Robin W. Yeo, PhD
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PROFESSIONAL SUMMARY

PhD in genetics with extensive genomics and bioinformatics experience including next-generation sequencing analysis and machine learning/deep learning expertise. 15+ years of research experience including molecular biology and genetic manipulation in numerous *in vitro* and *in vivo* systems. Expert in CRISPR-Cas systems and their therapeutic applications. Strong independent and collaborative publication record in both primary research and scientific literature reviews. Passionate about genome editing, aging biology, epigenetics, and neuroscience.

EDUCATION

Stanford University, Stanford, CA   *2014 – 2020*
Ph.D. in Genetics

Massachusetts Institute of Technology (MIT), Cambridge, MA   *2009 – 2013*
Bachelor's of Science in Biological Engineering
Major: Biological Engineering, Minor: Mathematics

SKILLS

Computational Languages: R, Python, PyTorch, Bash, Matlab
Bioinformatics: RNA-seq, ChIP-seq, ATAC-seq pipeline analysis (bowtie2, tophat, cufflinks, SAMtools, Bedtools, Picard, MACS2, DESeq2, EdgeR, deepTools, DiffBind, ChIPSeeker, Homer, NucleoATAC), scRNA-seq analysis (Seurat), long read sequencing analysis (NanoQC, Minimap2)
Machine Learning: Supervised machine learning (ElasticNet, SVM, Random Forest, XGBoost), Unsupervised machine learning (PCA, MDS, t-SNE, UMAP), Deep learning (CNNs, LLMs)
Molecular Biology: ATAC-seq library generation, CRISPR-Cas9 genome editing, lentiviral construction, FACS, immunofluorescence staining, tissue culture, cryosectioning, confocal microscopy, qPCR, western blots
Mouse Animal Procedures: Large-scale animal studies, mouse colony husbandry, brain microdissections, multi-tissue necropsies, paraformaldehyde perfusions
***C. elegans* Animal Procedures:** Animal husbandry, lifespan assays, genetic crosses, extrachromosomal microinjections, biolistic bombardment, UV integration

PROFESSIONAL EXPERIENCE

EpiCRISPR Biotechnologies, South San Francisco, CA
Head of Biological Data Science   *September 2023-Present*
- Managed a team of 2 PhD scientists and 1 engineer on multiple therapeutic and pre-clinical R&D projects (formal training including a 3 month CMC Management Certification)
- Supervised a bioinformatic CRO on RNA-seq+WGBS analysis for off-target analysis for a regulatory filing
- Study director on the in vitro and in vivo off-target characterization sections of IND filing for EPI-321
- Supervised clinical biostatistical analyses to identify clinical endpoints for a FIH PhI/II clinical trials for FSHD
- Drove multiple scientific partnerships for pre-clinical R&D platform development (e.g. Basecamp Research, CRISPRQC)

Biological Data Scientist II   *March 2022-September 2023*
Biological Data Scientist I   *June 2021-March 2022*
- Data science lead on all projects with Epic Bio's Technology Development team
- Designed 10+ peptide libraries for high-throughput screening experiments of novel epigenetic modulators
- Wrote custom alignment and analytical pipelines to process short and long-read sequencing high-throughput screens
- Integrated multi-omic datasets to characterize enhancer regions for CRISPR-Cas targeting
- Performed extensive feature engineering on aa sequences using biochemical encodings and protein language models
- Developed convolutional neural net architecture to predict epigenetic modulator function based on peptide sequence
- Lead architect for Epic Bio's ML platform for modulator discovery resulting in publication at NeurIPS 2023
- Developed our in-house algorithm for CasMINI guide design with extensive off-target characterization

- Created a back-end database of CasMINI gRNAs for genome-wide targeting with custom PAMs for a guide design website tool

- Founding member and treasurer of Epic Bio Culture Club – responsible for organizing multiple corporate events (e.g. Scientific Advisory Board Meeting, annual company retreat) and community outreach opportunities (e.g. beach cleanup, foodbank volunteering, patient advocacy walks/runs)
- Recipient of Epic Hero Award for outstanding performance and contributions beyond job description (Q3 2023)

Stanford University – Department of Genetics, Stanford, CA *Sep 2020-June 2021*
Postdoctoral scholar with Dr. Anne Brunet
- Integrated scRNA-seq data from SVZ niche cells during aging to orthogonally validate NSC cell adhesion changes
- Used molecular tension sensors to biophysically characterize focal adhesion strength in NSCs during aging
- Identified and functionally validated ROCK as a therapeutic target to reverse the migratory deficit of old NSCs
- Analyzed scRNA-seq data from mice with intracerebral infusions of ROCKi to identify ROCKi-mediated transcriptional changes in NSC populations from the SVZ

Stanford University – Department of Genetics, Stanford, CA *July 2015-Sep 2020*
PhD with Dr. Anne Brunet
Thesis Project: Chromatin accessibility dynamics underlie a decline in neural stem cell (NSC) migratory ability with age
- Isolated rare *in vivo* NSC populations from the mouse SVZ to assess chromatin accessibility (ATAC-seq) with FACS
- Bioinformatically processed ATAC-seq, RNA-seq, and ChIP-seq data to uncover NSC changes throughout aging
- Analyzed ATAC-seq data to identify aging changes in non-coding chromatin loci, TF motifs, and signaling pathways
- Functionally validated age-related NSC adhesion and migration changes using *in vitro* and *in vivo* techniques
- Characterized p16$^+$ senescent NSCs using *in vitro* assays and immunofluorescence staining of the SVZ *in vivo*
- Genetically engineered 100+ *C. elegans* strains to express extra-chromosomal arrays to characterize enhancer activity
- Spatiotemporally characterized regulatory activity of distal enhancers in *C. elegans* using fluorescence microscopy

Harvard School of Public Health – Department of GCD, Cambridge, MA *July 2013 – July 2014*
Research technician for Dr. William Mair
- Investigated AMPK and CRTC-1's role in cellular energy homeostasis in the context of *C. elegans* aging
- Synthesized and characterized *in vivo* fluorescent reporters to elucidate signalling interactions downstream of AMPK
- Created transgenic *C. elegans* lines by microinjection and biolistic bombardment to assess metabolic pathway activity

MIT – Guarente Lab for the Study of Aging, Cambridge, MA *Feb 2011 – May 2013*
Research Internship with Dr. Leonard Guarente
- Investigated the mechanisms of action underlying the Sirtuin family's critical role in *C. elegans* aging
- Isolated *C. elegans* mutants with combinatorial knock-out Sirtuin paralogs
- Conducted both small molecule and RNAi-based lifespan assays on overexpressing sir-2.1 strains

Hôpitale Pitié-Salpêtrière Neuroepidemiology Lab, Paris, France *Summer 2012*
Research Internship with Dr. Christophe Tzourio
- Investigated genome-wide SNP associations with metabolic syndrome, sirtuins, and neurovascular aging in humans

University of Toronto (MaRS Centre) – Rottapel Lab, Toronto, ON, Canada *Summer 2010*
Research Internship with Dr. Robert Rottapel
- Studied Tankyrase-2 knock-out mutations on murine osteoclast differentiation and growth
- Synthesized viral genome and adenoviruses for associated hematopoietic stem cell transduction experiments

MIT – Laboratory for Multiscale Regenerative Technologies, Cambridge, MA *Jan – April 2010*
Research Internship with Dr. Sangeeta Bhatia
- Utilized tissue engineering techniques in primary murine hepatocytes to stabilize morphology *in vitro*
- Assessed multiple small molecule inhibitors on hepatocyte differentiation and proliferation in high-throughput assays

University of Toronto (MaRS Centre) – Rottapel Lab, Toronto, ON, Canada *Nov 2008 – Sep 2009*
Research Internship with Dr. Robert Rottapel
- Investigated SH3-BP2 structure/function properties on various signal transduction pathways in mammalian cells
- Studied Tankyrase-2's role as a PARP in telomere length regulation through its interactions with TRF-1

PUBLICATIONS

Lopp, S.*, Borrman, T.*, Jha, N., Silvis, M., Swan, R., Yang, X., Alvarez, G., Klappenbach, C., Liu, Y., Hart, D. O., Qi, L.S., Daley, T. P.‡, & **Yeo, R.W.**‡ casmini-tool: a comprehensive database for efficient and specific guide RNA design using dCas-MINI. (***In preparation***) (https://www.biorxiv.org/content/10.1101/2023.09.17.558168v2)
‡co-corresponding author

Carosso, G., **Yeo, R. W.,** Gainous, T. B., Jawaid, M. Z., Yang, X., Kim, J. Y. S., Jadhav, K., Juan-Sing, N., Boregowda, S. V., Cutillas, V., Qi, L. S., Collin de l'Hortet, A., Daley, T. P. & Hart, D. O. (2024). Discovery of hypercompact epigenetic modulators for persistent CRISPR-mediated gene activation. (***In preparation***)
(https://www.biorxiv.org/content/10.1101/2023.06.02.543492v4)

Ruetz, T. J., Pogson, A. N., Kashiwagi C. M., Gagnon, S. D., Morton B., Sun, E. D., Na, J., **Yeo, R. W.,** Leeman, D. S., Morgens, D. W., Tsui, C. K., Li, A., Bassik, M. C. & Brunet, A. (2024). CRISPR–Cas9 screens reveal regulators of ageing in neural stem cells. ***Nature***, 634, 1150-1159.

Jawaid, M.Z., Gautam, A., Gainous, T. B., Hart, D. O., **Yeo, R. W.**‡, & Daley, T. P.‡ (2023) Improving few-shot learning-based protein engineering with evolutionary sampling. ***NeurIPS workshop on Generative AI and Biology (2023).***
‡co-corresponding author

Yeo, R. W*., Zhou, O. Y.*, Zhong, B. L., Sun, E. D., Navarro Negredo, P., Nair, S., Sharmin, M., Ruetz, T. J., Wilson, M., Kundaje, A., Dunn, A. R., & Brunet, A. (2023). Chromatin accessibility dynamics of neurogenic niche cells reveal defects in neural stem cell adhesion and migration during aging. ***Nature Aging***, 3, 866-893**.**
***co-first author**

Booth, L. N., Shi, C., Tantilert C., **Yeo, R. W.,** Miklas, J. W., Hebestreit K., Hollenhorst C. N., Maures, T. J., Buckley M. T., Murphy C. T., & Brunet, A. (2022). Males induce premature demise of the opposite sex by multifaced strategies. ***Nature Aging***, *2*, 809-823**.**

Navarro Negredo, P.*, **Yeo, R. W.***, & Brunet, A. (2020). Aging and Rejuvenation of Neural Stem Cells and Their Niches. ***Cell Stem Cell***, *27*(2), 202–223.
***co-first author**

Booth, L. N., Maures, T. J., **Yeo, R. W.,** Tantilert, C., & Brunet, A. (2019). Self-sperm induce resistance to the detrimental effects of sexual encounters with males in hermaphroditic nematodes. ***eLife***, *8*, e46418.

Leeman, D. S., Hebestreit, K., Ruetz, T., Webb, A. E., McKay, A., Pollina, E. A., Dulken, B. W., Zhao, X., **Yeo, R. W.,** Ho, T. T., Mahmoudi, S., Devarajan, K., Passegué, E., Rando, T. A., Frydman, J., & Brunet, A. (2018). Lysosome activation clears aggregates and enhances quiescent neural stem cell activation during aging. ***Science***, *359*(6381), 1277–1283.

Daugherty, A. C.*, **Yeo, R. W.***, Buenrostro, J. D., Greenleaf, W. J., Kundaje, A., & Brunet, A. (2017). Chromatin accessibility dynamics reveal novel functional enhancers in *C. elegans*. ***Genome research***, *27*(12), 2096–2107.
***co-first author**

Yeo, R., & Brunet, A. (2016). Deconstructing Dietary Restriction: A Case for Systems Approaches in Aging. ***Cell Metabolism***, *23*(3), 395–396. https://doi.org/10.1016/j.cmet.2016.02.018

Burkewitz, K., Morantte, I., Weir, H., **Yeo, R**., Zhang, Y., Huynh, F. K., Ilkayeva, O. R., Hirschey, M. D., Grant, A. R., & Mair, W. B. (2015). Neuronal CRTC-1 governs systemic mitochondrial metabolism and lifespan via a catecholamine signal. ***Cell***, *160*(5), 842–855.

Debette, S., Ibrahim Verbaas, C. A., Bressler, J., Schuur, M., Smith, […], **Yeo, R**., […], Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium (2015). Genome-wide studies of verbal declarative memory in nondemented older people: the Cohorts for Heart and Aging Research in Genomic Epidemiology consortium. ***Biological Psychiatry***, *77*(8), 749–763.

PATENTS

SYSTEMS AND METHODS FOR GENETIC MODULATION

SYSTEMS AND METHODS FOR GENETIC MODULATION TO TREAT OCULAR DISEASES

ENGINEERED GENE EFFECTORS, COMPOSITIONS, AND METHODS OF USE THEREOF

SYSTEMS AND METHODS FOR REGULATING TARGET GENES

SYSTEMS AND METHODS FOR GENE REGULATION

METHODS AND SYSTEMS FOR GENERATING FUNCTIONAL BIOLOGICAL SEQUENCES

METHODS AND SYSTEMS FOR IDENTIFYING GUIDE RNA SEQUENCES

AWARDS/FELLOWSHIPS

Genentech Foundation Pre-doctoral Fellowship - *$80,000 over 1 year*   *July 2018*
Office of Graduate Education Travel Grant - *$1000*   *March 2018*
Smith Fellowship (Stanford Graduate Fellowship) - $*250,000 over 3 years*   *2014-2017*

ORAL PRESENTATIONS

American Society for Gene & Cell Therapy – On- and Off-Target Method Development   *May 10, 2024*
- *Casmini-tool: a Comprehensive Database for Efficient and Specific Guide RNA Design using dCasMINI*

Stanford Genetics Departmental Seminar - Current Issues in Genetics (Stanford, CA)   *Nov 1, 2019*
- *Chromatin dynamics predict cell migration changes with age in neural stem cells*

Bay Area Aging Meeting (Buck Institute, CA)   *March 11, 2019*
- *The dynamic chromatin landscape of neural stem cell aging*

Stanford Genetics Departmental Seminar - Current Issues in Genetics (Stanford, CA)   *March 8, 2019*
- *The dynamic chromatin landscape of neural stem cell aging*

Stanford Genetics Department PhD Recruitment (Stanford, CA)   *February 28, 2019*
- *Epigenomics of neural stem cell aging*

Stanford Wu Tsai Neurosciences Institute - Brain Rejuvenation Symposia (Stanford, CA)   *February 1, 2019*
- *Epigenomics of neural stem cell aging*

Stanford Genetics Departmental Seminar - Current Issues in Genetics (Stanford, CA)   *May 18, 2018*
- *Epigenetic regulation of quiescence and activation in the neurogenic niche throughout aging*

Stanford Genetics Departmental Seminar - Current Issues in Genetics (Stanford, CA)   *August 4, 2017*
- *Chromatin accessibility of the neurogenic niche throughout aging*

Stanford Genome Training Program (SGTP) Seminar (Stanford, CA)   *June 2, 2016*
- *Investigating genome-wide chromatin accessibility changes in the NSC niche throughout aging*

POSTERS

American Society for Gene & Cell Therapy – Epigenetic Editing and RNA Editing   *May 10, 2024*
- *Accelerating the Discovery of Novel Hypercompact Transcriptional Activators with Machine Learning*

NeurIPS Workshop on Generative AI and Biology   *Dec 15, 2023*
- *Improving few-shot learning-based protein engineering with evolutionary sampling*

Keystone Conference – Epigenetics, Chromatin, Development, and Disease   *Mar 12-15, 2023*
- *Discovery and engineering of hypercompact transcriptional modulators for robust and durable target gene activation*

Cold Spring Harbor Laboratory – Mechanisms of Aging (Virtual)   *Sep 22-25, 2020*
- *Chromatin accessibility dynamics underlie a decline in neural stem cell migratory ability with age*

Bay Area Aging Meeting (Stanford, CA)   *Dec 5, 2019*
- *Chromatin dynamics predict age-related changes in migratory ability in subventricular neural stem cells*

Stanford Annual Genetics Department Retreat (Monterey, CA)   *Sep 11-13, 2019*
- *Chromatin dynamics and cell migration changes with age in subventricular neural stem cells*

Bay Area Aging Meeting (Buck Institute, CA)   *Mar 11, 2019*
- *Epigenetic regulation of quiescence and activation in the neurogenic niche throughout aging*

Bay Area Aging Meeting (UCSF, CA)   *Nov 9, 2018*
- *Epigenetic regulation of quiescence and activation in the neurogenic niche throughout aging*

Stanford Annual Genetics Department Retreat (Monterey, CA)   *Sep 19-21, 2018*
- *Epigenetic regulation of quiescence and activation in the neurogenic niche throughout aging*

Cancer Epigenetics Keystone Conference: New Mechanisms, New Therapies (Breckenridge, CO)   *Feb 10-14, 2018*
- *Epigenetic regulation of quiescence and activation in the neurogenic niche throughout aging*

Bay Area Aging Meeting (Berkeley, CA)   *May 17, 2018*
- *Epigenetic regulation of quiescence and activation in the neurogenic niche throughout aging*

16th Annual CS229 Stanford Machine Learning Poster Session   *Dec 13, 2017*
- *Predicting global gene expression from chromatin accessibility in the developing mammalian forebrain*

Bay Area Aging Meeting (Stanford, CA)   *Nov 3, 2017*
- *Investigating changes in chromatin accessibility in the neurogenic niche throughout aging*

Stanford Annual Genetics Department Retreat (Monterey, CA)   *Sep 13-15, 2017*
- *Investigating changes in chromatin accessibility in the neurogenic niche throughout aging*

Bay Area Aging Meeting (Buck Institute, CA)   *Mar 30, 2017*
- *Investigating changes in chromatin accessibility in the neurogenic niche throughout aging*

Bay Area Aging Meeting (UCSF, CA)   *Nov 7, 2016*
- *Investigating changes in chromatin accessibility in the neurogenic niche throughout aging*

Stanford Annual Genetics Department Retreat (Monterey, CA)   *Sep 21-23, 2016*
- *Investigating changes in chromatin accessibility in the neurogenic niche throughout aging*

Bay Area Aging Meeting (Berkeley, CA)   *May 26, 2016*
- *Investigating changes in chromatin accessibility in the neurogenic niche throughout aging*

MENTORSHIP

Olivia Zhou (Stanford MD/PhD student) *July 2020-July 2021*
- Trained Olivia in multiple murine neuroscience techniques including microdissections, cardiac perfusions, cryosectioning, immunohistochemistry, neural stem cell tissue culture, and flow cytometry
- Advised a project to investigate how neural stem cell localization and adhesion signatures change with age in the SVZ *in vivo* by immunofluorescent confocal imaging

Emily Greenwald (Stanford PhD Genetics rotation student) *Sep 2018 – Dec 2018*
- Designed a project to investigate age-dependent senescent signatures using immunohistochemical techniques in the SVZ, OB, cortex, liver, kidney, heart, and lung of aged mice *in vivo*
- Supervised *in vitro* research on over-expressing chromatin-modifying genes on NSC proliferative potential

Matthew Buckley (Stanford PhD Genetics rotation student) *Jan 2017 – March 2017*
- Devised a machine learning project to integrate genome-wide ATAC-seq data with RNA-seq transcriptomic data to predict expression from chromatin accessibility in sub-populations of the neural stem cell lineage
- Advised in proper machine learning practices for linear regression, logistic regression, SVMs, and random forests.
- Investigated different techniques for batch effect regression (Limma, ComBat, SVA) using R

Max Lenail (Palo Alto high school student) *Summer 2016*
- Advised a project in *C. elegans* husbandry, fluorescent microscopy and the characterization of genetic reporters

ADDITIONAL INFORMATION

- Fluency in English and French; proficiency in Spanish
- Avid marathon runner and triathlete (2016-present)
- Hiking & backpacking (CPR-certified (2010-present), Wilderness First Aid certified (2017-present))
- Contemporary literature, sci-fi, rock climbing, cooking, mathematics, ant sociobiology

REFERENCES

Anne Brunet, PhD
PhD Thesis Advisor
Stanford University, CA, USA
Department of Genetics
650 725 8042 | anne.brunet@stanford.edu

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CLASSES

	BIOMEDICAL			MATHEMATICS	
MIT 7.012	Intro Biology	2009	MIT 18.02A	Multivariable Calculus	2009
MIT 5.111	Principles of Chemistry	2010	MIT 8.01	Newtonian Mechanics	2009
MIT 5.12	Organic Chemistry	2010	MIT 8.02	Electromagnetism	2010
MIT 7.03	Genetics	2010	MIT 18.100B	Real Analysis	2010
MIT 20.111	Biomolecular Thermodynamics	2011	MIT 18.700	Theoretical Linear Algebra	2010
MIT 5.07	Biological Chemistry	2011	MIT 6.00	Introduction to Programming (Python)	2011
MIT 20.320	Analysis of Biomolecular & Systems Biology	2011	MIT 18.440	Probability & Random Variables	2011
MIT 20.109	Laboratory Fundamentals of Biological Engineering	2011	MIT 18.04	Complex Variables with Applications	2013
MIT 20.310	Molecular, Cellular & Tissue Biomechanics	2012	MIT 18.445	Introduction to Stochastic Processes	2013
MIT 20.330	Fields, Forces & Flows in Biological Systems	2012	SU STATS116	Theory of Probability	2015
MIT 7.06	Cell Biology	2012	SU CS106A	Programming Methodology (Java)	2015
MIT 20.201	Mechanisms of Drug Action	2012	SU STATS200	Introduction to Statistical Inference	2015
MIT 20.305	Principles of Synthetic Biology	2012	SU STATS260	Workshop in Advanced Biostatistics	2015
MIT 20.309	Instrumentation & Measurement in Biological Systems	2012	SU STATS216	Statistical Learning	2015
MIT 20.380	Biological Engineering Design	2013	SU CS161	Design and Analysis of Algorithms	2016
SU BIOS200	Foundations in Experimental Biology	2014	SU BIO329	Matrix Methods for Dynamic Models and Data Analysis	2016
SU GENE215	Frontiers in Biological Research	2014	SU BMI206	Informatics in Industry	2017
SU GENE205	Advanced Genetics	2015	SU CS229	Machine Learning	2017
SU GENE211	Genomics	2015			
SU GENE210	Genomics & Personalized Medicine	2015			
SU VSC0021	Mouse Handling & Basic Techniques	2016			
SU VSC0025	Stereotaxic Surgery in Rodents	2016			
SU GENE204	Essentials of Multidimensional Flow Cytometry	2017			
SOMGEN275	Leadership and Strategies for Health Care Delivery and Innovation	2018			
SU VSC0022	Rodent Aseptic Surgery Techniques	2019			