

RAHUL SATIJA
Curriculum Vitae

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101 Avenue of the Americas, 4th Floor
New York, NY 10013

EDUCATION

December 1, 2014 – Present

Core Member, New York Genome Center
Associate Professor, New York University, Center for Genomics and Systems Biology
Affiliate Faculty, NYU Langone Medical Center, Institute for Systems Genetics
Disciplines : Statistical learning, computational biology, single cell genomics

2011-2014 – Broad Institute of Harvard and MIT, Cambridge, MA

Ruth L. Kirchstein Postdoctoral Fellow
Advisor: Dr. Aviv Regev

2010-2011 – Medical Research Council, Mammalian Genetics Unit, Harwell UK

Medical Research Council Training Fellow in Biomedical Informatics
Advisor: Dr. Pat Nolan

2006-2010 - Oxford University, Balliol College, Oxford UK

Rhodes Scholar
Degree Course: D.Phil (Oxon) in Statistics, Advisor: Dr. Jotun Hein

2002-2006 - Duke University, Durham NC

Degree Course: B.Sc. in Biology, Music, Mathematics, *Summa Cum Laude*

HONORS AND AWARDS

2020	Director, NIH Center for Excellence in Genomic Science (CEGS)
2016	NIH ‘New Innovator’ Award
2016	Kavli Fellow, National Academy of Sciences
2012	Ruth L. Kirchstein National Research Service Award Postdoctoral Fellowship
2006	Rhodes Scholarship
2006	Hertz Foundation Graduate Fellowship Award

PUBLICATIONS (* - equal contribution, † - corresponding author)

Dictionary learning for integrative, multimodal, and scalable single-cell analysis

Y Hao, T Stuart, M Kowalski, S Choudhary, P Hoffman, A Hartman, A Srivastava, G Molla, S Madad, C Fernandez-Granda, **R Satija**†
Nature Biotechnology (In Press)

Efficient combinatorial targeting of RNA transcripts in single cells with Cas13 RNA Perturb-seq

HH Wessels*, A Mendez-Mancilla*, E Papalex, WM Mauck, L Lu, JA Morris, E Mimitou, P Smibert, NE Sanjana†, **R Satija**†
Nature Methods (2022)

Nanobody-tethered transposition allows for multifactorial chromatin profiling at single-cell resolution
T Stuart, S Hao, B Zhang, L Mekerishvili, DA Landau, S Maniatis, **R Satija**, I Raimondi
Nature Biotechnology (2022)

Characterizing cellular heterogeneity in chromatin state with scCUT&Tag-pro
B Zhang*, A Stivastava*, E Mimitou, T Stuart, I Raimondi, Y Hao, P Smibert, **R Satija**†
Nature Biotechnology (2022)

Comparison and evaluation of statistical error models for scRNA-seq
S Choudhary, **R Satija**†
Genome Biology (2022)

Single nucleus multi-omics identifies human cortical cell regulatory genome diversity
C Luo, H Lui, F Xie, E Armand, K Siletti, T Bakken, R Fang, W Doyle, T Stuart, R Hodge, L Hu, B Wang, Z Zhang, S Preissl, DS Lee, J Zhou, SY Niu, DA Davis, DC Mash, **R Satija**, JR Dixon, S Linnarsson, E Lein, MM Behrens, B Ren, E Mukamel, J Ecker
Cell Genomics (2022)

Integrated analysis of multimodal single-cell data
Y Hao*, S Hao*, E Andersen-Nissen, WM Mauck, S Zheng, A Butler, MJ Lee, AJ Wilk, C Darby, M Zager, P Hoffman, M Stoeckius, E Papalexi, EP Mimitou, J Jain, A Srivastava, T Stuart, LB Fleming, B Yeung, AJ Rogers, JM McElarth, CA Blish, R Gottardo, P Smibert†, **R Satija**†
Cell (2021)

Scalable, multimodal profiling of chromatin accessibility, gene expression, and protein levels in single cells
EP Mimitou*, CA Lareau*, KY Chen*, AL Zorzetto-Fernandes, Y Hao, Y Takeshima, W Luo, T Huang, BZ Yeung, EP Papalexi, PI Thaoke, T Kibayashi, HB Wing, M Hata, **R Satija**, KL Nazor, S Sakaguchi, LS Ludwin, VG Sankaran, A Regev, P Smibert
Nature Biotechnology (2021)

Characterizing the molecular regulation of inhibitory immune checkpoints with multi-modal single-cell screens
E Papalexi, E Mimitou, A Butler, S Foster, B Bracken, WM Mauck, H Wessels, BZ Yeung, P Smibert, **R Satija**†
Nature Genetics (2021)

Multimodal single-cell chromatin analysis with Signac
T Stuart†, A Srivastava, C Lareau, **R Satija**†
Nature Methods (2021)

A latent subset of human hematopoietic stem cells resists regenerative stress to preserve stemness
KB Kaufmann, AGX Zeng, E Coyaoud, L Garcia-Prat, E Papalexi, A Murison, EMN Laurent, OI Gan, K Pan, J McLeod, H Boutzen, S Zandi, S Takayanagi, **R Satija**, B Raught, SZ Xie, J Dick
Nature Immunology (2021)

geneBasis: an iterative approach for unsupervised selection of targeted gene panels from scRNA-seq
A Missarova, J Jain, A Butler, S Ghazanfar, T Stuart, M Brusko, C Wasserfall, H Nick, T Brusko, M Atkinson, **R Satija***†, J Marioni*†
Genome Biology (2021)

Selective metabolic redundancy of Gpi1 allows for specific inhibition of inflammatory Th17 cells.

L Wu, KER Hollinshead, Y Hao, C Au, L Kroehling, C Ng, L Woan-Yu, D Li, HM Silva, J Shin, JJ Lafaille, R Possemato, ME Pacold, TY Papagiannakopoulos, AC Kimmelman, **R Satija**, DR Littman
Cell (2020)

The strength and pattern of natural selection on gene expression in rice.

SC Groen, I Calic, Z Joly-Lopez, AE Platts, JY Choi, M Natividad, K Dorph, WM Mauck, B Bracken, CLU Cabral, A Kumar, RO Torres, **R Satija**, G Vergara, A Henry, SJ Franks, MD Purugganan
Nature (2020)

Comprehensive integration of single cell data

T Stuart*, A Butler*, P Hoffman, C Hafemeister, E Papalexi, WM Mauck, M Stoeckius, P Smibert,
R Satija†
Cell (2019)

The bone marrow micro-environment at single cell resolution

A Tikhonova, I Dolgalev, H Ku, K Sivaraj, E Hoxha, A Cuesta-Dominguez, S Pinho, I Akhmetzyanova , J Gao , M Witkowski , MR Guillaumot , M Gutkin , Y Zhang , C Marier , C Diefenbach , S Kousteni , A Heguy , H Zhong , D Fooksman , J Butler , A Economides , PS Frenette , R Adams , **R Satija**, A Tsimirgi, I Aifantis
Nature (2019)

A single cell transcriptional roadmap for cardiopharyngeal fate diversification

W Wang*, X Niu*, T Stuart, J Estelle, R Kelly, **R Satija*†**, L Christiaen*†
Nature Cell Biology (2019).

Normalization and variance stabilization of single-cell RNA-seq data using regularized negative binomial regression

C Hafemeister†, **R Satija†**
Genome Biology (2019)

Toward a Common Coordinate Framework for the Human Body

J Rood, T Stuart*, S Ghazanfar*, T Biancalini*, E Fisher, A Butler, A Hupalowska, L Gaffney, WM Mauck, G Eraslan, JC Marioni†, A Regev†, **R Satija†**
Cell (2019)

The human body at cellular resolution: the NIH Human Biomolecular Atlas Program

HuBMAP Consortium
Nature (2019)

Integrative single-cell analysis

T Stuart, **R Satija†**
Nature Reviews Genetics (2019)

Multiplexed detection of proteins, transcriptomes, clonotypes, and CRISPR perturbations in single cells.

E Mimitou, A Cheng, A Montalbano, S Hao, M Stoeckius, M Legut, T Roush, A Herrera, E Papalexi, Z Ouyang, **R Satija**, NE Sanjana, S Koralov, P Smibert
Nature Methods (2019)

Inhibitory neuron diversity originates from cardinal classes shared across germinal zones.

C Mayer*, C Hafemeister*, RC Bandler*, R Machold, G Fishell *†, **R Satija*†**

Nature (2018)

Integrated analysis of single cell transcriptomic data across conditions, technologies, and species

A Butler, P Hoffman, P Smibert, E Papalexi, **R Satija**†

Nature Biotechnology (2018)

Single-Cell RNA-Seq Of Rheumatoid Arthritis Synovial Tissue Using Low Cost Microfluidic Instrumentation

W Stephenson*, LT Donlin*, A Butler*, C Rozo, A Rashidfarrokhi, SM Goodman, LB Ivashkiv, VP Bykerk, DE Orange, RB Darnell, HP Swerdlow*†, **R Satija***†

Nature Communications (2018)

Molecular transitions in early progenitors during human cord blood hematopoiesis

S Zheng, E Papalexi, A Butler, W Stephenson, **R Satija**†

Molecular Systems Biology (2018)

Phenotypic convergence in the brain: distinct transcription factors regulate common terminal neuronal characters

N Konstantinides, K Kapuralin, C Fadil, L Barboza, **R Satija**, C Desplan

Cell (2018)

Cell 'hashing' with barcoded antibodies enables multiplexing and doublet detection for single cell genomics

M Stoeckius*, S Zheng*, B Houck-Loomis, S Hao, B Yeung, WM Mauck, P Smibert*†, **R Satija***†

Genome Biology (2018)

Kinetics of adult hematopoietic stem cell differentiation in vivo

S Upadhya, CM Sawai, E Papalexi, A Rashidfarrokhi, G Jang, P Chattopadhyay, **R Satija**, B Reizis

Journal of Experimental Medicine (2018)

Large-scale simultaneous measurement of epitopes and transcriptomes in single cells.

M Stoeckius, C Hafemeister, W Stephenson, B Houck-Loomis, H Swerdlow, **R Satija**, P Smibert

Nature Methods (2017).

Single-cell RNA-seq reveals new types of human blood dendritic cells, monocytes and progenitors

AC Villani*, **R Satija***, G Reynolds, K Shekhar, S Sarikova, A Butler, S Zheng, W Li, P Jager, O Rosenblatt-Rosen, M Hannifa, A Regev, N Hacohen.

Science (2017)

Single cell RNA-sequencing to explore immune cell heterogeneity

E Papalexi, **R Satija**†

Nature Reviews Immunology (2017).

Seq-Well: portable, low-cost RNA sequencing of single cells at high throughput

TM Gierahn, MH Wadsworth, TK Hughes, BD Bryson, A Butler, **R Satija**, S Fortune, JC Love, AK Shalek

Nature Methods (2017)

The Human Cell Atlas

A Regev, SA Teichmann, ES Lander, 56 named authors (including **R Satija**), Human Cell Atlas Meeting Participants

eLife (2017)

Landscape of X chromosome inactivation across human tissues

T Tukiainen, AC Villani, A Yen, MA Rivas, JL Marshall, **R Satija**, M Aguirre, L Gauthier, M Fleharty, A Kirby, BB Cummings, SE Castel, KJ Karczewski, F Aguet, A Byrnes, T Lappalainen, A Regev, KG Ardlie, N Hacohen, DG MacArthur, GTEx Consortium
Nature (2017).

A multi-step transcriptional and chromatin state cascade underlies motor neuron programming from embryonic stem cells

S Velasco, MM Ibrahim, A Kakumanu, G Garipler, B Aydin, MA Al-Sayegh, A Hirsekorn, F Abdul-Rahman, **R Satija**, U Ohler, S Mahony, EO Mazzoni
Cell Stem Cell (2016)

Human dendritic cells (DCs) are derived from distinct circulating precursors that are pre-committed to become CD1c+ or CD141+ DCs.

G Breton, S Zheng, R Valieris, I Silva, **R Satija**, M Nussenzweig.
Journal of Experimental Medicine (2016)

Root Regeneration Triggers an Embryo-like Sequence Guided by Hormonal Interactions

I Efroni, A Mello, T Nawy, PL Ip, R Rahni, N Delrose, A Powers, **R Satija**, K Birnbaum.
Cell (2016)

Single-cell analysis reveals key roles for Bcl11a in regulating stem cell fate decisions.

Powers AN, **Satija R**†.
Genome Biology (2015)

Spatial reconstruction of single-cell gene expression.

R Satija*, JA Farrell*, D Gennert, AF Schier, A Regev.
Nature Biotechnology (2015).

Highly Parallel Genome-wide Expression Profiling of Individual Cells Using Nanoliter Droplets

EZ Macosko, A Basu, **R Satija**, J Nemesh, K Shekhar, M Goldman, I Tirosh, A Bialas, N Kamitaki, E Martersteck, JT Trombetta, DA Weitz, JR Sanes, AK Shalek, A Regev, SA McCarroll.
Cell (2015).

MERFishing for spatial context.

AK Shalek, **R. Satija**†. **Trends in Immunology** (2015).

The Regulatory Factor ZFHX3 Modifies Circadian Function in SCN via an AT Motif-Driven Axis.

Parsons MJ, Brancaccio M, Sethi S, Maywood ES, **Satija R**, Edwards JK, et al. **Cell** (2015)

Pathogen cell-to-cell variability drives heterogeneity in host immune responses.

Avraham R, Haseley N, Brown D, Penaranda C, Jijon HB, Trombetta JJ, **Satija R**, Shalek AK, Xavier RJ, Regev A, Hung DT. **Cell** (2015)

Single-Cell Genomics Unveils Critical Regulators of Th17 Cell Pathogenicity.

Gaublomme JT, Yosef N, Lee Y, Gertner RS, Yang L V, Wu C, Pandolfi P, Mak T, **Satija R**, Shalek AK, Kuchrko VK, Park H, Regev A. **Cell** (2015)

A Generic and Cell-Type-Specific Wound Response Precedes Regeneration in Planarians.

Wurtzel O, Cote LE, Poirier A, **Satija R**, Regev A, Reddien PW. **Dev Cell** (2015)

Heterogeneity in immune responses- from populations to single cells.

R. Satija†, A.K. Shalek†. **Trends in Immunology** (2014).

Large-scale single cell RNA-Seq reveals dynamic paracrine control of cellular variation.

A.K. Shalek*, **R. Satija***†, J. Shuga*, J.J. Trombetta, D. Lu, D. Gennert, P. Chen, R.S. Gertner, J.T. Gaublomme, N. Yosef, S. Schwartz, B. Fowler, S. Weaver, J. Wang, X. Wang, R. Ding, R. Raychowdhury, N. Hacohen, H. Park, A.P. May†, A. Regev†. **Nature** (2014).

Single-cell transcriptomics reveals bimodality in expression and splicing in immune cells.

A.K. Shalek*, **R. Satija***, X. Adiconis, R.S. Gertner, J.T. Gaublomme, R. Raychowdhury, S. Schwartz, N. Yosef, C. Malboeuf, D. Lu, J.J. Trombetta, D. Gennert, A. Gnirke, A. Goren, N. Hacohen, J.L. Levin, H. Park, Regev, A. (2013). Single-cell transcriptomics reveals bimodality in expression and splicing in immune cells. **Nature** (2013).

Comparative analysis of RNA sequencing methods for degraded or low-input samples.

X. Adiconis*, D. Borges-Rivera*, **R. Satija**, D.S. DeLuca, M.A. Busby, A. Berlin, A. Sivachenko, D. A. Thompson, A. Wysocker, T. Fennell, A. Gnirke, N. Pochet, A. Regev, J.Z. Levin. Comparative analysis of RNA sequencing methods for degraded or low-input samples. **Nature Methods** (2013).

Dynamic regulatory network controlling TH17 cell differentiation. N. Yosef, A.K. Shalek, J.

Gaublomme, Y. Lee, A. Awasthi, H. Jin, C. Wu, K. Karwacz, S. Xiao, M. Jorgolli, D. Gennert, **R. Satija**, A. Shakya, D.Y. Lu, J.J. Trombetta, M. Pillai, P.J. Ratcliffe, M.L. Coleman, M. Bix, D. Tantin, H. Park, V.K. Kuchroo, A. Regev. **Nature** (2013).

High-Resolution Mapping Reveals a Conserved, Widespread, Dynamic mRNA Methylation Program in Yeast Meiosis. S. Schwartz*, S. Agarwala*, M.R. Mumbach, M. Jovanovic, P. Mertins, A. Shishkin, Y.

Tabach, T.S. Mikkelsen, **R. Satija**, G. Ruvkun, S. Carr, E.S. Lander, G.R. Fink, A. Regev. **Cell** (2013).

The TAGteam motif facilitates binding of 21 sequence-specific transcription factors in the *Drosophila* embryo. **R. Satija**, R.K. Bradley. **Genome Research** (2012)

The atypical calpains: evolutionary analyses and roles in *Caenorhabditis elegans* cellular degeneration.

P.I. Joyce, **R. Satija**, M. Chen, P.E. Kuwabara. **PLoS Genetics** (2012).

Genome-wide functional element detection using pairwise statistical alignment outperforms multiple genome footprinting techniques. **R. Satija**†, J. Hein, G. A. Lunter. **Bioinformatics** (2010).

BigFoot: Bayesian alignment and footprinting of large datasets. **R. Satija**†, I. Miklos, A. Novak, R. Lyngsoe, J. Hein. **BMC Evol. Biol** (2009).

Stochastic models of sequence evolution including insertion-selection events. I. Miklós, A. Novák, **R.**

Satija, R. Lyngsoe, J. Hein. **Statistical Methods in Medical Research** (2009).

Combining statistical alignment and phylogenetic footprinting to detect regulatory elements.

R. Satija†, L. Pachter, and J. Hein. **Bioinformatics** (2008).

The Genome of the Sea Urchin *Strongylocentrotus purpuratus*. Sea Urchin Genome Sequencing Consortium. **Science** (2006).

In situ neutron imaging technique for evaluation of water management systems in operating PEM fuel cells. **R. Satija**, D.L. Jacobson, M. Arif, S.A. Werner. **Journal of Power Sources** (2004).

PROFESSIONAL ACTIVITIES

Reviewer for: Science, Nature, Cell, Nature Biotechnology, Nature Immunology, Nature Methods, Science Signalling, Cell Stem Cell, Molecular Systems Biology, Trends in Immunology, Molecular Biology and Evolution, Genome Biology, Genome Research, PLoS Computational Biology, Bioinformatics, BMC Bioinformatics

I am a member of the Analysis working Group for the Human Cell Atlas, a group of eight scientists who recommend optimal experimental design and best computational practices for the broader consortium.

I have led the creation of two yearly symposia. Each year (2016-present), we host Single Cell Genomics Day, a practical workshop to teach others how to apply new techniques in the field. All talks are free for in-person attendees, and are openly live-streamed online. In 2019, we additionally launched the NYU-Nature conference “Next-generation genomics”, aiming to highlight new research in sequencing technology and analysis. We exclusively included junior faculty as invited speakers, to promote discoveries made by new investigators.

SOFTWARE PACKAGES

Seurat: R-toolkit for single cell genomics
<http://www.satijalab.org/seurat>

Azimuth: Automated mapping of single-cell sequencing datasets to reference atlases
<http://azimuth.hubmapconsortium.org>

GRAPeFoot: Simultaneous Bayesian pairwise genomic alignment and functional element annotation
<http://sourceforge.net/projects/grapefoot/>

BigFoot: Bayesian multiple alignment and phylogenetic footprinting with MCMC
<http://sourceforge.net/projects/bigfoot/>

TEACHING AT NYU

Instructor of Record

Fall 2020	BIOL-GA 2025 : Statistical learning for large-scale biological data 15 students; 15/15 classes
Fall 2019	BIOL-GA 2025 : Statistical learning for large-scale biological data 15 students; 15/15 classes
Fall 2017	BIOL-GA 2025 : Statistical learning for large-scale biological data 14 students; 15/15 classes
Fall 2016	BIOL-GA 2025 : Statistical learning for large-scale biological data 15 students; 15/15 classes

Contributing lecturer

Spring 2017 BIOL-GA 2020. Biocore IV; 1 class
 Spring 2017 BIOL-GA 2019. Biocore IV; 1 class
 Spring 2017 BIOL-GA 2004. Biocore IV; 1 class
 Spring 2016 BIOL-GA 2004. Biocore IV; 1 class
 Spring 2016 BIOL-GA 2131. Developmental and Stem Cell Systems II; 1 class
 Spring 2015 BIOL-GA 2004. Biocore IV; 1 class

STUDENT AND TRAINEE SUPERVISION

Postdoctoral	Christian Mayer (2014-2018), joint w/Gord Fishell Current position: Group Leader at Max Planck Institute for Neurobiology Lin Wu (2015-2021), joint w/Dan Littman Current position: Group Leader at Shenzhen Bay Laboratory Hans-Hermann Wessels (2018-Present) Tim Stuart (2018-Present) Bingjie Zhang (2018-Present) Saket Choudhary (2020-Present) John Blair (2020-Present) Kristof Torkenczy (2020-Present) Avi Srivastava (2020-Present) Longda Jiang (2021-Present)
Ph.D. students	Shiwei Zheng (2015-2019) Current Position: Postdoctoral Fellow, Harvard Medical School Andrew Butler (2016-2021) Current Position: Postdoctoral Fellow, Fred Hutchinson Cancer Research Institute Efi Papalexi (2016-Present) Current Position: Senior Research Scientist, Parse Biosciences Yuhan Hao (2018-Present) Madeline Kowalksi (2020-Present)
M.S. students	Xiang Niu (2015-2017) Bernadette Bracken (2016-2019) Ashley Powers (2015-2016) Shaista Madad (2020-2021)
Thesis Committees	Kristen Gulino (2016-2019) Chang Wang (2017-2019) Geraldine Cayanan (2019-present) Dalia Barkley (2018-2021) Soobeom Lee (2020-present) Daniel Obaji (2020-present)