

Benedict N. Anchang, PhD

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Academic Positions

Aug 2019 – Position: Stadtman Investigator: NIH/NIEHS/NCI
National Institute of Environmental Health Sciences
Biostatistics and Computational Biology Branch

Jan 2017 – Aug 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

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

Awards, Honors, Fellowships

1. NIH **Distinguished Scholar Program** award, 2019

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

June 2007 - Dec2011 Certificate: Ph.D. in Bioinformatics
 University: University of Regensburg, Germany
 Thesis title: *“Modeling the interplay of molecular signaling and gene expression using dynamic nested effects models”*
 Advisors: Prof Rainer Spang (Co-advisor Prof Gronwald Wolfram)

Oct 2005 - Nov 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
Oct 2004 - Sept 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
Oct 1998 - July 2002	Certificate: Bachelor of Science in Mathematics and Computer Science University: University of Buea, Cameroon

Research and Teaching Experience

Aug 2019-	Institution	NIH/NIEHS/NCI
	Research	<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 • Optimize combination therapy for complex mixtures
Jan 2017 – Aug 2019	Institution:	Stanford University
Instructor	Research:	<ul style="list-style-type: none"> • Develop computational models to visualize, improve our understanding of normal and disease progression

		<p>to help target the complex tumor microenvironment using high-dimensional single-cell data</p> <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. • Co-Investigator for the NIH 1U54HG010426-01 Center grant to map the complexity of cellular architecture and biomolecular profiles of the small bowel and colon (NIH HuBMAP project) • Single cell RNA-seq analysis lecture (CBIO243) for undergraduate and graduate cancer biology trainees.
Feb 2012 - Sep 2016	Teaching:	Stanford University, Center for Cancer Systems Biology
	Institution:	
Postdoctoral Scholar Computational Biology	Projects:	<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
June 2007 - Dec 2011	Institution:	Institute of Functional Genetics and Bioinformatics, Regensburg, Germany

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|---|---------------------|---|
| PhD Candidate
Research Assistant | Projects: | <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 |
| July 2006 - Sep 2006
Summer Intern | Institution: | <ul style="list-style-type: none"> • National Institute of Public Health and Environment Netherlands |
| | Function: | Data Analysis <ul style="list-style-type: none"> • Analyzed data and wrote a report on age profiles on campylobacter seroprevalence in the Netherlands |

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

1. 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
2. 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., **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).
3. **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.

4. 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
5. **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.
6. **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.
7. **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.
8. 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
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
10. Alper Yetil, **Benedict Anchang** Arvin Guow, Stacey J. Adam, Tahera Zabuwala, 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.
11. 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.
12. **Anchang, B.** (2011). Modeling molecular signaling and gene expression using Dynamic Nested Effects Models. PhD, Universität Regensburg. [urn:nbn:de:bvb:355-epub-229962](https://nbn-resolving.org/urn:nbn:de:bvb:355-epub-229962)

13. **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.
14. **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.

Manuscripts under review and preparations

1. Ameen A. Salahudeen, Junjie Zhu, Anchang Benedict et al. 2018. Organoid-based characterization of distal adult human lung at single cell resolution. Preparation for resubmission to Nature.
2. Feature selection for optimal visualization using Dynamic Spanning Forest applied to single cell based dynamic developmental processes
3. Interpretability of data reduction methods applied to dynamic biological processes using single-cell data.
4. Disparate Participation of Male and Female Conference Attendants in Scientific Discussions. Melika, Anchang et al. 2020

Invited talks and abstract presentations

Invited talks

1. Fall 2020 Reproductive Developmental Biology Laboratory (RDBL) Seminar Series, NIEHS, NC, USA
2. 2020 Spring seminar series for NSCP young Scholars. Emerging areas of research and career exploration series, NIEHS, NC, USA, 02/07, 2020.
3. 2019 Epigenetics and Stem Cell Biology Laboratory (ESCBL) Seminar Series, 11/14, NIEHS, NC, USA
4. 2019 Integrative Bioinformatics Core meeting on scRNA-seq method development. 12/03, NIEHS, NC, USA
5. Combining machine learning and single-cell analysis for individualize precision medicine. 22nd Annual ISMB/EECCB meeting, Basel, Switzerland, July 22, 2019

6. 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.
7. 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.
8. **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).
9. **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
10. 9th **European Conference on Computational Biology (ECCB)** Ghent, Belgium-September 26-29th 2010. **Workshop presentation:** Learning from perturbation effects.
11. 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
12. 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>
13. 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
14. **ISCB International Conference on Bioinformatics** Bamako, Mali December 1-4th 2009. **Presentation** on dynamic nested effects models.
15. 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: From Biology to Therapy; Jan 7-10, 2015; La Jolla, CA. Philadelphia (PA): AACR; Mol Cancer Res 2015; 13(10 Suppl): Abstract nr A48.
6. 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
7. 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”
8. 18th Annual International Conference on intelligent Systems for Molecular Biology (ISMB), Boston, USA, July 13, 2010. **Presentation on** dynamic modeling of cellular decision-making.
9. 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”.
10. 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.
11. 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”.
12. ISCB International Conference on Bioinformatics Bamako, Mali December 1-4th 2009. **Presentation on** dynamic nested effects models.

13. 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. Hosting the 2021 Martin Rodbell Memorial Lecture at the National Institute of Environmental Health Sciences
2. 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).
3. PI on a project funded by Silicon Valley Community Foundation in support of Chan Zuckerberg Initiative (CZI)
4. 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>).
5. Key participant in the Pilot Postdoctoral Mentoring program between Novartis Institutes for Biomedical Research (**NIBR**) and Stanford Bio-X (2016)
6. Supervising computational projects for young scholars in the Cancer Systems Biology Scholar Program (CSBS), Stanford University (2016-present)
7. Participated in the certified STEM and diversity Teaching and mentoring postdoctoral program at Stanford (Summer 2016)
8. 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).
9. 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) which resulted in bringing investigators with diverse expertise from different universities to work on particular project proposals with funding potential. This effort is still ongoing.
10. 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

11. Supervised NCI ICBP Summer Intent Student 2013, Brian Williamson (Undergraduate) at Stanford University. Now a graduate student studying Biostatistics at Washington State University.
12. Supervised NCI ICBP 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. Participated in the AstraZeneca-Sanger Drug Combination DREAM Challenge 2015
5. Reviewed submitted computational papers in Bioinformatics, PNAS, Plos Computational Biology, RNA Biology and Plos one
6. Part of the ApoNET project (2007-2011) - Systems Analysis of Death Receptor Signaling Networks. <http://www.erasysbio.net/index.php?index=273>
7. Alumni member in A2B2D (Biostatistics-Bioinformatics) Diepenbeek, Belgium. 2006-present

Implemented softwares

1. Author of the **R statistical package dnem**: dynamic nested effects models.
2. Author of **SPADE-Forest R package**: Single-cell visualization.
3. Author of the **R package CCAST**: Clustering, Classification and Sorting Tree
4. Author of the **R package PHENotypic STate MaP PHENOSTAMP**
5. Author of the **R package DRUGNEM**: Drug Nested Effects Models

Languages

English:	Mother Tongue
French:	Good both in speaking and writing
German:	Fair both in speaking and writing
Dutch:	Beginner