10.1101/2023.10.03.559369) 2023. Preprint: <https://doi.org/mcfs>

S8. **Mendez M**, Harshbarger J, **Hoffman MM**. [“Automated identification of cell-type–specific genes and alternative promoters.”](https://doi.org/10.1101/2021.12.01.470587) 2022. Preprint: <https://doi.org/mcfq>

S6. **Mendez M**, *(2 authors)*, **Hoffman MM**. [“Unsupervised analysis of multi-experiment transcriptomic patterns with SegRNA identifies unannotated transcripts.”](https://doi.org/10.1101/2020.07.28.225193) 2021. Preprint: <https://doi.org/jncp>

S5. **Cao C**\*, **Chicco D**\*, **Hoffman MM**. [“The MCC-F1 curve: a performance evaluation technique for binary classification.”](https://doi.org/10.48550/arXiv.2006.11278) 2020. Preprint: <https://doi.org/d6jp>

S4. **Chan RCW**, **McNeil M**, **Roberts EG**, **Mendez M**, Libbrecht MW, **Hoffman MM**. [“Semi-supervised segmentation and genome annotation.”](https://doi.org/10.1101/2020.01.30.926923) 2020. Preprint: <https://doi.org/mcfq>

S3. **Chicco D**, **Bi HS**, Reimand J, **Hoffman MM**. [“BEHST: genomic set enrichment analysis enhanced through integration of chromatin long-range interactions.”](https://doi.org/10.1101/168427) 2019. Preprint: <https://doi.org/fm2z>

S2. **Roberts EG**, **Mendez M**, **Viner C**, **Karimzadeh M**, **Chan R**, Ancar R, **Chicco D**, *(2 authors)*, **Hoffman MM**. [“Semi-automated genome annotation using epigenomic data and Segway.”](https://doi.org/10.1101/080382) 2016. Preprint: <https://doi.org/10.1101/080382>

E1. **Hoffman MM**. [“Readers respond to *Nature’s* Editorial on historical monuments”.](http://www.nature.com/news/readers-respond-to-nature-s-editorial-on-historical-monuments-1.22584) *Nature* 2017. <https://doi.org/10.1038/nature.2017.22584>

### 5. Other Scholarly Works (e.g., Policy Reports, Multimedia, Software, etc.)

X1. **Niu J**, **Denisko D**, **Hoffman MM**. [“The Browser Extensible Data (BED) format.”](https://samtools.github.io/hts-specs/BEDv1.pdf) 2021. Global Alliance for Genomics and Health (GA4GH) Approved Standard.

### 6. Additional Information Relevant to Proposal and Review

### Funding: lead principal investigator

F22. “Segway Suite.” UHN. CAD 75,000. 2023–2024.

F21. “Computational methods for chromatin data.” NSERC. CAD 240,000. 2022–2027.

F20. Essential Oncology Software for Research. UHN. CAD 16,500. 2021–2022.

F19. Canada Research Continuity Emergency Fund. CAD 65,452. 2020–2021.

F17. “Genome-wide cell-free DNA methylation enrichment and sequencing for preeclampsia diagnosis.” McLaughlin Centre. CAD 80,000. 2019–2020.

F16. “DNA methylation profiling in cell-free DNA: a non-invasive method to screen for pre-term birth.” CIHR. CAD 1,237,817. 2019–2023.

F11. “Comprehending epigenomic changes in gene dysregulation and cancer using machine learning.” CIHR New Investigator Salary Award. CAD 300,000. 2017–2022.

F10. “The expanded epigenetic alphabet: transcription factor binding in methylated DNA and beyond.” Ontario Early Researcher Award. CAD 140,000. 2016–2021.

F7. “Transcription factor recognition models with modified nucleobases.” NSERC. CAD 247,192.83. 2015–2022.

### Funding: co-principal investigator

F14. “Acute Leukemia Translational Research Initiative.” OICR. CAD 9,743,920. 2017–2021.

F13. “Deciphering and manipulating cell-specific regulatory network to produce therapeutic designer cells.” Medicine by Design. CAD 314,309. 2016–2019.

F12. “Regulatory network control of neural stem cells for endogenous repair.” Medicine by Design. CAD 3,053,789. 2016–2019.

### Funding: co-investigator

F21. “Phenomic liquid biopsy resource.” Canadian Cancer Society. CAD 125,000. 2022–2023.

F18. “Lung cancer early detection and classification using methylome analysis of plasma cell free DNA.” CIHR. CAD 995,264. 2019–2023.