Maria Nattestad

Bioinformatics visualization software specialist

Genomics PhD with 8 years of bio + software industry experience specializing in building visualization tools to make sense of complex biological datasets. Danish citizen educated in the USA, moving back to Denmark with husband and two small kids.

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LinkedIn • GitHub • Portfolio • Google Scholar

Work experience

Co-founder

OMGenomics Labs

March 2024 — October 2025 SF Bay Area, USA

- Built Circa 2.0, genomics data visualization software using Svelte JS.
- Created bioinformatics technical tutorials on the OMGenomics YouTube channel.
- Revamped visualization web apps for genomic data: Ribbon and SplitThreader.

Senior Software Engineer

Google

June 2019 — Sept 2023 SF Bay Area, USA

- On the Genomics team in Google Research. Coding primarily in Python.
- Made software and model improvements to **DeepVariant** (video), which uses AI (a CNN) for calling small germline variants. Wrote explainer blog post.
- Worked on **DeepConsensus** (video), which uses a transformer model for correcting PacBio long-read sequencing data. Tech lead for release 0.3 (tweet) that enabled integration into PacBio's Revio instrument (Google Keyword blog).

Scientific Visualization Lead

DNAnexus

August 2017 — April 2019 SF Bay Area, USA

- Led a team of engineers to build a modular and configurable visualization dashboard for the UK Biobank (UKBB) exomes + health dataset.
- **Dot**: interactive dot plot viewer for genome assemblies.
- **BigTop:** (10% time group project) virtual reality 3D Manhattan Circos plot.

Founder

OMGenomics

Feb 2017 — August 2017 SF Bay Area, USA

- Circa: intuitive GUI software for creating circos plots for genomics.
- OMGenomics YouTube channel teaching bioinformatics.

Education

PhD in Genomics

Cold Spring Harbor Laboratory

Aug 2013 — Feb 2017 New York, USA

Thesis: “Computational methods for analysis and visualization of long-read sequencing data in cancer genomics”

Advisor: Michael C. Schatz

- Studied large and complex structural variants in the SK-BR-3 breast cancer cell line using PacBio sequencing. Paper in Genome Research.
- **Assemblytics**: assembly-based variant caller: assemblytics.com
- **SplitThreader**: interactive visualization with graph-search algorithms for the analysis of long-range variants and copy number: splitthreader.com
- **Ribbon**: visualization of complex structural variation, tailored for long-read sequencing data: genomeribbon.com

Bachelor of Science in Biological Sciences

University of the Pacific

Aug 2009 — May 2013 California, USA

Phi Beta Kappa. Summa Cum Laude. GPA 3.97.

Included 3 years undergraduate research in wet lab molecular biology.

Languages

English: Professional native-level fluency.

Danish: Native unprofessional 🙂fluency.

Interests

Reading non-fiction

Cooking Japanese food

Taking long walks to explore cities

Peer-reviewed publications

1. Accurate human genome analysis with Element Avidity sequencing
   Carroll A, Kolesnikov A, Cook DE, Brambrink L, Wiseman KN, Billings SM, Kruglyak S, Lajoie BR, Zhao J, Levy SE, McLean CY, Shafin K, **Nattestad M**, Chang PC.
   BMC Bioinformatics. 2025 Jul 25;26(1):194. doi: 10.1186/s12859-025-06191-4.
2. Highly accurate assembly polishing with DeepPolisher
   Mastoras M, Asri M, Brambrink L, Hebbar P, Kolesnikov A, Cook DE, **Nattestad M**, Lucas J, Won TS, Chang PC, Carroll A, Paten B, Shafin K; and the Human Pangenome Reference Consortium.
   Genome Res. 2025 Jul 1;35(7):1595-1608. doi: 10.1101/gr.280149.124.
3. Local read haplotagging enables accurate long-read small variant calling
   Kolesnikov A, Cook D, **Nattestad M**, Brambrink L, McNulty B, Gorzynski J, Goenka S, Ashley EA, Jain M, Miga KH, Paten B, Chang PC, Carroll A, Shafin K.
   Nat Commun. 2024 Jul 13;15(1):5907. doi: 10.1038/s41467-024-50079-5.
4. A draft human pangenome reference
   Liao WW, Asri M, Ebler J, Doerr D, Haukness M, Hickey G, Lu S, Lucas JK, Monlong J, Abel HJ, Buonaiuto S, Chang XH, Cheng H, Chu J, Colonna V, Eizenga JM, Feng X, Fischer C, Fulton RS, Garg S, Groza C, Guarracino A, Harvey WT, Heumos S, Howe K, Jain M, Lu TY, Markello C, Martin FJ, Mitchell MW, Munson KM, Mwaniki MN, Novak AM, Olsen HE, Pesout T, Porubsky D, Prins P, Sibbesen JA, Sirén J, Tomlinson C, Villani F, Vollger MR, Antonacci-Fulton LL, Baid G, Baker CA, Belyaeva A, Billis K, Carroll A, Chang PC, Cody S, Cook DE, Cook-Deegan RM, Cornejo OE, Diekhans M, Ebert P, Fairley S, Fedrigo O, Felsenfeld AL, Formenti G, Frankish A, Gao Y, Garrison NA, Giron CG, Green RE, Haggerty L, Hoekzema K, Hourlier T, Ji HP, Kenny EE, Koenig BA, Kolesnikov A, Korbel JO, Kordosky J, Koren S, Lee H, Lewis AP, Magalhães H, Marco-Sola S, Marijon P, McCartney A, McDaniel J, Mountcastle J, **Nattestad M**, Nurk S, Olson ND, Popejoy AB, Puiu D, Rautiainen M, Regier AA, Rhie A, Sacco S, Sanders AD, Schneider VA, Schultz BI, Shafin K, Smith MW, Sofia HJ, Abou Tayoun AN, Thibaud-Nissen F, Tricomi FF, et al.
   Nature. 2023 May;617(7960):312-324. doi: 10.1038/s41586-023-05896-x. Epub 2023 May 10.
5. DeepConsensus improves the accuracy of sequences with a gap-aware sequence transformer
   Baid G, Cook DE, Shafin K, Yun T, Llinares-López F, Berthet Q, Belyaeva A, Töpfer A, Wenger AM, Rowell WJ, Yang H, Kolesnikov A, Ammar W, Vert JP, Vaswani A, McLean CY, **Nattestad M**, Chang PC, Carroll A.
   Nat Biotechnol. 2023 Feb;41(2):232-238. doi: 10.1038/s41587-022-01435-7. Epub 2022 Sep 1.
6. Ultrarapid Nanopore Genome Sequencing in a Critical Care Setting
   Gorzynski JE, Goenka SD, Shafin K, Jensen TD, Fisk DG, Grove ME, Spiteri E, Pesout T, Monlong J, Baid G, Bernstein JA, Ceresnak S, Chang PC, Christle JW, Chubb H, Dalton KP, Dunn K, Garalde DR, Guillory J, Knowles JW, Kolesnikov A, Ma M, Moscarello T, **Nattestad M**, Perez M, Ruzhnikov MRZ, Samadi M, Setia A, Wright C, Wusthoff CJ, Xiong K, Zhu T, Jain M, Sedlazeck FJ, Carroll A, Paten B, Ashley EA.
   N Engl J Med. 2022 Feb 17;386(7):700-702. doi: 10.1056/NEJMc2112090. Epub 2022 Jan 12.
7. Accelerated identification of disease-causing variants with ultra-rapid nanopore genome sequencing
   Goenka SD, Gorzynski JE, Shafin K, Fisk DG, Pesout T, Jensen TD, Monlong J, Chang PC, Baid G, Bernstein JA, Christle JW, Dalton KP, Garalde DR, Grove ME, Guillory J, Kolesnikov A, **Nattestad M**, Ruzhnikov MRZ, Samadi M, Sethia A, Spiteri E, Wright CJ, Xiong K, Zhu T, Jain M, Sedlazeck FJ, Carroll A, Paten B, Ashley EA.
   Nat Biotechnol. 2022 Jul;40(7):1035-1041. doi: 10.1038/s41587-022-01221-5. Epub 2022 Mar 28.
8. PrecisionFDA Truth Challenge V2: Calling variants from short and long reads in difficult-to-map regions
   Olson ND, Wagner J, McDaniel J, Stephens SH, Westreich ST, Prasanna AG, Johanson E, Boja E, Maier EJ, Serang O, Jáspez D, Lorenzo-Salazar JM, Muñoz-Barrera A, Rubio-Rodríguez LA, Flores C, Kyriakidis K, Malousi A, Shafin K, Pesout T, Jain M, Paten B, Chang PC, Kolesnikov A, **Nattestad M**, Baid G, Goel S, Yang H, Carroll A, Eveleigh R, Bourgey M, Bourque G, Li G, Ma C, Tang L, Du Y, Zhang S, Morata J, Tonda R, Parra G, Trotta JR, Brueffer C, Demirkaya-Budak S, Kabakci-Zorlu D, Turgut D, Kalay Ö, Budak G, Narcı K, Arslan E, Brown R, Johnson IJ, Dolgoborodov A, Semenyuk V, Jain A, Tetikol HS, Jain V, Ruehle M, Lajoie B, Roddey C, Catreux S, Mehio R, Ahsan MU, Liu Q, Wang K, Sahraeian SME, Fang LT, Mohiyuddin M, Hung C, Jain C, Feng H, Li Z, Chen L, Sedlazeck FJ, Zook JM.
   Cell Genom. 2022 May 11;2(5):100129. doi: 10.1016/j.xgen.2022.100129. Epub 2022 Apr 27.
9. Haplotype-aware variant calling with PEPPER-Margin-DeepVariant enables high accuracy in nanopore long-reads

Shafin K, Pesout T, Chang PC, **Nattestad M**, Kolesnikov A, Goel S, Baid G, Kolmogorov M, Eizenga JM, Miga KH, Carnevali P, Jain M, Carroll A, Paten B.
Nat Methods. 2021 Nov;18(11):1322-1332. doi: 10.1038/s41592-021-01299-w. Epub 2021 Nov 1.

10. Ribbon: intuitive visualization for complex genomic variation
Nattestad M, Aboukhalil R, Chin CS, Schatz MC.
Bioinformatics. 2021 Apr 20;37(3):413-415. doi: 10.1093/bioinformatics/btaa680.
11. BigTop: a three-dimensional virtual reality tool for GWAS visualization
Westreich ST, **Nattestad M**, Meyer C.
BMC Bioinformatics. 2020 Jan 31;21(1):39. doi: 10.1186/s12859-020-3373-5.
12. Complex rearrangements and oncogene amplifications revealed by long-read DNA and RNA sequencing of a breast cancer cell line
Nattestad M, Goodwin S, Ng K, Baslan T, Sedlazeck FJ, Rescheneder P, Garvin T, Fang H, Gurtowski J, Hutton E, Tseng E, Chin CS, Beck T, Sundaravadanam Y, Kramer M, Antoniou E, McPherson JD, Hicks J, McCombie WR, Schatz MC.
Genome Res. 2018 Aug;28(8):1126-1135. doi: 10.1101/gr.231100.117. Epub 2018 Jun 28.
13. Accurate detection of complex structural variations using single-molecule sequencing
Sedlazeck FJ, Rescheneder P, Smolka M, Fang H, **Nattestad M**, von Haeseler A, Schatz MC.
Nat Methods. 2018 Jun;15(6):461-468. doi: 10.1038/s41592-018-0001-7. Epub 2018 Apr 30.
14. GenomeScope: fast reference-free genome profiling from short reads
Vurture GW, Sedlazeck FJ, **Nattestad M**, Underwood CJ, Fang H, Gurtowski J, Schatz MC.
Bioinformatics. 2017 Jul 15;33(14):2202-2204. doi: 10.1093/bioinformatics/btx153.
15. Phased diploid genome assembly with single-molecule real-time sequencing
Chin CS, Peluso P, Sedlazeck FJ, **Nattestad M**, Concepcion GT, Clum A, Dunn C, O'Malley R, Figueroa-Balderas R, Morales-Cruz A, Cramer GR, Delledonne M, Luo C, Ecker JR, Cantu D, Rank DR, Schatz MC.
Nat Methods. 2016 Dec;13(12):1050-1054. doi: 10.1038/nmeth.4035. Epub 2016 Oct 17.
16. Assemblytics: a web analytics tool for the detection of variants from an assembly
Nattestad M, Schatz MC.
Bioinformatics. 2016 Oct 1;32(19):3021-3. doi: 10.1093/bioinformatics/btw369. Epub 2016 Jun 17.
17. Complete telomere-to-telomere de novo assembly of the Plasmodium falciparum genome through long-read (>11 kb), single molecule, real-time sequencing
Vembar SS, Seetin M, Lambert C, **Nattestad M**, Schatz MC, Baybayan P, Scherf A, Smith ML.
DNA Res. 2016 Aug;23(4):339-51. doi: 10.1093/dnares/dsw022. Epub 2016 Jun 26.
18. The effect of α-mating factor secretion signal mutations on recombinant protein expression in Pichia pastoris
Lin-Cereghino GP, Stark CM, Kim D, Chang J, Shaheen N, Poerwanto H, Agari K, Moua P, Low LK, Tran N, Huang AD, **Nattestad M**, Oshiro KT, Chang JW, Chavan A, Tsai JW, Lin-Cereghino J.
Gene. 2013 May 1;519(2):311-7. doi: 10.1016/j.gene.2013.01.062. Epub 2013 Feb 21.
19. Analysis of the 5' untranslated region (5'UTR) of the alcohol oxidase 1 (AOX1) gene in recombinant protein expression in Pichia pastoris
Staley CA, Huang A, **Nattestad M**, Oshiro KT, Ray LE, Mulye T, Li ZH, Le T, Stephens JJ, Gomez SR, Moy AD, Nguyen JC, Franz AH, Lin-Cereghino J, Lin-Cereghino GP.
Gene. 2012 Apr 1;496(2):118-27. doi: 10.1016/j.gene.2012.01.006. Epub 2012 Jan 25.

Preprints

1. Highly accurate assembly polishing with DeepPolisher
Mastoras M, Asri M, Brambrink L, Hebbar P, Kolesnikov A, Cook DE, **Nattestad M**, Lucas J, Won TS, Chang PC, Carroll A, Paten B, Shafin K.
bioRxiv [Preprint]. 2024 Sep 19:2024.09.17.613505. doi: 10.1101/2024.09.17.613505.
2. Local read haplotagging enables accurate long-read small variant calling
Kolesnikov A, Cook D, **Nattestad M**, McNulty B, Gorzynski J, Goenka S, Ashley EA, Jain M, Miga KH, Paten B, Chang PC, Carroll A, Shafin K.
bioRxiv [Preprint]. 2023 Sep 12:2023.09.07.556731. doi: 10.1101/2023.09.07.556731.

3. DeepTrio: variant calling in families using deep learning
   Kolesnikov A, Goel S, **Nattestad M**, Yun T, Baid G, Yang H, McLean CY, Chang PC, Carroll A
   bioRxiv [Preprint]. 2021 Apr 06. doi: 10.1101/2021.04.05.438434
4. SplitThreader: Exploration and analysis of rearrangements in cancer genomes
   Nattestad M, Alford MC, Sedlazeck FJ, Schatz MC
   bioRxiv [Preprint]. 2016 Nov 15. doi: 10.1101/087981.
5. Third-generation sequencing and the future of genomics
   Lee H, Gurtowski J, Yoo S, **Nattestad M**, Marcus S, Goodwin S, McCombie WR, Schatz MC

Blog Posts

1. DeepVariant over the years
   Gunjan Baid, **Maria Nattestad**, Alexey Kolesnikov, Daniel Cook, Howard Yang, Pi-Chuan Chang, Andrew Carroll
   Google DeepVariant Blog. 2021
2. Looking Through DeepVariant's Eyes
   Maria Nattestad, Gunjan Baid, Andrew Carroll, Pi-Chuan Chang
   Google DeepVariant Blog. 2020
3. One Genome Browser to Rule Them All?
   Maria Nattestad
   Medium. 2018
4. Making genomic data come alive with circos plots
   Maria Nattestad
   Medium. 2017

Press

1. Google Research Vs. Genomic Bias
   2023, Google Research (YouTube)
2. Building better pangenomes to improve the equity of genomics
   2023, Google Research
3. Guinness World Record Awarded for Fastest DNA Sequencing — Just 5 Hours
   2022, NVIDIA
4. Massive genome havoc in breast cancer is revealed
   2018, Cold Spring Harbor Laboratory