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## Education and Employment

- **2016-2017** Postdoctoral fellow, Noble lab, University of Washington
- **2011–2016** PhD, University of Washington  
Department of Computer Science and Engineering  
Advisors: William S. Noble and Jeffrey A. Bilmes
- **Summer 2011** Software engineer, DNAnexus, Palo Alto.
- **2007–2011** B.S., Stanford University  
Department of Computer Science; Theory focus  
Research advisor: Serafim Batzoglou

## Awards

- Libbrecht et al, *Genome Research* 2015 “Joint annotation of . . .”, named one of ISCB’s Top 10 Regulatory and Systems Genomics papers of 2015 (<https://goo.gl/CWoJtC>).
- Microsoft Research Machine Learning day 2015 2nd place poster prize (\$10,000 in compute credits). *Out of 28 posters.*
- Genome Training Grant 2012-2014 (tuition and stipend, two years). *Awarded to nine PhD students doing genomics-related research at UW each year.*
- NSF Graduate Research Fellowship honorable mention 2013. *Awarded to 1,700 students nationally in all fields in 2013.*
- Achievement Awards for College Scientists award 2011 (\$17,500 stipend bonus over three years). *Awarded to 25 PhD students in all fields at UW and WashU in 2011.*

- Anne Dinning—Michael Wolf Endowed Regental Fellowship in Computer Science and Engineering 2011-2012 (Tuition and stipend, one year). *Awarded to one UW CSE graduate student each year.*
- Putnam Math Competition — 2008: national rank #221. 2009: national rank #818. 2011: national rank #342. *~4,000 undergraduate entrants nationally each year*

## Research interests

- **Computational biology:** genomics, unsupervised genome annotation, chromatin state, chromatin conformation and 3D structure, replication timing, single cell genomics.
- **Machine learning and big data:** dynamic Bayesian networks, unsupervised methods, convex optimization, submodularity.

## Publications

1. **Maxwell W. Libbrecht\***, Oscar Rodriguez\* (\*contributed equally), Jeffrey A. Bilmes, Zhiping Weng, William S. Noble. “A unified encyclopedia of human functional elements through fully automated annotation of 164 human cell types.” *Submitted*. Preprint at <http://dx.doi.org/10.1101/086025>.
2. **Maxwell W. Libbrecht**, Jeffrey A. Bilmes, William S. Noble. “Eliminating redundancy among protein sequences using submodular optimization.” *Submitted*. Preprint at <http://dx.doi.org/10.1101/051201>.
3. Kai Wei\*, **Maxwell W. Libbrecht\*** (\*contributed equally), Jeffrey A Bilmes, William S. Noble. “Choosing panels of genomics assays using submodular optimization.” *Genome Biology*, In press. Preprint at <http://dx.doi.org/10.1101/036137>.
4. Owen K. Smith, RyanGuk Kim, Haiqing Fu, Melvenia Martin, Chii-Mei Lin, Koichi Utani, Marc Lalande, Stormy Chamberlaine, **Maxwell W. Libbrecht**, Eric E Bouhassira, Michael C Ryan, William S. Noble, Mirit I. Aladjem. “Distinct epigenetic features of differentiation-Regulated Replication Origins.” *Epigenetics Chromatin*, 2016; 9: 18.
5. **Maxwell W. Libbrecht**, William S. Noble. “Machine learning applications in genetics and genomics.” *Nature Reviews Genetics*, 16: 321-332, 2015. **48 citations (Google Scholar). 14,841 downloads.**  
**Cover article.**



6. **Maxwell W. Libbrecht**, Michael Hoffman, Jeff Bilmes, William Stafford Noble. “Entropic graph-based posterior regularization.” *Proceedings of the International Conference on Machine Learning (ICML) 2015*.
7. **Maxwell W. Libbrecht**, Ferhat Ay, Michael M. Hoffman, David M. Gilbert, Jeffrey A. Bilmes, and William S. Noble “Joint annotation of chromatin state and chromatin conformation reveals relationships among domain types and identifies domains of cell-type-specific expression.” *Genome Research*, 25: 544-557, 2015. **Named one of ISCB’s Top 10 Regulatory and Systems Genomics papers of 2015** (<https://goo.gl/CWoJtC>).

8. Ho *et al* (**Maxwell W. Libbrecht** author #49). “Comparative analysis of metazoan chromatin architecture.” *Nature*, 512, 449-452, 2014.
9. Michael M. Hoffman\*, Jason Ernst\* (\*contributed equally), Steven P. Wilder, Anshul Kundaje, Robert S. Harris, **Max W. Libbrecht**, Belinda Giardine, Jeffrey A. Bilmes, Ewan Birney, Ross C. Hardison, Ian Dunham, Manolis Kellis, and William Stafford Noble. “Integrative annotation of chromatin elements from ENCODE data.” *Nucleic Acids Research*, 41(2):827–841, 2013. **Featured article. 179 citations (Google Scholar)**.
10. Anshul Kundaje\*, Sofia Kyriazopoulou-Panagiotopoulou\*, **Max W. Libbrecht\*** (\*contributed equally), Serafim Batzoglou, Arend Sidow “Ubiquitous heterogeneity and asymmetry of the chromatin landscape at transcription regulatory elements.” *Genome Research*, 22(9):1735-1747, 2012. **95 citations (Google Scholar)**.
11. ENCODE Project Consortium. “An integrated encyclopedia of DNA elements in the human genome.” *Nature*, 489(7414):57-74, 2012. **4403 citations (Google Scholar) Cover article..**



12. The ENCODE Project Consortium. “A Users Guide to the Encyclopedia of DNA Elements (ENCODE) Functional Genomic Data.” *PLoS Biology*, vol. 9, issue 4, e1001046, 2011.
13. Kenneth Libbrecht, **Max Libbrecht**. “Interferometric measurement of the resonant absorption and refractive index in rubidium gases.” *American Journal of Physics*, 74:1055, 2006.

## Teaching

- **2015, 2016.** Instructor for one two-week unit of Genome 541, “Gene regulation and epigenomics”.
- **2015.** Teaching Assistant for Genome 540, “Computational Molecular Biology”.

## Professional activities

- Program committee member: International Conference on Machine Learning 2016.
- Referee for (number of reviews parenthesized): Nature Methods (1), Nature Scientific Reports (1), Genome Research (2), Genome Biology (1), Nucleic Acids Research (1), Journal of Machine Learning Research (JMLR; 1), Neural Information Processing Systems (NIPS; 5), Uncertainty in Artificial Intelligence (UAI; 5), International Conference on Machine Learning (ICML; 8), Research in Computational Biology (RECOMB; 1), Intelligent Systems for Molecular Biology (ISMB; 1), Association for the Advancement of Artificial Intelligence (AAAI; 3), IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB; 1), Data (1), Pacific Symposium on Biocomputing (PSB; 1)
- Reviewed applications for UW CSE graduate admissions for the entering classes of 2014, 2015 and 2016.

## Invited talks

- ENCODE User’s Meeting. Stanford, CA, June 2016. “Storing and analyzing genomics signal data sets with Genomdata, Segway and Segtools”.
- International Conference on Machine Learning (ICML). Lille, France July 2015. “Entropic Graph-based Posterior Regularization”. Video available at [http://videlectures.net/icml2015\\_libbrecht\\_posterior\\_regularization/](http://videlectures.net/icml2015_libbrecht_posterior_regularization/).
- ENCODE Consortium meeting. Cold Spring Harbor, March 2015. “Joint annotation of chromatin state and chromatin conformation reveals relationships among domain types and identifies domains of cell type-specific expression”.
- Intelligent Systems for Molecular Biology (ISMB) Late-Breaking Research talk. Boston, July 2014. “Genome annotation of multiple cell types and chromatin architecture using graph-based regularization”.
- ENCODE Analysis Working Group meeting. July 2014, Stanford. “Genome annotation of multiple cell types and chromatin architecture using graph-based regularization”.

## Student mentoring

- **Oscar Rodriguez**. Summer 2012 and Summer 2013–Summer 2014. Postbaccalaureate researcher. Project: “Curation of genomics data sets and semi-automated genome annotation on hundreds of human cell types”. Current position: PhD student, Genetics and Genomic Sciences, Icahn School of Medicine at Mount Sinai.
- **Timothy Durham**. Fall 2014 – current. Ph.D. student, Genome Sciences, University of Washington. Project: “Imputation of missing genomics data sets using singular value decomposition-based methods”.
- **Pascale Marie Wallace Patterson**. Fall 2014 – Spring 2016. Undergraduate, Computer Science and Engineering, University of Washington. Project: “Evaluation of entropic graph-based posterior regularization using synthetic data”.
- **Hasanthi Neti**. Fall 2014 – Winter 2016. Undergraduate, Computer Science and Engineering, University of Washington. Project: “Segway with graph-based regularization on the DNAnexus cloud platform”.
- **Kritin Vij**. Fall 2014 – Winter 2015. Undergraduate, Computer Science and Engineering, University of Washington. Project: “A modular interface to Segway that enables graph-based regularization”.
- **Jacob Schreiber**. Fall 2015 – current. PhD student, Computer Science and Engineering, University of Washington. Project “Understanding the influence of sequence on 3D chromatin architecture using deep neural networks”.
- **Zhexin Han** Winter 2016 – Spring 2016. Undergraduate, Computer Science and Engineering, University of Washington. Project: “Curating available genomics data sets”.
- **Shiqi Zou** Winter 2016 – Spring 2016. Undergraduate, Computer Science and Engineering, University of Washington. Project: “Semi-automated genome annotation using Gaussian mixture emission distributions.”
- **Michael Lee** Fall 2016 – current. Undergraduate, Computer Science and Engineering, University of Washington. Project: “Annotation of all human cell types with available data from ENCODE Phase 3”.

- **David Wadden** Fall 2016 – current. PhD student, Computer Science and Engineering, University of Washington. Project: “Detecting recently-acquired genomic functional elements using a supervised learning approach trained on genomics data”.