

# WOUTER MEULEMAN

Altius Institute for Biomedical Sciences  
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Principal Investigator in Computational Biology, with independent NIH funding and high-impact well-cited papers. Long term research goal is to make "augmented genomics" a reality: a new field in which the work of genome scientists is supplemented – not replaced! – by large-scale visualization and data-driven machine intelligence.

## RESEARCH POSITIONS

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### **Affiliate Associate Professor – University of Washington** **2021 - present**

Paul G. Allen School of Computer Science & Engineering, University of Washington, Seattle, WA USA

### **Principal Investigator (PI) – Altius Institute** **2016 - present**

Altius Institute for Biomedical Sciences, Seattle, WA USA

- Core institute leadership and founding faculty member
- Mentored and supervised 12+ FTEs (4 PhDs) in computational and experimental sciences.
- Set up infrastructure for machine learning in Biology, incl. human and computational resources.
- Research collaborations with Stanford (Anshul Kundaje), MIT (Manolis Kellis, Carles Boix), Harvard University (Nils Gehlenborg), University of Washington (Georg Seelig), Oregon State University (Cory Simon)

Research program centered on large-scale integrative analysis of genomics data:

- Comprehensive annotation of the human regulatory genome
- Data-driven design of synthetic regulatory elements
- Machine-assisted augmentation of the scientific process

### **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 (4400+ 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

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### **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

### **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.

## TEACHING EXPERIENCE

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**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”  
Interactive two-hour lecture on genome organization, chromatin states and gene regulation.

**2012-6 Guest lecturer**, Massachusetts Institute of Technology

Course: “Computational Biology: Genomes, Networks, Evolution” (6.047/6.878/HST.507)

Lectured on the three-dimensional organization of the human genome to classes of 50 MIT students.

**2015 Lecturer**, Massachusetts Institute of Technology, Educational Studies Program (ESP)

Taught a class on the cellular organization of DNA to a group of 70 middle school students.

**2015 Kaufman Teaching Certificate Program**, Massachusetts Institute of Technology

Successfully completed program, gaining skills in course design, lesson plan preparation, assessing and providing feedback to students & creating an effective classroom climate.

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

Lectured on clinical biomarker discovery using mass spectrometry and machine learning, and three-dimensional organization of the human genome, to classes of 30 graduate students.

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

Developed and led hands-on training to wet-lab biologists on data pre-processing, differential gene expression analysis, transcription factor binding site analysis and gene set enrichment.

**2005-9 Member of five MSc thesis committees**, Delft University of Technology

**2008 Instructor**, Delft University of Technology

Course: “Bioinformatics”, as part of the ASCI graduate school curriculum. Design and instruction of the lab section dealing with sequence analysis and transcription factor binding site discovery.

**2004 Teaching Assistant**, Leiden University

Course: “Computer architecture”, as part of the core Computer Science curriculum. Leading and grading lab practicals regarding the design and implementation of central processing unit (CPU) simulators.

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

## HONORS and AWARDS

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- 2020 Genomic Innovator Award**, regarding the elucidation of the organizing principles of the regulatory genome through large-scale data integration (NIH 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

## INVITED TALKS

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- 2021** Rocky 2021 conference, Snowmass, CO (**keynote**)
- 2021** Duke University, Center for Genomic and Computational Biology (virtual, **student invited**)
- 2021** University of Colorado, Anschutz Medical Campus, Center for Health AI (virtual)
- 2021** University of Washington, CS & Engineering seminar (virtual)
- 2020** ENCODE 2020 Research Applications & Users meeting (virtual)
- 2020** Mathematical Frameworks for Integrative Analysis of Emerging Biological Data Types (BIRS, virtual)
- 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, Germany
- 2016** Utrecht University, Utrecht, the Netherlands
- 2016** Vertex Pharmaceuticals, Boston, MA
- 2016** f-Tales "Light on the dark side of the genome", Ghent, Belgium (**keynote** and workshop)
- 2016** Roadmap Epigenomics Workshop, Epigenomics 2016, Puerto Rico
- 2015** International Human Epigenome Consortium annual meeting, Tokyo, Japan
- 2015** BroadE Workshop: Strategies for Visualizing Data, Broad Institute, Cambridge, MA
- 2015** UMASS Medical School, Worcester, MA
- 2015** Roadmap Epigenomics Workshop, Keystone meeting on Epigenomics, Keystone, CO
- 2015** Panel on Data Sharing and Standardization, Festival of Genomics, Boston, MA
- 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** UMASS Medical School, Worcester, MA
- 2011** Harvard University, Boston, MA
- 2011** Columbia University, New York, NY
- 2010** Utrecht University, Utrecht, the Netherlands
- 2009** Radboud University Nijmegen Medical Centre, Nijmegen, the Netherlands
- 2006** Clinical proteomics symposium, Utrecht, the Netherlands

## PROFESSIONAL SERVICE

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- Reviewer for Nature Genetics, Nature Structural and Molecular Biology, Nature Scientific Reports, Nature Communications, Molecular Systems Biology, Proteomics, Chromosome Research, RECOMB conference, BMC Biology, BMC Bioinformatics, BMC Microbiology, Cancer informatics, ISMB conference, PeerJ, Genome Biology.
- Program committee member for Intelligent Systems for Molecular Biology (ISMB), Regulatory and Systems Genomics Conference with DREAM Challenges (RSGDREAM).
- Steering committee member for Set Visualization and Reasoning (SetVR).
- Expert Member of the FWO Review College (Belgian national science funding agency, years 2021-2023).
- Organizing committee of the ENCODE Users meeting, Stanford University, 2016.

## PUBLICATIONS

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- M. Wainberg, R.A. Kamber, A. Balsubramani, R.M. Meyers, N. Sinnott-Armstrong, D. Hornburg, L. Jiang, J. Chan, R. Jian, M. Gu, A. Shcherbina, M.M. Dubreuil, K. Spees, 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**, Vol. 53, pp. 638–649 (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**, Vol. 590, pp. 300–307 (2021).
- W. Meuleman<sup>†</sup>, A. Muratov, E. Rynes, J. Halow, K. Lee, D. Bates, M. Diegel, D. Dunn, J. Neri, A. Teodosiadis, A. Reynolds, E. Haugen, J.S. Nelson, A. Johnson, M. Frerker, M. Buckley, R. Sandstrom, J. Vierstra, R. Kaul, J.A. Stamatoyannopoulos<sup>†</sup> – Index and biological spectrum of human DNase I hypersensitive sites, **Nature**, Vol. 584, pp. 244–251 (2020).
- J. Vierstra, J. Lazar, R. Sandstrom, J. Halow, K. Lee, D. Bates, M. Diegel, D. Dunn, F. Neri, E. Haugen, E. Rynes, A. Reynolds, J. Nelson, A. Johnson, M. Frerker, M. Buckley, R. Kaul, W. Meuleman, J.A. Stamatoyannopoulos – Global reference mapping of human transcription factor footprints, **Nature**, Vol. 583, pp. 729–736 (2020).
- C.E. Breeze, J. Lazar, T. Mercer, J. Halow, I. Washington, K. Lee, S. Ibarrientos, A. Castillo, F. Neri, E. Haugen, E. Rynes, A. Reynolds, D. Bates, M. Diegel, D. Dunn, R. Kaul, R. Sandstrom, 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, J.C. Haan, Y. Feodorova, D. Bijos, A. Weuts, K. Theunis, S.J.B. Holwerda, W. Meuleman, L. Pagie, K. Thanisch, P. Kumar, H. Leonhardt, P. Marynen, B. van Steensel, T. Voet, W. de Laat, I. Solovei, B. Joffe – Small chromosomal regions position themselves autonomously according to their chromatin class, **Genome Research**, Vol. 27 No. 6, pp. 922–933 (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**, Vol. 8, No. 15011 (2017).
- H.J.G. van de Werken, J.C. de Haan, Y. Feodorova, D. Bijos, A. Weuts, K. Theunis, S. Holwerda, W. Meuleman, L. Pagie, K. Thanisch, P. Kumar, H. Leonhardt, P. Marynen, B. van Steensel, T. Voet, W. de Laat, I. Solovei, B. Joffe – Small chromosomal regions position themselves autonomously according to their chromatin class, **Genome Research**, Vol. 27, pp. 922–933 (2017).
- A. Kundaje\*, W. Meuleman\*, J. Ernst\*, M. Bilenky\*, *et al.* (248 authors) – Integrative analysis of 111 reference human epigenomes, **Nature**, Vol. 518, No. 7539, pp. 317–330 (2015). **4400+ citations.**
- M. Claussnitzer, S.N. Dankel, K-H. Kim, G. Quon, W. Meuleman, C. Haugen, V. Glunk, I.S. Sousa, J.L. Beaudry, V. Puvion-Randall, N.A. Abdennur, J. Liu, P-A. Svensson, Y-H. Hsu, D.J. Drucker, G. Mellgren, C-C. Hui, H. Hauner, M. Kellis – FTO obesity variant circuitry and adipocyte browning in humans, **New England Journal of Medicine**, Vol. 373, No. 10 (2015). **1000+ citations.**

- R.A.H. van de Ven, M. Tenhagen\*, W. Meuleman\*, J.J.G. van Riel, R.C.J. Schackmann, P.W.B. Derksen – Nuclear p120-catenin regulates the anoikis resistance of mouse lobular breast cancer cells through Kaiso-dependent Wnt11 expression, **Disease models & mechanisms**, Vol. 8, No. 4 (2015).
- W. Akhtar, J. de Jong, A.V. Pindyurin, L. Pagie, W. Meuleman, J. de Ridder, A. Berns, L.F.A. Wessels, M. van Lohuizen, B. van Steensel – Chromatin position effects assayed by thousands of reporters integrated in parallel, **CELL**, Vol. 154, No. 4 (2013). **250+ citations**
- W. Meuleman\*, D. Peric-Hupkes\*, J. Kind, J.B. Beaudry, L. Pagie, M. Kellis, M.J.T. Reinders, L.F.A. Wessels, B. van Steensel – Constitutive nuclear lamina-genome interactions are highly conserved and associated with A/T-rich sequence, **Genome Research**, Vol. 23, No. 2, pp. 270–280 (2013). **350+ citations**.
- W. Meuleman, Computational Biology in Clinical Proteomics and Chromatin Genomics – PhD thesis (2012).
- N. Kubben, M. Adriaens, W. Meuleman, J.W. Voncken, B. van Steensel, T. Misteli – Mapping of lamin A-and progerin-interacting genome regions, **Chromosoma**, Vol. 121, No. 5 (2012).
- D. Peric-Hupkes\*, W. Meuleman\*, L. Pagie, S. Bruggeman, I. Solovei, W. Brugman, S. Gräf, P. Flicek, R. Kerkhoven, M. van Lohuizen, M.J.T. Reinders, L.F.A. Wessels, B. van Steensel – Molecular maps of the reorganization of genome – nuclear lamina interactions during differentiation, **Molecular Cell**, Vol. 38, No. 4, pp. 603–613 (2010). **900+ citations**.
- J. van Bommel, L. Pagie, U. Braunschweig, W. Brugman, W. Meuleman, R. Kerkhoven, B. van Steensel – The insulator protein SU(HW) fine-tunes nuclear lamina interactions of the *Drosophila* genome, **PLoS One**, Vol. 5, No. 11, pp. e15013 (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**, Vol. 10 Suppl 1, No. S51 (2009).
- L. Guelen, L. Pagie, E. Brassat, W. Meuleman, M.B. Faza, W. Talhout, B.H. Eussen, A. de Klein, L.F.A. Wessels, W. de Laat, B. van Steensel – Domain organization of human chromosomes revealed by mapping of nuclear lamina interactions, **Nature**, Vol. 453, pp. 948–951 (2008). **1800+ citations**.
- W. Meuleman, J.Y.M.N. Engwegen, M.C. Gast, J.H. Beijnen, M.J.T. Reinders, L.F.A. Wessels – Comparison of normalisation methods for surface-enhanced laser desorption and ionisation (SELDI) time-of-flight (TOF) mass spectrometry data, **BMC Bioinformatics**, Vol. 9, No. 88 (2008).
- M. van Uiter, W. Meuleman, L.F.A. Wessels – Biclustering Sparse Binary Genomic Data, **Journal of Computational Biology**, Vol. 15, pp. 1329–1345 (2008).
- J.Y.M.N. Engwegen, A.C.T.M. Depla, M.E. Smits, A. Cats, H. Tuynman, H.A. van Heukelem, P. Snel, W. Meuleman, L.F.A. Wessels, J.H.M. Schellens, J.H. Beijnen – Detection of colorectal cancer by serum and tissue protein profiling: a prospective study in a population at risk, **Biomarker insights**, Vol. 3 (2008).
- W. Meuleman, M. Welten, F. Verbeek – Construction of correlation networks with explicit time-slices using time-lagged, variable interval standard and partial correlation coefficients, Computational Life Sciences II: Second International Symposium CompLife 2006, Cambridge (UK), **Lecture Notes in Bioinformatics**, Vol. 4216, pp. 236–246 (2006).

\*: equal contributions

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