

Personal Data

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Academic Positions

08/2019 - Present Position Stadtman Tenure-Track Investigator
 Department: Biostatistics and Computational Biology Branch
 National Institute of Environmental Health Sciences

08/2019 - Present Position: Adjunct Investigator
 Department: Cancer Data Science Laboratory
 National Cancer Institute (NCI)

01/2017 – 08/2019 Position Instructor
 Department: Radiology & Biomedical Data Science
 Integrative Biomedical Imaging
 Stanford University, School of Medicine,
 James H. Clark Center, Room S255
 318 Campus Drive West Stanford, CA 94305

Administrative Appointments

10/2017- 08/2019 Position: Chair for Diversity Trainee Subcommittee, Radiology
 Department
 Website <https://web.stanford.edu/dept/radiology/cgi-bin/raddiversity/>

Awards, Honors, Fellowships

1. Grant on Chan Zuckerberg Initiative award on Ancestry Networks for the Human Cell Atlas, 10/2021. Amount: ~\$820k
2. NICHD Collaboration Award
3. Lab Winner, 2022 NIH/NIEHS Fellows Award for Research Excellence (FARE)
4. Featured among 1000 inspiring Black scientists in America by Cell Mentor
5. Host of the NIEHS 2021 Martin Rodbell Memorial Lecture
6. Certificate of Accomplishment, 2020-2021 Biomedical Data Science Innovation Lab on Challenges in Brain Analytics and Data Integration sponsored by NIH
7. Special Act Award as a Tenure-Track Investigator in 2019-2020
8. NIH Distinguished Scholar Program award, 2019
9. Grant on Collaborative Computational Tools for the Human Cell Atlas project, Chan Zuckerberg Initiative (CZI) DAF (2018 - 2019)

10. Best oral presentation International Conference on Intelligent Systems for Molecular Biology /European Conference on Computational Biology (ISMB/ECCB), TransMed Proceedings, Basel Switzerland, July 2019
11. American Association for Cancer Research (AACR) Minority and/or Minority-Serving Institution Faculty Scholar in Cancer Research Award (2018)
12. 2018 Delegate for BD2K NIH sponsored Data Science Innovation Lab: Mathematical Challenges of Single Cell Dynamics
13. Sponsored Faculty delegate in the NIH extramural 2021 Biomedical Data Science Innovation Lab program challenge in brain analytics and data Integration taking place in Virginia.
14. Certification award on College Science Teaching and STEM, University of Michigan (2016)
15. Travel fellowship for International Conference on Intelligent Systems for Molecular Biology (ISMB) international conference in Boston, USA (July 2010)
16. Travel fellowship for International Society of Computational Biology (ISCB) international conference in Bamako, Mali (December 2009)
17. Postdoctoral Scholar Certificate, Stanford University (2016)

Patent Applications

1. Anchang Benedict & Sylvia K. Plevritis (2017). Systems and Methods for Targeted Therapy Based on Single-Cell Stimulus Perturbation Response. Patent PCT/US2017/026243, 12/10/2017.

Education

06/2007- 12/2011	Certificate: Ph.D. in Statistical Bioinformatics University: University of Regensburg, Germany Thesis title: <i>“Modeling the interplay of molecular signaling and gene expression using dynamic nested effects models”</i> Advisors: Prof Rainer Spang (Co-advisor Prof Gronwald Wolfram)
10/2005 – 11/2006	Certificate: Master of Science in Biostatistics University: University of Hasselt, Diepenbeek, Belgium Thesis title: <i>“Age profiles of campylobacter seroprevalence from hierarchical distribution mixtures”</i> Advisors: Prof Ziv Shkedy, Dr Peter Teunis, Dr Harriet Namata
10/2004 – 09/2005	Certificate: Master of Science in Applied Statistics University: Limburgs Center for Statistics, Diepenbeek, Belgium Thesis title: <i>“Determination of critical values of oscillatory gas exchange parameters during exercise in healthy children using mixed effects models”</i> Advisors: Prof Hebert Thijs and Prof Geert Molenberghs
10/1998 – 07/2002	Certificate: Bachelor of Science in Mathematics and Computer Science University: University of Buea, Cameroon

Research and Teaching Experience

08/2019- Principal Investigator	Institution Research	NIH/NIEHS/NCI <ul style="list-style-type: none">• Develop and apply methods for visualizing and modelling temporal and spatial high-dimensional single-cell data• Develop methods for integration of molecular and pathological features to differentiate between chemically induced, adverse biological processes at a systems level associated with neoplastic and non-neoplastic lesions• Measure and optimize synergy in complex mixtures• Environment exposures and interference with the endocrine system.
01/2017 – 08/2019 Instructor	Institution: Research: Teaching:	Stanford University <ul style="list-style-type: none">• Develop computational models to visualize, improve our understanding of normal and disease progression to help target the complex tumor microenvironment using high-dimensional single-cell data• PI on Chan Zuckerberg Initiative grant entitled “<i>Detection and Visualization of Temporal Partitioned Cellular States using Single-cell Analysis</i>” with main focus on EMT in lung cancer.• Co-Investigator for the NIH U54-CA209971 Center grant on Modeling the Role of Lymph Node Metastasis in Tumor-Mediated Immunosuppression. <ul style="list-style-type: none">• Single cell RNA-seq analysis lecture (CBIO243) for undergraduate and graduate cancer biology trainees.
02/2012 – 09/2016 Postdoctoral Scholar Computational Biology	Institution: Projects:	Stanford University, Center for Cancer Systems Biology <ul style="list-style-type: none">• Develop algorithms for analyzing high throughput single cell drug screening data with the goal of achieving better-individualized combination therapy by accounting for intratumor heterogeneity.• Develop computational tools for sorting and analyzing single cell fluorescence and mass cytometry data.• Develop computational tools for the analysis of oncogenic survival mechanisms related to biological processes like senescence and innate immunity based on high content genomic data
06/2007 – 12/2011 PhD Candidate	Institution:	Institute of Functional Genetics and Bioinformatics, Regensburg, Germany

- Research Assistant Projects:
- Modeling the dynamics of signaling and gene expression using high throughput genomic data
 - Develop and apply methodology called Dynamic Nested Effects Models
 - Network reconstruction on Wnt signaling pathway using next generation RNAi sequencing data from colon cancer cell lines
- 07/2006 – 09/2006 Institution: National Institute of Public Health and Environment
Summer Intern Netherlands
- Projects:
- Analyzed data and wrote a report on age profiles on campylobacter seroprevalence in the Netherlands

Implemented published software

1. Author of the Dynamic Spanning Forest Mixture (**DSFMix**) **R statistical package**
2. Author of the **R statistical package dnem**: dynamic nested effects models.
3. Author of the **SPADE-Forest R package**: Single-cell visualization.
4. Author of the **R package CCAST**: Clustering, Classification and Sorting Tree
5. Author of the **R package PHENotypic STate MaP PHENOSTAMP**
6. Author of the **R package DRUGNEM**: Drug Nested Effects Models
7. Co-Author of **ODE-based Multiscale Multicellular Quantitative Evaluator (MMQE)** implemented in MATLAB

Research Interests / Methods & Techniques

Systems biomedicine, Cancer Systems Biology, Endocrine disruptors, Perturbation network analysis, Translational Systems Biology, Single-cell analysis, Trajectory modeling, Mixtures, Toxicology, Immunology, Neuroscience, Synthetic biology, Drug combination optimization, biomarker discovery, neural networks, deep learning, dynamic and spatial inference, causal inference and modeling of biological networks, integration of genomic and clinical data, clinical informatics, Data Reduction and high-dimensional multi-scale modeling.

Publications (Peer-reviewed)

1. **Anchang B**, Mendez-Giraldez R, et al. (2022). Visualization, Benchmarking and Characterization of Nested Single-cell Heterogeneity as Dynamic Forest Mixtures, **Accepted** 01/13, *Briefings in Bioinformatics*.
2. Atitey K and **Anchang B** (2022). Mathematical Modeling of Proliferative Immune Response Initiated by Interactions Between Classical Antigen-Presenting Cells Under Joint Antagonistic IL-2 and IL-4 Signaling. *Front. Mol. Biosci.* 9:777390. <https://www.frontiersin.org/article/10.3389/fmolb.2022.777390>
3. Bushel, P.R., Ward, J., Burkholder, A., Jianying Li & **Anchang B**. Mitochondrial-nuclear epistasis underlying phenotypic variation in breast cancer pathology. *Sci Rep* 12, 1393 (2022). <https://doi.org/10.1038/s41598-022-05148-4>
4. Rezaee M, Verde A, **Anchang B**, Mattonen SA, Garcia-Diaz J, Daldrup-Link H (2022) Disparate participation by gender of conference attendants in scientific discussions. **PLoS ONE** 17(1): e0262639. <https://doi.org/10.1371/journal.pone.0262639>
5. Green AJ, **Anchang B**, Akhtari FS, Reif DM, Motsinger-Reif A. Extending the lymphoblastoid cell line model for drug combination pharmacogenomics. *Pharmacogenomics*. 2021 Jun;22(9):543-551. doi: 10.2217/pgs-2020-0160. Epub 2021 May 28. PMID: 34044623.

6. Salahudeen A, Choi S, Rustagi A, Zhu J, van Unen V, de la O S, Flynn R, Margalef-Català M, Santos A, Ju J, Batish A, Usui T, Zheng G, Edwards C, Wagar L, Luca V, **Anchang B**, Nagendran M, Nguyen K, Hart D, Terry J, Belgrader P, Ziraldo S, Mikkelsen T, Harbury P, Glenn J, Garcia K, Davis M, Baric R, Sabatti C, Amieva M, Blish C, Desai T, Kuo C. 2020. Progenitor identification and SARS-CoV-2 infection in human distal lung organoids. *Nature*. Nov 25. doi: 10.1038/s41586-020-3014-1. PMID: 33238290
7. Karacosta, L.G., **Anchang, B.**, Ignatiadis, N. *et al.* Mapping lung cancer epithelial-mesenchymal transition states and trajectories with single-cell resolution. *Nat Commun* **10**, 5587 (2019) doi:10.1038/s41467-019-13441-6 PMID: 31811131 PMCID: PMC6898514
8. Michael Patrick Menden, Dennis Wang, Yuanfang Guan, Michael Mason, Bence Szalai, Krishna C Bulusu, Thomas Yu, Jaewoo Kang, Minji Jeon, Russ Wolfinger, Tin Nguyen, Mikhail Zaslavskiy, [et al. Including **Benedict Anchang**], AstraZeneca-Sanger Drug Combination DREAM Consortium. Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen *Nature Communications*, **10**: 2674 (2019). PMID: 31811131 PMCID: PMC6898514
9. **Anchang B**, Kara Davis, Brian Williamson, Harris Fienberg, Loukia Karacosta, Sean C Bendall, Robert Tibshirani, Garry Nolan and Sylvia K Plevritis. (2018). DRUG-NEM: Optimizing drug combinations using single-cell perturbation response to account for intratumoral heterogeneity. *Proceedings of the National Academy of Sciences* 2018; 115 (18): E4294–E4303.
10. Yan, K., Gevaert, O., Zheng, G., **Anchang, B.** et al. (2017). Intestinal Enteroendocrine Lineage Cells Possess Homeostatic and Injury-Inducible Stem Cell Activity. *Cell Stem Cell* 21(1):78- 90.e6 PMID: 31811131 PMCID: PMC6898514
11. **Anchang B**, Tom DP Hart, Sean C Bendall, Peng Qiu, Zach Bjornson, Michael Linderman, Gary Nolan, and Sylvia Plevritis. (2016). Visualization and cellular hierarchy inference of single-cell data using SPADE. *Nature Protocols*, 11, 1264–1279. PMID: 31811131 PMCID: PMC6898514
12. **Anchang B**, Harris Fienberg, Sean Bendall, Robert Tibshirani, Sylvia K. Plevritis. Multi-target drug combinations from single drug responses measured at the level of single cells using Mixture Nested Effects Models (MNEMs) applied to cancer. In: *Proceedings of the American Association for Cancer Research (AACR) Special Conference on Computational and Systems Biology of Cancer*, Feb 8-11, 2015; San Francisco, CA. Philadelphia (PA): AACR; Cancer Res 2015; 75 (22 Suppl 2): Abstract nr B1-39.
13. **Anchang B.**, Do, M.T., Zhao, X., Plevritis S.K. (2014). CCAST: A model-based gating strategy to isolate homogeneous subpopulations in heterogeneous population of single cells. *Plos Computational Biology*, 10(7): e1003664. PMID: 27310265
14. Dumcke, S., Brauer J., **Anchang, B.**, Spang R., Beerenwinkel, N., Tresch A. (2014). Exact likelihood computation in Boolean networks with probabilistic time delays, and its application in signal network reconstruction. *Bioinformatics*, 30(3): 414-9
15. Oksana Voloshanenko, Gerrit Erdmann, Taronish D. Dubash, Iris Augustin, Marie Metzigg, Giusi Moffa, Christian Hundsrucker, Grainne Kerr, Thomas Sandmann, **Benedict Anchang**, Kubilay Demir, Christina Boehm, Svenja Leible, Claudia R. Ball, Hanno Glimm, Rainer Spang and Michael Boutros. (2013). Wnt secretion is required to maintain canonical Wnt signaling in colon cancer cell lines. *Nature Communications*, 4:2610 PMID: 24162018 PMCID: PMC3826636
16. Alper Yetil, **Anchang B.**, Arvin Guow, Stacey J. Adam, Tahera Zabuawala, Ramya Parameswaran, Jan van Riggelen Sylvia Plevritis and Dean W. Felsher. (2015). p19ARF is a critical mediator of cellular senescence and the innate immune response associated with MYC suppression in acute leukemia. *Oncotarget*, **6(6)**, 3563-3577. PMCID: PMC4414137 PMID: 25784651

17. Kearney AY, **Anchang B**, Plevritis S, Felsher DW. ARF: Connecting senescence and innate immunity for clearance. *Aging* (Albany NY). 2015 Sep 25; PubMed PMID: 26412380.
18. **Anchang B** (2011). Modeling molecular signaling and gene expression using Dynamic Nested Effects Models. PhD, Universität Regensburg. urn:nbn:de:bvb:355-epub-229962
19. **Anchang, B et al. (2010)**. Modeling the temporal interplay of molecular signaling and gene expression by using dynamic nested effects models. *Highlight track proceedings* of the 18th Annual International Conference on intelligent Systems for Molecular Biology (**ISMB**), Boston, USA.
20. **Anchang, B.**, Sadeh M., Jacob, J., Tresch, A., Vlad, O.M., Oefner, P., Spang R. (2009). Modeling the temporal interplay of molecular signaling and gene expression by using dynamic nested effects models. *Proceedings of the National Academy of Sciences*, 106(16): 6447 - 6452. PMID: 19329492 PMCID: PMC2672479

Manuscripts under preparation, submitted or under review

1. Benchmarking framework for optimal visualization and interpretability of high-dimensional separable data. Under preparation
2. Optimal drug combinations for large scale heterogeneous perturbation screens using single-cell analysis. Under preparation

Invited talks and abstract presentations

Invited talks

1. Plenary talk invitation in the Mathematical and Computational Modeling session during the 3rd Annual AFROBIOTECH Conference, October 25-26, 2021
2. ISMB/ECCB 2021 presentation as part of the BioVis COSI proceedings.
3. 2020 Summer short talk on single-cell analysis organized by Washington state University attended by ~150 graduate students.
4. Fall 2020 Reproductive Developmental Biology Laboratory (RDBL) Seminar Series, NIEHS, NC, USA
5. 2020 Spring seminar series for NSCP young Scholars. Emerging areas of research and career exploration series, NIEHS, NC, USA, 02/07, 2020.
6. 2019 Epigenetics and Stem Cell Biology Laboratory (ESCBL) Seminar Series, 11/14, NIEHS, NC, USA
7. 2019 Integrative Bioinformatics Core meeting on scRNA-seq method development. 12/03, NIEHS, NC, USA
8. Combining machine learning and single-cell analysis for individualize precision medicine. 22nd Annual ISMB/EECCB meeting, Basel, Switzerland, July 22, 2019
9. Loukia Karacosta, Benedict Anchang et al. 2018. AACR Annual Meeting, Chicago Illinois. Identifying Dynamic EMT Transition States and Constructing a Proteomic EMT Landscape of Lung Cancer Using Single Cell Multidimensional Analysis.
10. Inaugural meeting for Systems Approaches to Cancer Biology sponsored by Association of Early Career Cancer Systems Biology and National Cancer Institute of the National Institute of Health, Woods Hole, MA, USA. April 3-6, 2016. DRUG-NEM: an optimized drug combination strategy using single-cell perturbation response that accounts for intratumoral heterogeneity.
11. **Anchang et. al.** 2016. Short presentation on precision medicine using single-cell perturbation analysis during the inaugural Artificial Intelligence in Medicine (AI Med) meeting at the Ritz Carlton in Laguna Niguel, CA (December 12-15, 2016).

12. **NCI ICBP** Mathematical Modeling of Cancer Systems Meeting. CCAST: A model-based gating strategy to isolate homogeneous subpopulations in heterogeneous population of single cells, Tampa, Florida, February 26-28, 2015
13. 9th European Conference on Computational Biology (ECCB) Ghent, Belgium-September 26-29th 2010. **Workshop presentation**: Learning from perturbation effects.
14. 18th Annual ISMB conference, Boston, USA, July 13, 2010. **Highlight track presentation** on dynamic modeling of cellular decision-making. Video: http://www.iscb.org/cms_addon/multimedia/flvmedia.php?i=698
15. 5th RECOMB Conference on Regulatory and Systems Genomics, with DREAM Challenges San Francisco, USA, November 12-15, 2012. Systems Biology Session presentation on "A non-parametric model-based framework to quantify heterogeneous populations in fluorescence activated cell sorting data". Video: <https://www.iscb.org/recomb-mm/media-recombrsg2012>
16. 22nd Annual **ISMB conference**, Boston, USA, July 13, 2014. **Short presentation** on DRUGMNEM: an optimization strategy for targeted combination of drugs using single-drug screening single cell data
17. ISCB International Conference on Bioinformatics Bamako, Mali December 1-4th 2009. **Presentation** on dynamic nested effects models.
18. Bioinformatics seminar at the Schleusenwerterhaus Regensburg, Germany, June 19, 2009.

Peer reviewed Abstract and Poster Presentations

1. Benchmarking framework for optimal visualization and interpretability of high-dimensional separable data, ISMB/ECCB 2021, BioVis COSI proceedings.
2. Assessment of data reduction models including autoencoders for optimal visualization, interpretability, and speed. 2020 Joint Statistical Meetings, Philadelphia, Pennsylvania, USA, 8/04.
3. Combining machine learning and single-cell analysis for individualize precision medicine. 22nd Annual ISMB/EECCB meeting, Basel, Switzerland, July 22, 2019
4. Anchang et al. 2018. AACR Annual Meeting, Chicago Illinois. **Presentation on** Individualized drug combination based on single-cell drug perturbations.
5. Anchang et al. 2015 AACR Translation of the Cancer Genome and Computational and Systems Biology Conferences. **Presentation on** Multi-target drug combinations from single drug responses measured at the level of single cells using Mixture Nested Effects Models (MNEMs) applied to cancer. 7-11 February 2015, San Francisco, CA, USA.
6. Daniel Koch, Stacey Adams, Andrew Gentles, **Benedict Anchang**, Delaney Sullivan, Sylvia Plevritis, Dean Felsher. Gene expression signatures associated with MYC oncogene addiction in lymphoma. **abstract**. In: Proceedings of the **AACR** Special Conference on Myc: From Biology to Therapy; Jan 7-10, 2015; La Jolla, CA. Philadelphia (PA): AACR; Mol Cancer Res 2015; 13(10 Suppl): Abstract nr A48.
7. 22nd Annual International Conference on intelligent Systems for Molecular Biology (ISMB), Boston, USA, July 13, 2014. **Presentation on** DRUGMNEM: an optimization strategy for targeted combination of drugs using single-drug screening single cell data
8. Keystone Symposia on Molecular and Cellular Biology: Engineering Cell Fate and Function, Olympic Valley, California, USA, April 6-11, 2014. **Presentation on** "An optimal gating strategy isolates homogeneous cell subpopulations in heterogeneous single cell data"
9. 18th Annual International Conference on intelligent Systems for Molecular Biology (ISMB), Boston, USA, July 13, 2010. **Presentation on** dynamic modeling of cellular decision-making.

10. 5th RECOMB Conference on Regulatory and Systems Genomics, with DREAM Challenges San Francisco, USA, November 12-15, 2012. **Presentation** on “A non-parametric model-based framework to quantify heterogeneous populations in fluorescence activated cell sorting data”.
11. Cell Symposia: Hallmarks of Cancer Meeting, San Francisco, USA, October 29-31, 2012. **Presentation** on Maintenance of Cellular Phenotypes in Breast Cancer Cell Lines from Sorted Cells.
12. CCSB EAB/NCI site meeting Stanford, USA. October 22, 2012. **Presentation** on “A Non-parametric Model-based Framework to identify and quantify Heterogeneous populations in FACS Data”.
13. ISCB International Conference on Bioinformatics Bamako, Mali December 1-4th 2009. **Presentation** on dynamic nested effects models.
14. Anchang et al. 2009. **IEEE** International Conference on Bioinformatics and Biomedicine Workshop Bethesda, MD, USA, November 1-4th 2009. **Presentation** on Modeling the Temporal Interplay of Molecular Signaling and Gene Expression by using Dynamic Nested Effects Models

Mentoring, Outreach and Leadership Activities

1. Leading a joint international effort to create an African-Materno-Fetal system cell atlas during pregnancy using single-cell analysis to be funded by the Chan Zuckerberg Initiative as part of the Ancestry Networks for the Human Cell Atlas project.
2. Hosting of the NIEHS 2021 Martin Rodbell Memorial Lecture
3. 2021 NIEHS host for Summer Internship Program Intern, Fatima Ahmed
4. Mentoring 2 postdoctoral scientists: Dr. Komlan Atitey and Dr. Raul Mendez
5. Workshop subcommittee chair: Modernizing Neurotoxicology at NIEHS: Technologies to Applications in Environmental Health Sciences
6. Participant of the Ancestry Networks for the Human Cell Atlas program
7. PI on a submitted international fellowship grant application on “The African Materno-Fetal System during Pregnancy at Single-cell Resolution” in response to Request for Applications: Ancestry Networks for the Human Cell Atlas by CZI
8. Summer short talk on single-cell analysis organized by Washington state University attended by about 150 graduate students.
9. Invited to motivate young scholars into STEM fields during the NIEHS 2020 Spring seminar series for NSCP young Scholars.
10. Submitted manuscript under review on collaboration research with Heike et al. at Stanford on “Disparate Participation of Male and Female Conference Attendants in Scientific Discussions”.
11. Hosting the 2021 Martin Rodbell Memorial Lecture at the National Institute of Environmental Health Sciences
12. Promote Diversity in the department of Radiology by increasing awareness within the Stanford community using surveys and publishing monthly newsletters on diversity, helping to attract and recruit new trainees, organizing social events and inviting guest speakers who promote diversity e.g., Hannah Valentine, MD (former NIH Chief Officer for Scientific Workforce Diversity).
13. PI on a project funded by Silicon Valley Community Foundation in support of Chan Zuckerberg Initiative (CZI)
14. Participated in a project highlighting the critical contributions of Bay Area immigrants to the social, cultural, and economic betterment of America initiated by an international freelance photographer Mark Tuschman (<http://tuschmanphoto.com>).

15. Key participant in the Pilot Postdoctoral Mentoring program between Novartis Institutes for Biomedical Research (NIBR) and Stanford Bio-X (2016)
16. Supervising computational projects for young scholars in the Cancer Systems Biology Scholar Program (CSBS), Stanford University (2016-present)
17. Participated in the certified STEM and diversity Teaching and mentoring postdoctoral program at Stanford (Summer 2016)
18. Wrote a peer reviewed and scored NIH Research Scientist Development K01 Award application, which involved bringing together a team of mentors and collaborators (2015-2016).
19. Participated as a delegate in a 5-day intensive BD2K NIH sponsored Data Science Innovation Lab: Mathematical Challenges of Single Cell Dynamics in Oregon (2018).
20. Planning committee member and Chair of the discussion session on "Mechanisms of Acquired Resistance in cancer" during the Integrative Cancer Biology Program (ICBP) Junior Investigator Meeting, November 13-15, 2013, Bethesda
21. Supervised NCI ICBP Summer Intent Student 2013, Brian Williamson (Undergraduate) at Stanford University (Now a graduate student studying Biostatistics at Washington State University) and Summer Intent Student 2014, Tom Hart (Undergraduate) at Stanford University (Now a graduate student studying at Rockefeller University).

Professional Memberships and Other activities

1. Advisory board member of charitable foundation: Mendem Foundation
2. Member of the Ancestry Networks for the Human Cell Atlas program
3. Member of Human Cell Atlas Reproductive Network
4. Participant of the Human Cell Atlas Pediatric Network
5. ISCB student member 2009-2011
6. ISCB Postdoc member 2012-2019
7. ISCB Professional member 2020-Present
8. AACR member 2015-2018
9. MICR member 2018
10. DDIR external branch review committee representative for Tenure-Track positions
11. Recruitment committee member for staff and tenure-track investigators for the Epigenetics & Stem Cell Biology Laboratory, National Toxicology Program and IIDL
12. Search committee member for the recruitment of a Tenure Eligible Investigator for the Biostatistics and Computational Biology Branch (BCBB), Division of Intramural Research (DIR) at NIEHS
13. Participated in the AstraZeneca-Sanger Drug Combination DREAM Challenge 2015
14. Reviewed submitted computational papers in Bioinformatics, PNAS, Plos Computational Biology, RNA Biology and Plos one
15. Alumni member in A2B2D (Biostatistics-Bioinformatics) Diepenbeek, Belgium. 2006-present