

# Samson Koelle

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I am a researcher and engineer with diverse skills in artificial intelligence, interpretable machine learning, and computational biology. I am looking for team-based work with real-world impact.

## Skills

Methods:	Python	PyTorch	GitHub	Sequence models	Unsup. learn.	Full stack
Domains:	Generative AI	TTS	Neuro.	Mol. dynamics	Hematology	

## Experience

<b>Uberduck</b>	Cofounder	Seattle, WA	08/2021 – 03/2024
Headed text-to-speech development for startup at 0-60k MRR			
<b>Allen Institute for Brain Science</b>	Graduate assistant	Seattle, WA	01/2020 – 12/2020
Statistical methods development for modeling brain connectivity			
<b>Amazon SCOT Forecasting Science</b>	Research Intern	Seattle, WA	06/2017 – 09/2017
Online training of fine-tuned forecasting models			
<b>Fred Hutchinson CRC</b>	Graduate assistant	Seattle, WA	09/2015 – 06/2017
Computational analysis of single cell RNA sequencing			
<b>National Heart, Lung, &amp; Blood Inst.</b>	IRTA	Bethesda, MD	07/2013 – 05/2015
Studied distribution of clonality in hematopoiesis			

## Education

<b>Y Combinator</b>	San Francisco, CA	01/2022 – 03/2022
<b>Ph.D. Statistics</b>	University of Washington, Seattle, WA	09/2015 – 03/2022
Thesis: <i>Geometric algorithms for interpretable manifold learning</i> .		
Committee: Marina Meila (advisor), Yen-Chi Chen, Zaid Harchaoui, John Lee		
<b>B.A. Mathematics</b>	Columbia University, New York, NY	09/2009 – 05/2013

## References

<b>Zach Ocean</b>	Uberduck, Inc.	z@uberduck.ai
<b>Marina Meila</b>	University of Washington Department of Statistics	mmp@uw.edu
<b>Stefan Mihalas</b>	Allen Institute for Brain Science	stefanm@alleninstitute.org
<b>Cynthia Dunbar</b>	National Heart Lung and Blood Institute	dunbarc@nhlbi.nih.gov

## Service

<b>Reviewer</b>	AISTAT	2023
<b>Reviewer</b>	JMLR	2021
<b>Reviewer</b>	UAI	2020-2021
<b>Organizer</b>	UW Geometric Data Analysis reading group (uwgeometry.github.io)	2017-2021

## Publications

Koelle, Samson et al. (Dec. 2023). “Modeling the cell-type-specific mesoscale murine connectome with anterograde tracing experiments”. en. In: *Netw Neurosci* 7.4, pp. 1497–1512.

Zhang, Hanyu et al. (Feb. 2023). “Dictionary-based Manifold Learning”. In: *AISTATS 2024 (to appear)*. arXiv: 2302.00263 [cs.LG].

- Koelle, Samson (2022). “Geometric Algorithms for Interpretable Manifold Learning”. en. PhD thesis. Ann Arbor, United States: University of Washington.
- Koelle, Samson J et al. (2022). “Manifold Coordinates with Physical Meaning”. In: *J. Mach. Learn. Res.* 23.133, pp. 1–57.
- Buenfil, James et al. (2021). “Tangent Space Least Adaptive Clustering”. en. In: *2021 ICML Unsupervised Learning for Reinforcement Learning Workshop*.
- Espinoza, Diego A et al. (Apr. 2021). “Interrogation of clonal tracking data using barcodetrackR”. en. In: *Nat Comput Sci* 1.4, pp. 280–289.
- Xu, Jason et al. (2019). “Statistical inference for partially observed branching processes with application to cell lineage tracking of in vivo hematopoiesis”. In: *Ann. Appl. Stat.* 13.4, pp. 2091–2119.
- Meila, Marina et al. (Nov. 2018). “A regression approach for explaining manifold embedding coordinates”.
- Paulson, K G et al. (Sept. 2018). “Acquired cancer resistance to combination immunotherapy from transcriptional loss of class I HLA”. en. In: *Nat. Commun.* 9.1, p. 3868.
- Wu, Chuanfeng et al. (Nov. 2018a). “Clonal expansion and compartmentalized maintenance of rhesus macaque NK cell subsets”. en. In: *Sci Immunol* 3.29.
- Wu, Chuanfeng et al. (Jan. 2018b). “Geographic clonal tracking in macaques provides insights into HSPC migration and differentiation”. en. In: *J. Exp. Med.* 215.1, pp. 217–232.
- Yabe, Idalia M et al. (Dec. 2018). “Barcoding of Macaque Hematopoietic Stem and Progenitor Cells: A Robust Platform to Assess Vector Genotoxicity”. en. In: *Mol Ther Methods Clin Dev* 11, pp. 143–154.
- Yu, Kyung-Rok et al. (Mar. 2018). “The impact of aging on primate hematopoiesis as interrogated by clonal tracking”. en. In: *Blood* 131.11, pp. 1195–1205.
- Koelle, Samson J et al. (Mar. 2017). “Quantitative stability of hematopoietic stem and progenitor cell clonal output in rhesus macaques receiving transplants”. en. In: *Blood* 129.11, pp. 1448–1457.
- Wu, Chuanfeng et al. (Apr. 2014). “Clonal tracking of rhesus macaque hematopoiesis highlights a distinct lineage origin for natural killer cells”. In: *Cell Stem Cell* 14.4, pp. 486–499.