# Keynote speakers

## Naomi HABIB, PhD | Edmond & Lily Safra Center for Brain Sciences (ELSC), Israel

Naomi Habib is an assistant professor at the ELSC Brain Center at the Hebrew University of Jerusalem since July 2018. Habib's research focuses on understanding how complex interactions between diverse cell types in the brain and between the brain and other systems in the body, are mediating neurodegenerative diseases and other aging-related pathologies. Naomi combines in her work computational biology, genomics and genome-engineering, and is a pioneer in single nucleus RNA-sequencing technologies and their applications to study cellular diversity and molecular processes in the brain. Naomi did her postdoctoral at the Broad Institute of MIT/Harvard working with Dr. Feng Zhang and Dr. Aviv Regev, and earned her PhD in computational biology from the Hebrew University of Jerusalem in Israel, working with Prof. Nir Friedman and Prof. Hanah Margalit.

*Selected publications:*

- *Habib N, McCabe C*, Medina S*, Varshavsky M*, Kitsberg D, Dvir R, Green G, Dionne D, Nguyen L, Marshall J.L, Chen F, Zhang F, Kaplan T, Regev A, Schwartz M. (2019) Unique disease-associated astrocytes in Alzheimer's disease. Nature Neuroscience. In Press.*
- *Habib N*, Basu A*, Avraham-Davidi I*, Burks T, Choudhury SR, Aguet F, Gelfand E, Ardlie K, Weitz DA, Rozenblatt-Rosen O, Zhang F, and Regev A. (2017). Deciphering cell types in human archived brain tissues by massively-parallel single nucleus RNA-seq. Nature Methods. Oct;14(10):955-958.*
- *Habib N*, Li Y*, Heidenreich M, Sweich L, Avraham-Davidi I, Trombetta J, Hession C, Zhang F, Regev A. (2016) Div-Seq: Single-nucleus RNA-Seq reveals dynamics of rare adult newborn neurons. Science. 353, 925-928.*

## Kenneth HARRIS, PhD | London's Global University (UCL), UK

Kenneth Harris studied mathematics at Cambridge University, did a PhD in robotics at UCL, then moved to Rutgers University in the United States for postdoctoral work in neuroscience. He was an Associate Professor of Neuroscience at Rutgers and Professor of Neurotechnology at Imperial College London, before returning to UCL as Professor of Quantitative Neuroscience. His research aims to understand how the brain processes sensory signals, and integrates them with internal signals to guide decision and action. Together with Matteo Carandini, he co-direct the Cortical Processing Laboratory at UCL (www.ucl.ac.uk/cortexlab), addressing these questions using a combination of experiment and computational analysis. The lab work mostly on the mouse brain, using experimental techniques such as single-cell and in situ transcriptomics, high-count electrodes, optogenetics, 2-photon and widefield calcium imaging, operant conditioning, and virtual

reality simulation. They also develop and deploy new computational techniques to turn the "big data" produced by these experiments into conclusions about brain function.

*Selected publications:*

- *Qian X, Harris KD, Hauling T, Nicoloutsopoulos D, Manchado AM, Skene N, Hjerling-Leffler J, Nilsson M. (2019) Probabilistic cell typing enables fine mapping of closely related cell types in situ. Nature Methods doi:10.1038/s41592-019-0631-4.*
- *Harris, K.D., Hochgerner, H., Skene, N., Magno, L., Katona, L., Bengtsson Gonzales, C., Somogyi, P., Kessaris, N., Linnarsson, S., Hjerling-Leffler, J. (2018). Classes and continua of hippocampal CA1 inhibitory neurons revealed by single-cell transcriptomics. PLoS Biology 16 (6), e2006387*
- *Stringer C, Pachitariu M, Steinmetz NA, Carandini M, Harris KD (2019). High-dimensional geometry of visual cortical population activity. Nature 571(7765):361-365 (full article)*
- *Stringer C, Pachitariu M, Steinmetz NA, Reddy CB, Carandini M, Harris KD (2019). Spontaneous behaviors drive multidimensional, brainwide activity. Science 364(6437):255 (full article)*
- *Steinmetz NA, Zatka-Haas P Carandini M, Harris KD (2019). Distributed networks for choice, action, and engagement across the mouse brain. Nature doi:10.1038/s41586-019-1787-x (full article)*

## Ed LEIN, PhD | Allen Institute for Brain Science, USA

Ed Lein is an Investigator at the Allen Institute for Brain Science and an Affiliate Professor in the Department of Neurological Surgery at the University of Washington. He received a B.S. in biochemistry from Purdue University and a Ph.D. in neurobiology from UC Berkeley, and performed postdoctoral work at the Salk Institute for Biological Studies. He joined the Allen Institute in 2004 and has led the creation of large-scale gene expression atlases of the adult and developing mammalian brain as catalytic community resources, including the inaugural Allen Mouse Brain Atlas and developing and adult human and non-human primate brain atlases. Dr. Lein has driven a number of advances in using the tools of modern molecular genomics techniques to study brain organization at the regional, cellular and functional brain level, to understand what is unique about human brain, and to understand what is disrupted in brain diseases. He now leads the Human Cell Types program at the Allen Institute, which aims to create a comprehensive map of human brain cell types and circuits using quantitative single cell transcriptomic, anatomical and functional methods, and is a member of the NIH BRAIN Initiative Cell Census Network and the Human Cell Atlas.

*Selected publications:*

- *Hodge RD, Bakken TE, Miller JA, Smith KA, Barkan ER, Graybuck LT… Lein ES. Conserved cell types with divergent features in human versus mouse cortex. Nature. 2019 Sep;573(7772):61-68. doi: 10.1038/s41586-019-1506-7. Epub 2019 Aug 21.*
- *Bakken TE, Hodge RD, Miller JA, Yao Z, Nguyen TN, Aevermann B, Barkan E, Bertagnolli D, Casper T, Dee N, Garren E, Goldy J, Graybuck LT, Kroll M, Lasken RS, Lathia K, Parry S, Rimorin C, Scheuermann RH, Schork NJ, Shehata SI, Tieu M, Phillips JW, Bernard A, Smith KA, Zeng H, Lein ES, Tasic B. Single-nucleus and single-cell transcriptomes compared in matched cortical cell types. PLoS One. 2018 Dec 26;13(12):e0209648. doi: 10.1371/journal.pone.0209648. eCollection 2018.*

- *Boldog E, Bakken TE, Hodge RD, Novotny M, Aevermann BD, … Lein ES, Tamás G. Transcriptomic and morphophysiological evidence for a specialized human cortical GABAergic cell type. Nat Neurosci. 2018 Sep;21(9):1185-1195. doi: 10.1038/s41593-018-0205-2. Epub 2018 Aug 27.*
- *Tasic B, Yao Z, Graybuck LT, Smith KA, Nguyen TN, Bertagnolli D, … Lein E, Hawrylycz M, Svoboda K, Jones AR, Koch C, Zeng H. Shared and distinct transcriptomic cell types across neocortical areas. Nature. 2018 Nov;563(7729):72-78. doi: 10.1038/s41586-018-0654-5. Epub 2018 Oct 31.*
- *Hawrylycz MJ, Lein ES, Guillozet-Bongaarts AL, Shen EH, Ng L... An anatomically comprehensive atlas of the adult human brain transcriptome. Nature. 2012 Sep 20;489(7416):391-399. doi: 10.1038/nature11405.*

## Sten LINNARSSON, PhD | Karolinska Institute, Sweden

Sten Linnarsson took his PhD in 2001, studying neurotrophic factors regulating neuronal survival, growth and plasticity. Instead of a postdoc, he founded a company to develop methods for gene expression analysis and single-molecule DNA sequencing. In 2007, he was appointed assistant professor and in 2015 Professor of Molecular Systems Biology at Karolinska Institute. He was awarded the 2015 Erik K. Fernström Prize for his work in single-cell biology, and is a member of the European Molecular Biology Organization (EMBO), the Organizing Committee of the Human Cell Atlas initiative and the Nobel Assembly at Karolinska Institutet. Since 2007, Linnarsson has pursued single-cell biology with the ultimate aim to discover the complete branching manifold of cell states in the developing human nervous system. To achieve this goal, his group pioneered single-cell RNA sequencing, RNA single-molecule FISH, and advanced computational methods. In 2011, Linnarsson showed that cell types could be directly discovered and distinguished de novo, by unbiased sampling and sequencing of large numbers of single cells, without use of previously known markers, thus laying a conceptual foundation for the single-cell genomics field. He has made important contributions to single-cell technology: unique molecular identifiers (UMIs) for accurate quantification; Patch-seq for combined electrophysiology, morphology and transcriptomics; RNA velocity to extract dynamic information from snapshot measurements, and more. In a series of recent papers he has used these methods to explore the mammalian brain, culminating in a complete single-cell atlas of the mouse nervous system in 2018.

*Selected publications*

- *Amit Zeisel, Hannah Hochgerner, Peter Lönnerberg, Anna Johnsson, Fatima Memic, Job van der Zwan, Martin Häring, Emelie Braun, Lars E. Borm, Gioele La Manno, Simone Codeluppi, Alessandro Furlan, Kawai Lee, Nathan Skene, Kenneth D. Harris, Jens Hjerling Leffler, Ernest Arenas, Patrik Ernfors, Ulrika Marklund, Sten Linnarsson. Molecular architecture of the mouse nervous system. Cell 2018 Aug 8.*
- *Gioele La Manno, Ruslan Soldatov, Amit Zeisel, Emelie Braun … Sten Linnarsson* and Peter V. Kharchenko*. RNA Velocity of Single Cells. Nature 2018, Aug 7.*
- *Hochgerner H, Zeisel A, Lönnerberg P, Linnarsson S. Conserved properties of dentate gyrus neurogenesis across postnatal development revealed by single-cell RNA sequencing. Nature Neuroscience 2018 Feb*

- *Gioele La Manno, Daniel Gyllborg, Simone Codeluppi, Kaneyasu Nishimura, Carmen Salto, Amit Zeisel, Lars Eliot Borm, Simon R.W. Stott, Enrique M. Toledo, J. Carlos Villaescusa, Peter Lönnerberg, Jesper Ryge, Roger Alistair Barker, Ernest Arenas, Sten Linnarsson. Molecular Diversity of Midbrain Development in Mouse, Human and Stem Cells. Cell. 2016 Oct 9.*
- *Amit Zeisel*, Ana Munoz Manchado*, Simone Codeluppi, Peter Lönnerberg, Gioele La Manno, Anna Juréus, Sueli Marques, Hermany Munguba, Liqun He, Christer Betsholtz, Charlotte Rolny, Gonçalo Castelo-Branco, Jens Hjerling-Leffler, Sten Linnarsson. Cell types in the mouse cortex and hippocampus revealed by single-cell RNA-seq. Science 2015 Mar 6;347(6226):1138-42*

## John MARIONI, PhD | European Bioinformatics Institute (EMBL-EBI), UK

John Marioni is a Research Group Leader at the EMBL-European Bioinformatics Institute, a Senior Group Leader at the CRUK Cambridge Institute within the University of Cambridge and an Associate Faculty member of the Wellcome Sanger Institute. John read for his PhD at the University of Cambridge under the supervision of Professor Simon Tavaré before becoming a postdoctoral scholar under the supervision of Professor Matthew Stephens at the University of Chicago. John's lab has pioneered the development of methods for the analysis of singlecell genomics data. Subsequently, his lab has applied them, in conjunction with outstanding experimental collaborators, to understand cell fate decisions in early mammalian development. Complete list of Published Work in MyBibliography: www.ebi.ac.uk/research/marioni/publications

*Selected publications:*

- *MOFA+: a probabilistic framework for comprehensive integration of structured single-cell data; Argelaguet R, Arnol D, Bredikhin D, Deloro Y, Velten B, Marioni JC, Stegle O in Nature, Volume (2019) p.*
- *A single-cell molecular map of mouse gastrulation and early organogenesis; Pijuan-Sala B, Griffiths JA, Guibentif C, Hiscock TW, Jawaid W, Calero-Nieto FJ, Mulas C, Ibarra-Soria X, Tyser RCV, Ho DLL, Reik W, Srinivas S, Simons BD, Nichols J, Marioni JC, Göttgens B. in Nature, Volume 566 (2019) p.490-495*
- *Batch effects in single-cell RNA-sequencing data are corrected by matching mutual nearest neighbors; Haghverdi L, Lun ATL, Morgan MD, Marioni JC. in Nature Biotechnology, Volume 36 (2018) p.421-427*
- *Pooling across cells to normalize single-cell RNA sequencing data with many zero counts; Lun AT, Bach K, Marioni JC. in Genome Biology, Volume 17 (2016) p.75*
- *High-throughput spatial mapping of single-cell RNA-seq data to tissue of origin; Achim K, Pettit JB, Saraiva LR, Gavriouchkina D, Larsson T, Arendt D, Marioni JC. in Nature Biotechnology, Volume 33 (2015) p.503-509*

## Ana MARTIN VILLALBA, PhD | German Cancer Research Center (DKFZ), Germany

Ana Martin-Villalba studied medicine in Murcia, Spain and Leeds, UK and received her Ph.D. from the University of Heidelberg for investigating the role of death ligands in the ischemic brain. Thereafter she moved to the german cancer research center (DKFZ) where she further worked on devicing strategies for CNS repair following stroke, spinal cord injuries or chronic CNS disorders with a focus on the interaction of the CNS with the innate immune system and activation of endogenous stem cells. This work has also generated some understanding of how cancer stem cell contribute to tumor progression and set the basis for a phase-II clinical trial that successfully increased the overall survival of a subgroup of glioblastoma patient. She was awarded the prestigious Paul Ehrlich and Ludwig Darmstaedter Prize and the Heinz Maier-Leibnitz Prize for the development of pro-regenerative brain therapies. She was awarded an ERC grant in 2018. Her research now centers in understanding stem cell behaviour in homeostasis and disease including CNS-injuries and cancer, for which she has pioneered the application of single cell technologies.

*Selected publications:*


- *Baser, A., Skabkin, M., Kleber, S., Dang, Y., Guelcueler Balta, G.S., Kalamakis, G., Goepferich, M., Schefzik, R., Santos Lopez, A., Llorens Bobadilla, E., Schultz, C., Fischer , B., and Martin-Villalba, A.: (2019). Onset of differentiation is posttranscriptionally controlled in adult neural stem cells. Nature 566, 100-104*
- *Kalamakis, G., Bruene, D., Ravichandran, S., Bolz, J., Fan, W., Ziebell, F., Stiehl, T., Catalá-Martinez, F., Kupke, J., Zhao, S., Llorens-Bobadilla, E., Bauer, K., Limpert, S., Berger, B., Christen, U., Schmezer, P., Mallm, J.P., Berninger, B., Anders, S., Del Sol, A., Marciniak-Czochra, A., and Martin-Villalba, A. (2019). Quiescence modulates stem cell maintenance and regenerative capacity in the aging brain. Cell 176, 1407-1419*
- *Ziebell, F., Dehler, S., Martin-Villalba, A., and Marciniak-Czochra, A. (2017). Revealing age-related changes of adult hippocampal neurogenesis using mathematical models. Development, 145, doi:10.1242/dev.153544.*
- *Llorens E, Zhao S, Baser A, Saiz-Castro G, Zwadlo K, Martin-Villalba A (2015) Single cell-transcriptomics reveals a population of dormant neural stem cells that become activated upon brain injury. Cell Stem Cell 17:329-340*
- *Seib, D.R.M., Corsini, N.S., Ellwanger, K., Plass, C., Mateos, A., Pitzer, C., Niehrs, C., Celikel, T. and Martin-Villalba, A. (2013). Loss of Dickkopf-1 restores neurogenesis in old age and counteracts cognitive decline. Cell Stem Cell 12, 204-214*

## Sarah TEICHMANN, PhD | Wellcome Sanger Institute, UK

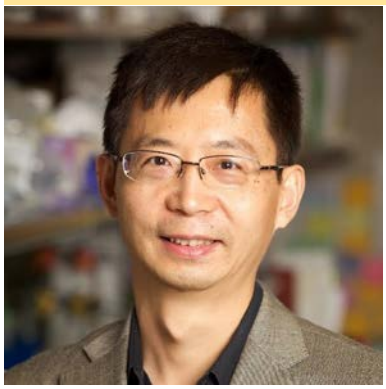
Sarah Teichmann did her PhD at the MRC Laboratory of Molecular Biology, Cambridge, UK and was a Beit Memorial Fellow at University College London. She started her group at the MRC Laboratory of Molecular Biology in 2001, developing computational methods, creatively combining them with structural biology and genomics. She showed that protein complexes assemble *via* stereotypical pathways, helping us understand genetic diseases including cancer mutations. Moving to the Wellcome Genome Campus in 2013, Sarah became the first faculty member to be jointly appointed between the EMBL-European Bioinformatics Institute & Wellcome Sanger Institute. She was one of the co-founders of the highly successful Sanger-EBI Single Cell Genomics Centre in 2012/13, and pioneered the application of single cell genomics to the study of lymphocytes, their development and their antigen receptor sequence repertoires.

From 2016, Sarah has been Head of the Cellular Genetics Programme at the Wellcome Sanger Institute. Sarah has steered the programme towards a strong focus on "cell atlas" technologies, coupled with human genetics at the cellular level and application of these methodologies for further understanding of human health, development and disease. In parallel with this role, Sarah was a co-founder and co-leader of the "Human Cell Atlas" (HCA) international consortium. Her work has been recognized by a number of prizes, including the Lister Prize, Biochemical Society Colworth Medal and GSK Award, Royal Society Crick Lecture, EMBO Gold Medal and the Genetics Society Mary Lyon Medal. She is a member of EMBO, and a Fellow of the Academy of Medical Sciences and of the Royal Society.

*Selected publications:*

- *M Litviňuková, C Talavera-López, H Maatz, D Reichart, CL Worth, ... (2020) Cells of the adult human heart. Nature, 1-10*
- *Z Miao, P Moreno, N Huang, I Papatheodorou, A Brazma, SA Teichmann. (2020) Putative cell type discovery from single-cell gene expression data. Nature Methods, 1-8*
- *JE Park, RA Botting, CD Conde, DM Popescu, M Lavaert, DJ Kunz, I Goh, ... A cell atlas of human thymic development defines T cell repertoire formation. Science 367 (6480)*
- *FAV Braga, G Kar, M Berg, OA Carpaij, K Polanski, LM Simon, S Brouwer, ... (2019) A cellular census of human lungs identifies novel cell states in health and in asthma. Nature medicine 25 (7), 1153-1163*
- *R Vento-Tormo, M Efremova, RA Botting, MY Turco, M Vento-Tormo, ... (2018) Single-cell reconstruction of the early maternal–fetal interface in humans. Nature 563 (7731), 347-353*

## Kun ZHANG, PhD | University of California San Diego, USA



Dr. Kun Zhang is a Professor of Bioengineering in the University of California at San Diego. After obtaining his Ph.D. in Human and Molecular Genetics from the University of Texas at Houston/MD Anderson Cancer Center, he received his post-doctoral training with George Church at Harvard Medical School. He joined the faculty of UCSD Department of Bioengineering in 2007. His current group is developing molecular techniques and engineering platforms for building single-cell maps of multiple human organs. Dr. Zhang became an elected fellow of AIMBE in 2017, and started to serve as Department Chair in 2018.

*Selected publications:*

- *Chen S, Lake BB, Zhang K. (2019) High-throughput sequencing of the transcriptome and chromatin accessibility in the same cell. Nature Biotechnology, 37:1452-7*
- *Lake BB*, Chen S*, Hoshi M*, Plongthongkum N*, Salamon D, Knoten A, Vijayan A, Venkatesh R, Kim EH, Gao D, Gaut J, Zhang K, Jain S. (2019) A single-nucleus RNA-sequencing pipeline to decipher the molecular anatomy and pathophysiology of human kidneys. Nature Communications. 10:2832.*
- *Wu Y, Tamayo P, Zhang K. (2018) Visualizing single-cell RNA-seq datasets with Similarity Weighted Nonnegative Embedding (SWNE). Cell Systems, 7:656-666.e4*
- *Lake BB*, Chen S*, Sos B*, Fan J*, Yung Y, Kaeser G, Duong T, Gao D, Chun J, Kharchenko P, Zhang K. (2018) Integrative single-cell analysis by transcriptional and epigenetic states in human adult brain. Nature Biotechnology, 36:70–80*
- *Lake BB*, Ai R*, Kaeser GE*, Salathia NS*, Yung YC, Liu R, Wildberg A, Gao D, Fung HL, Chen S, Vjayaraghavan R, Wong J, Chen A, Sheng X, Kaper F, Shen R, Ronaghi M, Fang JB, Wang W, Chun J, Zhang K. (2016) Neuronal subtypes and diversity revealed by single-nucleus RNA sequencing of the human brain. Science, 352:1586-90*