

CURRICULUM VITAE**Interests**

Evolution of protein expression, role of protein stability in evolution and disease
 Digital pathology
 AI and ML applications in biology and health
 Big data, data interoperability, data visualization
 Open science, science communication

Positions

2024-	Senior Director, Applied AI Research
2023-2024	Director, Applied AI
2021-2023	Director of Bioinformatics and Computational Biology Ellison Medical Institute, Los Angeles, CA
2019-2021	Director of Bioinformatics and Computational Biology
2014-2019	Director of Data Management and Analytics The Lawrence J. Ellison Institute for Transformative Medicine of USC The University of Southern California, Los Angeles, CA
2026-	Visiting Scholar
2019-2020, 2023-2026	Adjunct Assistant Professor, Biology, Computer Science, Engineering [sequential appointments]
2014-2020	Visiting Scientist, Biology Harvey Mudd College, Claremont, CA
2011-2014	Adjunct Assistant Professor, Ecology and Evolutionary Biology The University of Arizona, Tucson, AZ
2014	Scientific Lead and Communications Director
2011-2014	Scientific Lead
2010-2011	Engagement Team Analyst The iPlant Collaborative (later CyVerse) BIO5-Institute, The University of Arizona, Tucson, AZ
2009	Postdoctoral Fellow, Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany

Education

2004-2009	Ph.D., Biology (Dr. rer. nat., <i>magna cum laude</i>) International Max Planck Research School “The Leipzig School of Human Origins” (University of Leipzig), Germany Thesis: <i>Insights into the Evolution of Primate Protein Expression through Comparative Proteomics</i>
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	Advisor: Prof. Dr. Svante Pääbo
1999-2004	M.Sc., Molecular biology (Minors: Computer Science, Biomathematics) University of Zurich, Switzerland Thesis: <i>Did Domestication Reduce the Fraction of Functional Olfactory Receptors in Pig?</i> Supervisor: Dr. Yoav Gilad; Advisor: Prof. Dr. Walter Schaffner
Teaching	
2011-2014	Workshop Instructor, iPlant Tools and Services The iPlant Collaborative, Tucson, AZ
2002	Teaching Assistant, Biomathematics III University of Zurich, Switzerland
Advising	
2019-2020, 2023-2026	Faculty Advisor, Clinic Program, Harvey Mudd College, Claremont, CA
2011-2014	Dissertation Committee (Kurt Michels), Statistics, University of Arizona, Tucson, Arizona.
Scholarships & Fellowships	
2009	Max Planck Society (MPG) Foreign Postdoctoral Fellow
2006	Max Planck International Research School of Human Evolution
2004	Max Planck Society (MPG) Foreign Doctoral Student
2002	German Academic Exchange Service (DAAD) scholarship
Service	
2026-2024	Project EAGER (NIH/NHGRI), External Scientific Advisor
2024	FASEB Generative AI Task Force, Member
2022-2024	FASEB DataWorks! Advisory Committee, Member
Outreach	
2012-2014	Mentor, Arizona Assurance Scholars Program

PUBLICATIONS & PRESENTATIONS

Peer-reviewed publications

Chi BT*, Fulcar S*, Ipe J*, Schleifer O*, Subramanian R*, Vlases C*, Matasci N, Georgouli K, Pottier L, Hsu T, Carpenter TS, Nissley DV, Lightstone FC, Streitz FH, Ingólfsson HI, Aydin F. Integrating Ultra-Coarse-Grained Protein Models into Accessible Workflows for Multiscale Molecular Dynamics. *ACS Omega*. 2025;10(43):51726-51737. doi:[10.1021/acsomega.5c07601](https://doi.org/10.1021/acsomega.5c07601)

Chen X, Ligumsky H, Ambrose C, Sibrian D, Tran B, Arif D, Castellanos O, Kessner D, Luo H, Ubale M, Coleman A, Mahaganapathy V, Jönsson TJ, Basho RK, Lee JSH, Matasci N, Agus DB. Monitoring the rate and variability of somatic genomic alterations using long-read sequencing. *Scientific Reports*. 2025;15(1):18397. doi:[10.1038/s41598-025-01690-z](https://doi.org/10.1038/s41598-025-01690-z)

Elton E, Strelez C, Ung N, Perez R, Ghaffarian K, Hixon D, Matasci N, Mumenthaler SM. A novel thin plate spline methodology to model tissue surfaces and quantify tumor cell invasion in organ-on-chip models. *SLAS Discovery*. 2024;29(4). doi:[10.1016/j.slasd.2024.100163](https://doi.org/10.1016/j.slasd.2024.100163)

Chambliss AB, Aljehani M, Tran B, Chen X, Elton E, Garri C, Ung N, Matasci N, Gross ME. Immune biomarkers associated with COVID-19 disease severity in an urban, hospitalized population. *Practical Laboratory Medicine*. 2023;36:e00323. doi:[10.1016/j.plabm.2023.e00323](https://doi.org/10.1016/j.plabm.2023.e00323)

Ung N, Goldbeck C, Man C, Hoeflich J, Sun R, Barbeta A, Matasci N, Katz J, Lee JSH, Chopra S, Asgharzadeh S, Warren M, Sher L, Kohli R, Akbari O, Genyk Y, Emamaullee J. Adaptation of Imaging Mass Cytometry to Explore the Single Cell Alloimmune Landscape of Liver Transplant Rejection. *Frontiers in Immunology*. 2022;13. doi:[10.3389/fimmu.2022.831103](https://doi.org/10.3389/fimmu.2022.831103)

Spiller ER, Ung N, Kim S, Patsch K, Lau R, Strelez C, Doshi C, Choung S, Choi B, Juarez Rosales EF, Lenz HJ, Matasci N, Mumenthaler SM. Imaging-Based Machine Learning Analysis of Patient-Derived Tumor Organoid Drug Response. *Frontiers in Oncology*. 2021;11:771173. doi:[10.3389/fonc.2021.771173](https://doi.org/10.3389/fonc.2021.771173)

Patsch K, Matasci N, Soundararajan A, Diaz P, Agus DB, Ruderman D, Gross ME. Monitoring dynamic cytotoxic chemotherapy response in castration-resistant prostate cancer using plasma cell-free DNA (cfDNA). *BMC Research Notes*. 2019;12(1):275. doi:[10.1186/s13104-019-4312-2](https://doi.org/10.1186/s13104-019-4312-2)

One Thousand Plant Transcriptomes Initiative. One thousand plant transcriptomes and the phylogenomics of green plants. *Nature*. 2019;574(7780):679-685. doi:[10.1038/s41586-019-1693-2](https://doi.org/10.1038/s41586-019-1693-2)

Carpenter EJ, Matasci N, Ayyampalayam S, Wu S, Sun J, Yu J, Jimenez Vieira FR, Bowler C, Dorrell RG, Gitzendanner MA, Li L, Du W, K. Ullrich K, Wickett NJ, Barkmann TJ, Barker MS, Leebens-Mack JH, Wong GKS. Access to RNA-sequencing data from 1,173 plant species: The 1000 Plant transcriptomes initiative (1KP). *GigaScience*. 2019;8(10):giz126. doi:[10.1093/gigascience/giz126](https://doi.org/10.1093/gigascience/giz126)

Martin L, Cook C, Matasci N, Williams J, Bastow R. Data mining with iPlant: A meeting report from the 2013 GARNet workshop, Data mining with iPlant. *Journal of Experimental Botany*. 2015;66(1):1-6. doi:[10.1093/jxb/eru402](https://doi.org/10.1093/jxb/eru402)

Wickett NJ, Mirarab S, Nguyen N, Warnow T, Carpenter E, Matasci N, Ayyampalayam S, Barker MS, Burleigh JG, Gitzendanner MA, Ruhfel BR, Wafula E, Der JP, Graham SW, Mathews S, Melkonian M, Soltis DE, Soltis PS, Miles NW, Rothfels CJ, Pokorny L, Shaw AJ, DeGironimo

L, Stevenson DW, Surek B, Villarreal JC, Roure B, Philippe H, dePamphilis CW, Chen T, Deyholos MK, Baucom RS, Kutchan TM, Augustin MM, Wang J, Zhang Y, Tian Z, Yan Z, Wu X, Sun X, Wong GKS, Leebens-Mack J. Phylotranscriptomic analysis of the origin and early diversification of land plants. *Proc Natl Acad Sci USA*. 2014;111(45). doi:[10.1073/pnas.1323926111](https://doi.org/10.1073/pnas.1323926111)

Matasci N, Hung LH, Yan Z, Carpenter EJ, Wickett NJ, Mirarab S, Nguyen N, Warnow T, Ayyampalayam S, Barker M, Burleigh JG, Gitzendanner MA, Wafula E, Der JP, dePamphilis CW, Roure B, Philippe H, Ruhfel BR, Miles NW, Graham SW, Mathews S, Surek B, Melkonian M, Soltis DE, Soltis PS, Rothfels C, Pokorný L, Shaw JA, DeGironimo L, Stevenson DW, Villarreal JC, Chen T, Kutchan TM, Rolf M, Baucom RS, Deyholos MK, Samudrala R, Tian Z, Wu X, Sun X, Zhang Y, Wang J, Leebens-Mack J, Wong GKS. Data access for the 1,000 Plants (1KP) project. *GigaScience*. 2014;3(1):17. doi:[10.1186/2047-217X-3-17](https://doi.org/10.1186/2047-217X-3-17)

Stoltzfus A, Lapp H, Matasci N, Deus H, Sidlauskas B, Zmasek CM, Vaidya G, Pontelli E, Cranston K, Vos R, Webb CO, Harmon LJ, Pirrung M, O'Meara B, Pennell MW, Mirarab S, Rosenberg MS, Balhoff JP, Bik HM, Heath TA, Midford PE, Brown JW, McTavish EJ, Sukumaran J, Westneat M, Alfaro ME, Steele A, Jordan G. Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. *BMC Bioinformatics*. 2013;14(1):158. doi:[10.1186/1471-2105-14-158](https://doi.org/10.1186/1471-2105-14-158)

Miller AJ, Matasci N, Schwaninger H, Aradhya MK, Prins B, Zhong GY, Simon C, Buckler ES, Myles S. Vitis Phylogenomics: Hybridization Intensities from a SNP Array Outperform Genotype Calls. *PLOS ONE*. 2013;8(11):e78680. doi:[10.1371/journal.pone.0078680](https://doi.org/10.1371/journal.pone.0078680)

Matasci N, McKay S. Phylogenetic Analysis with the iPlant Discovery Environment. *Current protocols in bioinformatics*. 2013;Chapter 6:Unit6.13. doi:[10.1002/0471250953.bi0613s42](https://doi.org/10.1002/0471250953.bi0613s42)

Boyle B, Hopkins N, Lu Z, Raygoza Garay JA, Mozzherin D, Rees T, Matasci N, Narro ML, Piel WH, McKay SJ, Lowry S, Freeland C, Peet RK, Enquist BJ. The taxonomic name resolution service: an online tool for automated standardization of plant names. *BMC bioinformatics*. 2013;14(1):16. doi:[10.1186/1471-2105-14-16](https://doi.org/10.1186/1471-2105-14-16)

Goff S, Vaughn M, McKay S, Lyons E, Stapleton A, Gessler D, Matasci N, Wang L, Hanlon M, Lenards A, Muir A, Merchant N, Lowry S, Mock S, Helmke M, Kubach A, Narro M, Hopkins N, Micklos D, Hilgert U, Gonzales M, Jordan C, Skidmore E, Dooley R, Cazes J, McLay R, Lu Z, Pasternak S, Koesterke L, Piel W, Grene R, Noutsos C, Gendler K, Feng X, Tang C, Lent M, Kim S jin, Kvilekval K, Manjunath BS, Tannen V, Stamatakis A, Sanderson M, Welch S, Cranston K, Soltis P, Soltis D, O'Meara B, Ane C, Brutnell T, Kleibenstein D, White J, Leebens-Mack J, Donoghue M, Spalding E, Vision T, Myers C, Lowenthal D, Enquist B, Boyle B, Akoglu A, Andrews G, Ram S, Ware D, Stein L, Stanzione D. The iPlant Collaborative: Cyberinfrastructure for Plant Biology. *Frontiers in Plant Science*. 2011;2. doi:[10.3389/fpls.2011.00034](https://doi.org/10.3389/fpls.2011.00034)

* Supervised undergraduate students

Preprints & conference proceedings

Zalach J, Gazy I, Avinoam A, Sinai R, Shmuel E, Gilboa I, Swisher C, Matasci N, Basho R, Agus DB. CanvOI, an Oncology Intelligence Foundation Model: Scaling FLOPS Differently. Published online September 4, 2024. <http://arxiv.org/abs/2409.02885>

Chen X*, Dougherty T*, Hong C*, Schibler R*, Zhao YC*, Sadeghi R, Matasci N, Wu YC, Kerman I. Predicting Antibody Developability from Sequence using Machine Learning. Published online June 20, 2020:2020.06.18.159798. doi:[10.1101/2020.06.18.159798](https://doi.org/10.1101/2020.06.18.159798)

Rogowitz BE, Matasci N. Metadata Mapper: a web service for mapping data between independent visual analysis components, guided by perceptual rules. In: Rogowitz BE, Pappas TN, eds. *IS&T/SPIE Electronic Imaging*. International Society for Optics and Photonics; 2011:78650I-78650I - 13. doi:[10.1117/12.881734](https://doi.org/10.1117/12.881734)

*Supervised undergraduate students

Oral Presentations

Matasci Naim, Boyle Brad, Lu Zhenyuan, Hopkins Nicole, Piel William H., Raygoza Garay Juan Antonio, Gregory Steven, Lowry Sonya, McKay Sheldon J., Narro Martha L., Skidmore Edwin, Enquist Brian J., “iPlant’s Taxonomic Name Resolution Service”, Oral presentation, Botany 2012, Columbus, OH

Matasci Naim, Cranston Karen, Donoghue Michael J, Leebens-Mack Jim, O'Meara Brian, Piel William H, Sanderson Michael, Soltis Douglas, Soltis Pamela, Stamatakis Alexandros, Tannen Val, Vision Todd J, McKay Sheldon, Goff Stephen A, “The iPlant Tree of Life Project and Toolkit: Building a Cyberinfrastructure for Plant Science Research”, Oral presentation, Evolution 2011, Norman, OK

Matasci Naim, Boyle Brad, Lu Zhenyuan, Hopkins Nicole, Piel William H., Raygoza Garay Juan Antonio, Narro Martha L., Lowry Sonya, McKay Sheldon J., Enquist Brian J., “The TNRS, a Taxonomic Name Resolution Service for Plants”, Oral presentation, iEvoBio 2011, Norman, OK

Matasci Naim, Boyle Brad, Lu Zhenyuan, Hopkins Nicole, Piel William H., Raygoza Garay Juan Antonio, Narro Martha L., Lowry Sonya, McKay Sheldon J., Enquist Brian J., “Correcting and Standardizing Taxonomic Names with the Taxonomic Name Resolution Service”, Oral presentation, TDWG 2011, New Orleans, LA

Matasci Naim, “Primate Protein Expression Evolution”, Oral presentation, SMCB 2007, Halifax, Canada.

Invited Talks

2023

“An interactive multidimensional image data management and analysis system to support AI applications”, SLAS2023 International Conference and Exhibition, San Diego, CA

2022

“Unleashing the Power of AI in Digital Pathology for Cancer Care”, Oracle CloudWorld, Las Vegas, NV

“An Interactive 5D Image Data Management and Analysis System to Support AI Applications”, SLAS 2022 AI Data Pipelines for Life Sciences Symposium, Seattle, WA

“Digitizing Your Lab”, DataWorks! Salon, Virtual

2012

“The iPlant Collaborative – Building a Cyberinfrastructure for the Life Sciences”, Western Association of Core Directors Annual Meeting, Portland, OR

2011

“The iPlant Collaborative: A Cyberinfrastructure for the Life Sciences”, Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, AZ

“What Can iPlant Do for You?”, Department of Plant Sciences, University of Arizona, Tucson, AZ

“The iPlant Tree of Life Project and Toolkit: Building a Cyberinfrastructure for Plant Science Research”, National Museum of Natural History, Washington, DC

“The iPlant Tool Integration Process”, Generation Challenge Program, San Diego, CA

2007

“Protein Evolution and Localization”, University of Maryland, College Park, MD.

Posters

Basho R, Heredia E, McArthur H, Fang Z, Narumi V, LeVee A, Jonsson T, Dadmanesh F, Bose S, Patre S, Keller T, Paine J, Tran B, Simental B, Castellanos O, Lee J, Shiao S, Agus D, Matasci N. Abstract PS3-04-01: Prediction of pathologic complete response from histopathology images of HER2+ breast cancer using an AI foundation model. Clin Cancer Res.

2026;32(4_Supplement):PS3-04-01. Presented at San Antonio Breast Cancer Symposium 2025. doi:[10.1158/1557-3265.SABCS25-PS3-04-01](https://doi.org/10.1158/1557-3265.SABCS25-PS3-04-01)

Heredia EA, Paine J, Patre S, Jonsson T, Keller T, Fang Z, Narumi V, Katiyar I, Lagerstrom I, Lombardo J, Lee JSH, Agus DB, Basho R, Matasci N. Abstract B039: Detecting obesity-associated histopathology characteristics in breast cancer using an AI foundation model. In: *Clinical Cancer Research*. Vol 31. ; 2025:B039. Presented at AACR Special Conference in Cancer Research: Artificial Intelligence and Machine Learning. doi:[10.1158/1557-3265.AIMACHINE-B039](https://doi.org/10.1158/1557-3265.AIMACHINE-B039)

Heredia EA, Patre S, Paine J, Chen X, Lagerstrom I, Jonsson J, Lee JSH, Lombardo J, Matasci N, Agus DB. An AI Research Platform for Computational Pathology. Presented at Digital Pathology & AI Congress: USA, 2024.

Srivatsa S, Walsh D, Aljehani M, Weinreb J, Becker N, Ellis BH, George R, Chen X, Matasci N, Basho R, Gross ME, Swisher CL. Abstract 6467: Causal personalized treatment estimation framework using real-world electronic health record (EHR) data to inform cancer care decisions. In: *Cancer Research*. Vol 84. ; 2024:6467. Presented at AACR Annual Meeting 2024. doi:[10.1158/1538-7445.AM2024-6467](https://doi.org/10.1158/1538-7445.AM2024-6467)

Chambliss AB, Aljehani M, Tran B, Chen X, Elton E, Garri C, Ung N, Matasci N, Gross ME. A-229 Immune Biomarkers Associated with COVID-19 Disease Severity in an Urban, Hospitalized Population. In: *Clinical Chemistry*. Vol 69. ; 2023:hvad097.206. Presented at 2023 AACC Annual Scientific Meeting & Clinical Lab Expo. doi:[10.1093/clinchem/hvad097.206](https://doi.org/10.1093/clinchem/hvad097.206)

Chen X, Heredia E, Patre S, Lee JSH, Matasci N, Agus DB. SPE3D: A Distributed and scalable 2D/3D digital pathology platform. Presented at: Pacific Symposium on Biocomputing, 2023. doi:[10.7490/f1000research.1119248.1](https://doi.org/10.7490/f1000research.1119248.1)

Emamaullee J, Ung N, Man C, Hoeflich J, Goldbeck C, Barbetta A, Sun RX, Matasci N, Katz J, Lee JSH, Chopra S, Sher L, Asgharzadeh S, Akbari O, Genyk Y. Multiplexed Imaging Mass Cytometry of the Alloimmune Landscape of Rejection in Clinical Liver Transplantation. In: *American Journal of Transplantation*. Vol 21. ; 2021:348-348.

Emamaullee J, Man C, Hoeflich J, Ung N, Sun RX, Matasci N, Katz J, Lee JSH, Chopra S, Sher L, Shahab Asgharzadeh, Akbari O, Genyk Y. Multiplexed Imaging Mass Cytometry Analysis Reveals a New Role for CD68+ Macrophages in Chronic Liver Transplant Rejection. In: *American Journal of Transplantation*. Vol 20. ; 2020:324-324.

Chiang CT, Ung N, Demetriou AN, Chiu CL, Choudhury N, Arnesano C, Fraser SE, Agus DB, Matasci N, Ruderman DL, Mumenthaler SM. Abstract 2414: Interrogating cellular metabolism reveals mTORC2 as a new biomarker to stratify epidermal growth factor receptor-mutant non-small cell lung cancer. In: *Cancer Research*. Vol 78. ; 2018:2414. Presented at AACR Annual Meeting 2018. doi:[10.1158/1538-7445.AM2018-2414](https://doi.org/10.1158/1538-7445.AM2018-2414)

Shah PP, Patsch K, Matasci N, Soundararajan A, Diaz P, Agus DB, Ruderman D, Gross ME. Abstract 3731: A novel multidimensional cfDNA assay for real time analysis of chemotherapy response. In: *Cancer Research*. Vol 77. ; 2017:3731. Presented at AACR Annual Meeting 2017. doi:[10.1158/1538-7445.AM2017-3731](https://doi.org/10.1158/1538-7445.AM2017-3731)

Ruderman D, Patsch K, Matasci N, Soundararajan A, Diaz P, Gross ME. Abstract A20: Use of cell-free plasma DNA for dynamic monitoring of response to cytotoxic chemotherapy. In: *Cancer Research*. Vol 77. ; 2017:A20. Presented at AACR Special Conference: Engineering and Physical Sciences in Oncology, 2016. doi:[10.1158/1538-7445.EPSO16-A20](https://doi.org/10.1158/1538-7445.EPSO16-A20)

Patsch K, Matasci N, Soundararajan A, Nicoll J, Katz J, Sanchez A, Feierstein E, Loy CV, Xu Z, Agus DB, Gross ME, Ruderman D. Abstract 3934: Bladder cancer tumor heterogeneity: development of a system-level mutation assay. In: *Cancer Research*. Vol 77. ; 2017:3934. Presented at AACR Annual Meeting 2017. doi:[10.1158/1538-7445.AM2017-3934](https://doi.org/10.1158/1538-7445.AM2017-3934)

Matasci N, Boyd B, Lu Z, Hopkins N, Piel WH, Garay JAR, Gregory S, Lowry S, McKay SJ, Narro ML. Correcting and Standardizing Taxonomic Names with the Taxonomic Name Resolution Service. Presented at TDWG 2011 Annual Conference.

Matasci N, Cranston K, Donoghue MJ, Leebens-Mack J, O'Meara B, Piel WH, Sanderson M, Soltis D, Soltis P, Stamatakis A, Tannen V, Vision TJ, McKay S, Goff SA. The iPlant Collaborative: a Cyberinfrastructure to Support Next-generation Phylogeny-based Research. Presented at Plant Genomes and Biotechnology, 2011.

Matasci N, Vaughn M, Skidmore E, Merchant N. Using R to Empower a New Plant Biology. Presented at User! 2011.

Matasci N, Paavilainen L, Wester K, Pontén F, Uhlén M, Pääbo S. Evolution of Protein Expression and Localization. Presented at SMP Proteomics Symposium 2007.

Lee YS, Matasci N, Serre D, Wiebe V, Vigilant L, Pääbo S. Investigation of some genes putatively under positive selection in humans. Presented at 16th Annual Meeting, Korean Society for Molecular and Cellular Biology 2004.

Workshops

2013

“Phylotastic II”, University of Arizona, Tucson, AZ*

“Tucson Winter Plant Breeding Institute”, University of Arizona, Tucson, AZ*

2012

“Phylotastic Hackathon”, NESCent, Durham, NC

“iPlant Tools and Services”, UC Davis, Davis, CA*

“iPlant Tools and Services”, UC Riverside, Riverside, CA*

“iPlant Tools and Services”, Purdue University, West Lafayette, IN*

“iPlant Tools and Services”, North Carolina State University, Raleigh, NC*

“iPlant Tools and Services”, Botany 2012, Columbus, OH*

“QIIME”, University of Arizona, Tucson, AZ**

“iPlant Tools and Services”, iDigBio's Specimen Digitization Tools and Practices, Columbus OH

2011

“Phylogenetics Workflows Part II: Post-tree Analyses”, Botany 2011, Saint Louis, MO*

“Post Tree Analyses”, NESCent, Durham, NC*

“iPlant Tree of Life”, Plant and Animal Genome 2011, San Diego, CA*

“Phylogenetic Workflows: Tree Building and Post-tree Analyses”, Plant Biology 2011, Minneapolis, MI*

*Instructor; **Organizer