

Benedict N. Anchang, PhD

Personal Data

Name: Benedict N. Anchang
Address: Biostatistics and Computational Biology Branch,
National Institute of Environmental Health Sciences
111 T W Alexander Dr, Rall Building
Research Triangle Park, NC 27709
Email: benedict.anchang@nih.gov
TEL: 984-287-3350
eFAX: benedict.anchang%4802455@fax.nih.gov
FAX: 301 - 480 - 2455
Website: <https://www.niehs.nih.gov/research/atniehs/labs/bb/staff/anchang/index.cfm>

Academic Positions

08/2019 - Present Position: Stadtman Tenure-Track Investigator (NIH/NIEHS/NCI)
 Department: Biostatistics and Computational Biology Branch (NIEHS)

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. Special Act Award as a Tenure-Track Investigator in 2019-2020
2. NIH Distinguished Scholar Program award, 2019
3. Grant on Collaborative Computational Tools for the Human Cell Atlas project, Chan Zuckerberg Initiative DAF (2018 - 2019)
4. Best oral presentation International Conference on Intelligent Systems for Molecular Biology /European Conference on Computational Biology (ISMB/ECCB), TransMed Proceedings, Basel Switzerland, July 2019
5. American Association for Cancer Research (AACR) Minority and/or Minority-Serving Institution Faculty Scholar in Cancer Research Award (2018)
6. 2018 Delegate for BD2K NIH sponsored Data Science Innovation Lab: Mathematical Challenges of Single Cell Dynamics
7. 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.
8. Certification award on College Science Teaching and STEM, University of Michigan (2016)
9. Travel fellowship for International Conference on Intelligent Systems for Molecular Biology (ISMB) international conference in Boston, USA (July 2010)
10. Travel fellowship for International Society of Computational Biology (ISCB) international conference in Bamako, Mali (December 2009)
11. Postdoctoral Scholar Certificate, Stanford University (2016)

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12. Host of the NIEHS 2021 Martin Rodbell Memorial Lecture
13. Bio-X Corporate Forum Liaison sponsorship to attend the PMWC 2014 World Conference on Personalized Medicine 2014 in Silicon Valley

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• Perturbation Network Analysis |
| 01/2017 – 08/2019
Instructor | Institution:
Research: | 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 |

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		microenvironment using high-dimensional single-cell data
		<ul style="list-style-type: none">• 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.
	Teaching:	<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 ultimate 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 Research Assistant	Institution: Projects:	Institute of Functional Genetics and Bioinformatics, Regensburg, Germany <ul style="list-style-type: none">• 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 Summer Intern	Institution: Projects:	National Institute of Public Health and Environment Netherlands <ul style="list-style-type: none">• 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 dnm**: 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

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Research Interests / Methods & Techniques

Systems biomedicine, Cancer Systems Biology, 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. 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
2. Karacosta, L.G., Anchang, B., Ignatiadis, N. *et al.* (2019) Mapping lung cancer epithelial-mesenchymal transition states and trajectories with single-cell resolution. *Nat Commun* **10**, 5587 doi:10.1038/s41467-019-13441-6 PMID: 31811131 PMCID: PMC6898514
3. 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**], (2019). AstraZeneca-Sanger Drug Combination DREAM Consortium. Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen *Nature Communications*, 10: 2674 PMID: 31811131 PMCID: PMC6898514
4. **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.
5. 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
6. **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
7. **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.
8. **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

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- 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
- 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
- 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
- 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.
- Anchang B** (2011). Modeling molecular signaling and gene expression using Dynamic Nested Effects Models. *PhD, Universität Regensburg*. urn:nbn:de:bvb:355-epub-229962
- 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.
- 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

- Combining Shape and Time-dependent Decision trees with Spanning Forests for Optimal Visualization, Testing and Characterization of Single-cell Heterogeneity. Anchang et al. 2020. Under review
- Melika, Anchang et al. 2020. Disparate Participation of Male and Female Conference Attendants in Scientific Discussions. Submission under second review.
- Unbiased Assessment of data visualization and model interpretability of data reduction methods applied to dynamic biological processes using single-cell data. Under preparation.
- Extending the Lymphoblastoid Cell Line Model for Drug Combination Pharmacogenomics. Under full consideration for potential publication in Pharmacogenomics.

Invited talks and abstract presentations

Invited talks

- 2020 Summer short talk on single-cell analysis organized by Washington state University attended by ~150 graduate students.
- Fall 2020 Reproductive Developmental Biology Laboratory (RDBL) Seminar Series, NIEHS, NC, USA
- 2020 Spring seminar series for NSCP young Scholars. Emerging areas of research and career exploration series, NIEHS, NC, USA, 02/07, 2020.
- 2019 Epigenetics and Stem Cell Biology Laboratory (ESCBL) Seminar Series, 11/14, NIEHS, NC, USA

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5. 2019 Integrative Bioinformatics Core meeting on scRNA-seq method development. 12/03, NIEHS, NC, USA
6. Combining machine learning and single-cell analysis for individualize precision medicine. 22nd Annual ISMB/EECCB meeting, Basel, Switzerland, July 22, 2019
7. 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.
8. 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.
9. 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).
10. **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
11. 9th **European Conference on Computational Biology (ECCB)** Ghent, Belgium-September 26-29th 2010. **Workshop presentation**: Learning from perturbation effects.
12. 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
13. 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>
14. 22nd Annual **ISMB conference**, Boston, USA, July 13, 2014. **Short presentation** on DRUGMNE: an optimization strategy for targeted combination of drugs using single-drug screening single cell data
15. **ISCB International Conference on Bioinformatics** Bamako, Mali December 1-4th 2009. Presentation on dynamic nested effects models.
16. Bioinformatics seminar at the Schleusenwerterhaus Regensburg, Germany, June 19, 2009.

Peer reviewed Abstract and Poster Presentations

1. Assessment of data reduction models including autoencoders for optimal visualization, interpretability and speed. 2020 Joint Statistical Meetings, Philadelphia, Pennsylvania, USA, 8/04.
2. Combining machine learning and single-cell analysis for individualize precision medicine. 22nd Annual ISMB/EECCB meeting, Basel, Switzerland, July 22, 2019.
3. Anchang et al. 2018. AACR Annual Meeting, Chicago Illinois. **Presentation on** Individualized drug combination based on single-cell drug perturbations.
4. 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.
5. 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**:

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- From Biology to Therapy; Jan 7-10, 2015; La Jolla, CA. Philadelphia (PA): AACR; Mol Cancer Res 2015; 13(10 Suppl): Abstract nr A48.
- 22nd Annual International Conference on intelligent Systems for Molecular Biology (ISMB), Boston, USA, July 13, 2014. **Presentation** on DRUGMNM: an optimization strategy for targeted combination of drugs using single-drug screening single cell data
 - 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”
 - 18th Annual International Conference on intelligent Systems for Molecular Biology (ISMB), Boston, USA, July 13, 2010. **Presentation** on dynamic modeling of cellular decision-making.
 - 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”.
 - 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.
 - 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”.
 - ISCB International Conference on Bioinformatics Bamako, Mali December 1-4th 2009. **Presentation** on dynamic nested effects models.
 - 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

- Mentoring to 2 postdoctoral scientists: Dr. Komlan Atitey and Dr. Raul Mendez
- Summer short talk on single-cell analysis organized by Washington State University attended by about 150 graduate students.
- Invited to motivate young scholars into STEM fields during the NIEHS 2020 Spring seminar series for NSCP young Scholars.
- 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”.
- Hosting the NIEHS 2021 Martin Rodbell Memorial Lecture at the National Institute of Environmental Health Sciences
- 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 (NIH Chief Officer for Scientific Workforce Diversity).
- PI on a project funded by Silicon Valley Community Foundation in support of Chan Zuckerberg Initiative (CZI).
- 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>).
- Key participant in the Pilot Postdoctoral Mentoring program between Novartis Institutes for Biomedical Research (NIBR) and Stanford Bio-X (2016).
- Supervising computational projects for young scholars in the Cancer Systems Biology Scholar Program (CSBS), Stanford University (2016-present)

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11. Participated in the certified STEM and diversity Teaching and mentoring postdoctoral program at Stanford (Summer 2016).
12. 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).
13. 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).
14. 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.
15. 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. ISCB member since 2009
2. AACR member since 2015
3. MICR member since 2018
4. DDIR's Representative for recruiting Investigators (Tenure-Track) in BBB, NICHD/DIPHR.
5. Recruitment committee member for staff and tenure-track investigators for the Epigenetics & Stem Cell Biology Laboratory, National Toxicology Program and IIDL.
6. Participated in the AstraZeneca-Sanger Drug Combination DREAM Challenge 2015.
7. Reviewed submitted computational papers in Bioinformatics, PNAS, Plos Computational Biology, RNA Biology and Plos one.
8. Alumni member in A2B2D (Biostatistics-Bioinformatics) Diepenbeek, Belgium. 2006-present.