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Benjamin E. Decato, Ph.D.

Curriculum vitae

Executive Summary

- Bioinformatician and quantitative thinker with experience developing and communicating efficient algorithms and statistical modeling pipelines for integrative analysis of large-scale genomic and biomedical datasets.
- 8 years of experience building tools for and analyzing bulk and single-cell next-generation sequencing data
- Broad therapeutic area experience that spans oncology, immunology, cardiovascular, and fibrotic disease areas as well as all stages of drug development

Skills

Programming languages & tools:	R/Markdown, C++, *nix shell scripting, LaTeX, Java, C, Python, SQL, GNU make, git, Docker, Domino, Jira, AWS/SGE/PBS, and the ability and enthusiasm to learn others!
Relevant domain areas:	Machine learning, Probability, Statistics, Data Visualization, Algorithms, Molecular Biology, Databases, Statistical Genetics, Single-cell & bulk [epigen/transcript/prote]-omics
Interpersonal & other skills:	Public speaking, reproducible research, growth mindset, active listener, self-motivating

Positions Held

2021–Present **City of Hope, Department of Medical Oncology and Therapeutics Research**, *Monrovia, CA*.

Assistant Research Professor, Bioinformatics

- Work in the lab of Dr. Andrea Bild to study tumor heterogeneity using whole genome sequencing and single cell sequencing approaches
- Lead efforts to analyze high throughput sequencing data for detection of tumor heterogeneity and subclonal populations in clinical trial data
- Manage analysis and interpretation of genomics data from patient cohorts to understand cancer progression and resistant tumor phenotypes that emerge during therapy

2018–2021 **Bristol Myers Squibb (BMS)**, *Princeton, NJ.*

- 2020-2021 Senior Scientist, Translational Bioinformatics
  - Collaborate with late-stage asset development stakeholders to plan and lead translational biomarker analysis, PK/PD, and patient stratification modeling in phase 2 and 3 clinical trials.
- 2018-2020 Research Investigator, Translational Bioinformatics
  - As part of the internal UK Biobank working group, perform GWAS, PheWAS, and loss-of-function burden tests to drive genetic target identification, existing target prioritization, and risk assessment in immunoscience, cardiovascular, and fibrosis phenotypes
  - As part of the Genetically Modified Animals (GMA) consortium, interact with and provide bioinformatics expertise to partner CROs to design and execute the production of 10+ CRISPR knock-in, knock-out, and humanized preclinical mouse models.
  - Designed and managed a summer internship project exploring epigenetic signatures of fibrosis

2012–2018 **University of Southern California**, *Los Angeles, CA.*

- 2012-2018 Research Assistant / Ph.D. Candidate
  - Developed software pipelines for the analysis of DNA methylation and other epigenetic data, and fostered collaborations on projects exploring the DNA methylation dynamics of embryonic development and tumorigenesis.
- 2015 Teaching Assistant, BISC307: General Physiology
  - Supervised and evaluated student work for a range of physiology related experiments on topics including the cardiovascular, renal, muscular, and respiratory systems.
  - Led dissections and proctored/graded exams.

2011 **Corteva Agriscience (formerly Dow AgroSciences)**, *Indianapolis, IN.*

Summer Intern, Human Health Assessment

- Designed and implemented a SQL database for the predictive toxicology group. Interfaced with users to develop a C# GUI and set of useful database queries.

2009–2012 **University of New Hampshire**, *Durham, NH.*

- 2012 Consultant, Programming Assistance Center
- 2010–2012 Undergraduate Research Assistant, Computer Science Department
- 2009–2010 Resident Assistant, Department of Residential Life

Education

2012–2018 **Ph.D. Computational Biology & Bioinformatics**, *University of Southern California*, Los Angeles, CA.

Dissertation Title: Identification and analysis of shared epigenetic changes in extraembryonic development and tumorigenesis

Dissertation Committee: Andrew D. Smith, Ph.D. (advisor); Remo Rohs, Ph.D.; Matthew D. Dean, Ph.D.; Peter Calabrese, Ph.D.

2008–2012 **B.S. Computer Science**, *University of New Hampshire*, Durham, NH.

Department option, Bioinformatics

Magna cum laude

Publications

- Luo Y, Wadhawan S, Greenfield A, **Decato BE**, Oseini A, Collen R, Shevell D, Thompson J, Jarai G, Charles ED, Sanyal AJ. "SOMAscan proteomics identifies serum biomarkers associated with liver fibrosis in patients with nonalcoholic steatohepatitis: development and validation of a prediction model" *Hepatology Communications*, in press. **[PubMed]**

- **Decato BE**, Qu J, Ji X, Wagenblast E, Knott SRV, Hannon GJ, Smith AD. "Characterization of universal features of partially methylated domains across tissues and species" *Epigenetics & Chromatin*, 2020. **[PubMed]**

- Barnett KR, **Decato BE**, Scott T, Hansen T, Chen B, Attalla J, Smith AD, Hodges E. "Spatiotemporal dynamics of DNA methylation across the chromatin accessible genome during a monocyte to macrophage transition" *Molecular Cell*, 2020. **[PubMed]**

- **Decato BE**, Lopez-Tello J, Sferruzzi-Perri AN, Smith AD, Dean MD. "DNA methylation divergence and tissue specialization in the developing mouse placenta" *Molecular Biology & Evolution* 34(7): 1702-1712, 2017. **[PubMed]**

- Song Q, **Decato BE**, Hong EE, Zhou M, Fang F, Qu J, Garvin T, Kessler K, Zhou J, Smith AD. "A reference methylome database and analysis pipeline to facilitate integrative and comparative epigenomics." *PLoS ONE* 8(12): e81148, 2013. **[PubMed]**

- Kaaij LT, van de Wetering M, Fang F, **Decato BE**, Molaro A, van de Werken HJ, van Es JH, Schuijers J, de Wit E, de Laat W, Hannon GJ, Clevers HC, Smith AD, Ketting RF. "DNA methylation dynamics during intestinal stem cell differentiation reveals enhancers driving gene expression in the villus." *Genome Biology*, 14:R50, 2013. **[PubMed]**

Submitted Journal Articles

- **Decato BE***, Ammar R*, Reinke-Breen L*, Thompson JR, Azzara A. "Exploring the transcriptional landscape of insult and intervention in a bleomycin model of systemic sclerosis." *Submitted.*
  (* denotes co-first author)

- Chirinos A, Zhao L, Reese-Petersen AL, Genovese F, Jia Y, Basso M, Wang Z, Fronheiser M, **Decato BE**, Cvijic ME, Koenitzer J, Yarde M, Zamani P, Cohen J, Prenner P, Hanff T, Kumar A, Hayes W, Seiffert D, Karsdal MA, Gordon DA, Cappola T. "Endotrophin, a collagen VI formation-derived bioactive peptide, in Heart Failure with Preserved Ejection Fraction." *Submitted.*

Selected Posters and Presentations

- Luo Y, **Decato BE**, Palmer S, Du S, Charles ED, Sand JMB, Leeming DJ, Karsdal M, Minnich A. "Evaluation of Collagen Neoepitope Biomarkers in a Phase 2 Trial of BMS-986020, a Lysophosphatidic Acid Receptor Antagonist, for the Treatment of Idiopathic

Pulmonary Fibrosis" *American Thoracic Society* international conference, 2020.

- Minnich A, Yang M, Du S, Soule B, **Decato BE**, Luo Y. "Effect of MUC5b Genetic Polymorphism on Response to Lysophosphatidic Acid Receptor 1 (LPA1) Antagonist BMS-986020 in a Phase 2 Clinical Trial in Idiopathic Pulmonary Fibrosis" *American Thoracic Society* international conference, 2019.

- **Decato B**, Lopez-Tello J, Sferruzzi-Perri AN, Smith AD, Dean MD. "DNA methylation divergence and tissue specialization in the developing mouse placenta" *Society for Molecular Biology & Evolution* annual meeting, 2017.

Honors & Awards

- Volunteering
  - Career Panelist, Korean American Scientists & Engineers Seminar Series 2020
  - Invited Talk, Seacoast School of Technology 2020
  - Invited Talk, QBIO Graduate Student Association 2020

- Professional Awards & Activities – Bristol Myers Squibb
  - Bravo Well Done Award – Core Value Innovation June 2020
  - Bravo Well Done Award – Core Value Accountability June 2020
  - Analytics Exchange – Selective internal professional society for technical skills development, networking, and cross-functional project work cohort 2019
  - Bravo Well Done Award – Core Value Speed August 2019
  - Bravo Well Done Award – Core Value Passion July 2019
  - Bravo Well Done Award – Core Value Speed March 2019
  - BMS Internal Statistical Horizons Multilevel & Mixed Models coursework January 2019

- Graduate Awards & Activities – University of Southern California
  - Subreviewer – *Genome Research* 2018
  - NCBI Hackathon Participant, Bethesda MD 2017
  - ISMB and RECOMB Attendee 2012, 2016
  - Provost's Fellowship 2012-2017
  - Provost's Fellowship Travel Award 2017
  - SMBE Young Investigator Travel Award 2017
  - Subreviewer – *Bioinformatics* 2016, 2017
  - Volunteer, STEM Career Day 2017
  - Reviewer – *Algorithms in Bioinformatics*, WABI Conference Proceedings 2015

- Undergraduate Awards & Activities — University of New Hampshire
  - Summer Undergraduate Research Fellowship 2010
  - Fred G. and Gertrude A. Howell Memorial Scholarship 2010-2011
  - Volunteer, Seacoast School of Technology, Technology Fun Nights 2010
  - Presidential Scholarship 2008-2012

References

References available upon request.