WOUTER MEULEMAN, PhD

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Computational Biology | Regulatory Genomics | Epigenomics | Data Visualization | Machine Learning

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Principal Investigator and computational biology leader with a strong record of NIH funding (Genomic Innovator Award, R35 HG011317) and highly cited publications (*Nature*, *NEJM*, *Nature Genetics*, *Molecular Cell*). Research at the interface of regulatory genomics, large-scale data integration, and machine learning.

RESEARCH POSITIONS

Affiliate Associate Professor – University of Washington   2021 - present
Paul G. Allen School of Computer Science & Engineering, University of Washington, Seattle, WA USA
Collaborative research and teaching activities with UW researchers in genomics and systems biology.

Principal Investigator (PI) – Altius Institute for Biomedical Sciences   2016 - 2025
Altius Institute for Biomedical Sciences, Seattle, WA USA

- Core institute leadership and founding faculty member with independent research program.
- Mentored 25+ researchers over tenure (10 at post-PhD level) in computational and experimental sciences.
- Research program pillars: (i) comprehensive annotation of the human regulatory genome, (ii) data-driven design of synthetic regulatory elements, (iii) machine-assisted augmentation of the scientific process.
- Collaborations with Stanford (Anshul Kundaje), MIT (Manolis Kellis, Carles Boix), Harvard (Luca Pinello, Nils Gehlenborg), University of Washington (Georg Seelig), among others.

Postdoctoral Associate – Massachusetts Institute of Technology   2012 - 2016
Massachusetts Institute of Technology & Broad Institute of MIT and Harvard, Cambridge, MA USA
Research in computational biology in general and regulatory genomics in particular.

- **Advisor:** Prof. Manolis Kellis, MIT
- Lead scientist and data coordinator for the integrative analysis of the NIH Common Fund's Roadmap Epigenomics Program, resulting in widely-used reference maps published in Nature (6900+ citations).
- Research collaborations with Harvard University, Massachusetts General Hospital (Brad Bernstein), Dana Farber Cancer Institute (Guo-Cheng Yuan), Washington University (Ting Wang)
- Supervised 15+ students at undergraduate and graduate levels during thesis, rotation and class projects. Taught classes on three-dimensional genome organization to undergraduate and graduate MIT students.

PhD Researcher – Netherlands Cancer Institute   2005 - 2012
Netherlands Cancer Institute, Amsterdam & Delft University of Technology, Delft, the Netherlands

- **Thesis:** *Computational Biology in Clinical Proteomics and Chromatin Genomics*
- **Advisors:** Prof. Bas van Steensel, Prof. Marcel Reinders & Prof. Lodewyk Wessels
- Co-discovered and characterized Lamina Associated Domains (LADs) in human and mouse. Analyzed dynamics of LADs during stem cell differentiation, performed comparative studies between human and mouse, and developed models for predicting LADs from DNA sequence features.
- Developed methods for the analysis of mass spectrometry data, including a systematic comparison of normalization methods and an improved method for peak detection and quantification.

EDUCATION

PhD in Computational Biology – Delft University of Technology   2012
Delft University of Technology, Delft & Netherlands Cancer Institute, Amsterdam, the Netherlands
- **Thesis:** *Computational Biology in Clinical Proteomics and Chromatin Genomics*
- **Advisors:** Prof. Bas van Steensel, Prof. Marcel Reinders & Prof. Lodewyk Wessels

MSc in Computer Science – Leiden University   2005
Leiden Institute of Advanced Computer Science, Leiden University, Leiden, the Netherlands
- **Thesis:** *Integration and analysis of zebrafish microarray data*
- MSc thesis work performed at the Sanger Institute, Hinxton, and Brunel University, London, UK.
- Major in Computer Science, Minor in Molecular Biology. Awarded *met genoegen* (with distinction).

BSc in Computer Science – The Hague University   2002
The Hague University of Applied Sciences, The Hague, the Netherlands
- **Thesis:** *Application of high-speed Linux clusters to bioinformatics problems*
- BSc thesis work performed at the University of Cambridge, UK. Awarded 10 out of 10.

HONORS and AWARDS

2020-5   **NIH Genomic Innovator Award**, regarding the elucidation of the organizing principles of the regulatory genome through large-scale data integration (R35 HG011317-01, $300k direct/year, 5 years)

2015   Best talk prize at International Human Epigenome Consortium annual meeting, Tokyo, Japan

2015   Best poster prize at Broad Institute CBBO retreat, Cambridge, MA

2014   Contributed to a successfully funded R01 grant regarding the post-GWAS interpretation of genetic variants using epigenomic reference maps (HG008155-01, $499k direct/year)

2014   Co-wrote a funded R01 grant regarding epigenomic comparison and clustering, predicting the three-dimensional genome organization and gene-enhancer linking (GM113708-01, $250k direct/year).

2014   Best poster prize at Broad Institute retreat, Boston, MA

2011   Best poster prize at Netherlands Bioinformatics Centre (NBIC) conference

2010   EMBO Short Term Fellowship to visit lab of Manolis Kellis at MIT

2010   Best poster prize at ISMB student council conference, Boston, MA

2003-   Various fellowships for attending (inter)national conferences

PROFESSIONAL SERVICE

- Reviewer for Nature journals, Molecular Systems Biology, Genome Biology, BMC journals, and major bioinformatics conferences (RECOMB, ISMB)
- Grant reviewer for NIH; Expert Member of FWO Review College (Belgian national funding, 2021-2023)
- Program committee: ISMB, RSGDREAM; Organizing committee: ENCODE Users meeting (2016)
- PhD committee member, University of Washington (ongoing)
- Member of five MSc thesis committees, Delft University of Technology

PATENTS

- Analyzing characteristics of genomic regions of a genome (2016, US11195596B2).
- Methods of analyzing microscopy images using machine learning (2018, US12322101B2).

TEACHING EXPERIENCE

2021-2 **Co-organizer**, University of Washington, CSE590C Reading & Research in Computational Biology.

2018 **Guest lecturer**, Cold Spring Harbor Laboratory, "Chromatin, Epigenetics and Gene Expression"

2012-6 **Guest lecturer**, MIT, "Computational Biology" (6.047/6.878/HST.507). Lectured on genome organization to 50+ students.

2015 **Lecturer**, MIT Educational Studies Program. Organization of DNA to 70 middle school students.

2015 **Kaufman Teaching Certificate Program**, MIT. Completed program in course design and pedagogy.

2010-1 **Guest lecturer**, Delft University of Technology, "Genome-scale data analysis"

2010-1 **Course co-designer and instructor**, Netherlands Cancer Institute, "R and statistics for Biologists"

2008 **Instructor**, Delft University of Technology, "Bioinformatics" (ASCI graduate curriculum)

2004 **Teaching Assistant**, Leiden University, "Computer architecture"

2003-4 **Member of Curriculum Committee**, Leiden University

INVITED TALKS

2025 ENCODE Consortium coordination meeting (virtual)

2021 Rocky 2021 conference (**keynote**); Duke University (**student invited**); University of Colorado; University of Washington

2020 ENCODE Research Applications meeting; Mathematical Frameworks for Integrative Analysis (BIRS)

2019 Pacific Symposium on Biocomputing, Big Island of Hawai'i, HI

2018 "Chromatin, Epigenetics and Gene Expression course", CSHL, Cold Spring Harbor, NY

2018 Panels on career development, ENCODE Consortium meeting, Palo Alto, CA

2016 Ludwig Maximilian University, Munich; Utrecht University; Vertex Pharmaceuticals; f-Tales, Ghent (**keynote**); Roadmap Epigenomics Workshop, Puerto Rico

2015 International Human Epigenome Consortium, Tokyo; BroadE Workshop, Broad Institute; UMASS Medical School; Roadmap Epigenomics, Keystone; Festival of Genomics, Boston

2013 Delft University of Technology, Delft, the Netherlands

2013 Translating Epigenomes into Function: a Next Generation Challenge for Human Disease, Capri, Italy

2011 Massachusetts Institute of Technology, Cambridge, MA

2011 Harvard University, Boston; Columbia University, New York; UMASS Medical School, Worcester

2010 Utrecht University, Utrecht, the Netherlands

2009 Radboud University Nijmegen Medical Centre, Nijmegen, the Netherlands

2006 Clinical proteomics symposium, Utrecht, the Netherlands

SELECTED PUBLICATIONS (h-index: 22)

- L.F. DaSilva, S. Senan, J.F. Kribelbauer-Swietek, . . . , <u>W. Meuleman</u>, L. Pinello – Designing synthetic regulatory elements using the generative AI framework DNA-Diffusion, **Nature Genetics** (2025, accepted)

- S.M. Castillo-Hair, C. Yin, L. VandenBosch, T.J. Cherry, <u>W. Meuleman</u>, Georg Seelig – Programming human cell type-specific gene expression via an atlas of AI-designed enhancers, **bioRxiv** (2025)

- C. Yin, S. Castillo-Hair, . . . , <u>W. Meuleman</u>[†], G. Seelig[†] – Iterative deep learning-design of human enhancers exploits condensed sequence grammar to achieve cell type-specificity, **Cell Systems** (2025)

- J. Quon, A. Reynolds, N. Tripician, E. Rynes, A. Teodosiadis, M. Kellis, <u>W. Meuleman</u>[†] – Epilogos: information-theoretic navigation of multi-tissue functional genomic annotations, **bioRxiv** (2025)

- A. Kundaje[†], W. Meuleman[†] – Automated sequence-based annotation and interpretation of the human genome, **Nature Genetics** (2022).

- M. Wainberg, R.A. Kamber, . . . , W. Meuleman, M.P. Snyder, M.C. Bassik, A. Kundaje – A genome-wide atlas of co-essential modules assigns function to uncharacterized genes, **Nature Genetics** (2021).

- C.A. Boix, B.T. James, Y.P. Park, W. Meuleman, M. Kellis – Regulatory genomic circuitry of human disease loci by integrative epigenomics, **Nature** (2021). **400+ citations**.

- W. Meuleman[†], A. Muratov, E. Rynes, . . . , R. Sandstrom, J. Vierstra, R. Kaul, J.A. Stamatoyannopoulos[†] – Index and biological spectrum of human DNase I hypersensitive sites, **Nature** (2020). **370+ citations**.

- J. Vierstra, J. Lazar, R. Sandstrom, J. Halow, . . . , R. Kaul, W. Meuleman, J.A. Stamatoyannopoulos – Global reference mapping of human transcription factor footprints, **Nature** (2020). **390+ citations**.

- The ENCODE Project Consortium – Expanded encyclopaedias of DNA elements in the human and mouse genomes, **Nature** (2020). **1900+ citations**.

- C.E. Breeze, J. Lazar, T. Mercer, . . . , W. Meuleman, M.A. Bender, M. Groudine, J.A. Stamatoyannopoulos – Atlas and developmental dynamics of mouse DNase I hypersensitive sites, **bioRxiv** (2020)

- H.J.G. van de Werken, . . . , W. Meuleman, . . . , W. de Laat, I. Solovei, B. Joffe – Small chromosomal regions position themselves autonomously according to their chromatin class, **Genome Research** (2017).

- E. Marco*, W. Meuleman*, J. Huang*, K. Glass, L. Pinello, J. Wang, M. Kellis, G.C. Yuan – Multi-scale chromatin state annotation using a hierarchical hidden Markov model, **Nature communications** (2017).

- A. Kundaje*, W. Meuleman*, J. Ernst*, M. Bilenky*, . . . , B. Ren, J. Stamatoyannopoulos, T. Wang, M. Kellis – Integrative analysis of 111 reference human epigenomes, **Nature** (2015). **6900+ citations**.

- M. Claussnitzer, S.N. Dankel, K-H. Kim, G. Quon, W. Meuleman, . . . , M. Kellis – FTO obesity variant circuitry and adipocyte browning in humans, **New England Journal of Medicine** (2015). **1600+ citations**.

- W. Akhtar, J. de Jong, A.V. Pindyurin, L. Pagie, W. Meuleman, . . . , B. van Steensel – Chromatin position effects assayed by thousands of reporters integrated in parallel, **Cell** (2013). **390+ citations**.

- W. Meuleman*, D. Peric-Hupkes*, . . . , B. van Steensel – Constitutive nuclear lamina-genome interactions are highly conserved and associated with A/T-rich sequence, **Genome Research** (2013). **540+ citations**.

- N. Kubben, M. Adriaens, W. Meuleman, J.W. Voncken, B. van Steensel, T. Misteli – Mapping of lamin A-and progerin-interacting genome regions, **Chromosoma** (2012).

- D. Peric-Hupkes*, W. Meuleman*, . . . , B. van Steensel – Molecular maps of the reorganization of genome – nuclear lamina interactions during differentiation, **Molecular Cell** (2010). **1200+ citations**.

- J. van Bemmel, L. Pagie, . . . , W. Meuleman, R. Kerkhoven, B. van Steensel – The insulator protein SU(HW) fine-tunes nuclear lamina interactions of the *Drosophila* genome, **PLoS One** (2010).

- W. Meuleman, J.Y.M.N Engwegen, M.C. Gast, L.F.A. Wessels, M.J.T. Reinders – Analysis of mass spectrometry data using sub-spectra, **BMC Bioinformatics** (2009).

- L. Guelen, L. Pagie, E. Brasset, W. Meuleman, . . . , B. van Steensel – Domain organization of human chromosomes revealed by mapping of nuclear lamina interactions, **Nature** (2008). **2300+ citations**.

- W. Meuleman, *et al.* – Comparison of normalisation methods for surface-enhanced laser desorption and ionisation (SELDI) time-of-flight (TOF) mass spectrometry data, **BMC Bioinformatics** (2008).

- M. van Uitert, W. Meuleman, L.F.A. Wessels – Biclustering Sparse Binary Genomic Data, **Journal of Computational Biology** (2008).

- W. Meuleman, M. Welten, F. Verbeek – Correlation networks with explicit time-slices using time-lagged, variable interval standard and partial correlation coefficients, **Lecture Notes in Bioinformatics** (2006).

    *: equal contributions; [†]: (co-)corresponding authors