

Anthony Almudevar, PhD

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PROFILE

Statistician with over 30 years of experience spanning academia and private industry. Broad expertise across statistical modeling, AI/ML, operations research, and applied mathematics, with a strong track record of developing novel solutions to complex, open-ended problems. Extensive project experience across biomedical research, insurance industry, software development, and algorithm development and deployment, with deep domain knowledge in computational biology (including transcriptomics, proteomics, and microbiomics), drug discovery, systems biology, immunology, oncology, statistical genetics and smart home sensor networks. Strong foundation in traditional biostatistics, including clinical trials, experimental design and power analysis, statistical analysis plans, and grant writing. Accomplished educator and author, with extensive lecturing and course development experience, approximately 100 peer-reviewed publications, and two textbooks in advanced applied mathematics. See projects section at <https://www.linkedin.com/in/anthony-almudevar-37108994/details/projects/>.

PROFESSIONAL EXPERIENCE

Distinguished Scientist, Empress Therapeutics, Boston MA (2022 – 2025)

Machine learning support for drug discovery:

- Created a **novel target identification** ML pipeline for analysis of Perturb-seq experiments resulting in 70% identification of targets for arbitrary molecules.
- **Causal models for drug discovery.** Invented and implemented in C++ a novel regularization method for LASSO, expanded to include multinomial response models.
- **Multi-stage estimation of cytokine networks** with exogenous inputs based on Markov blankets.
- **Batch learning and correction methods** based on supervised learning of laboratory metadata.

Department of Biostatistics and Computational Biology, University of Rochester Medical Center Assistant Professor (2003-2009); Associate Professor (2009–2021); currently Professor Emeritus

Selection of projects with representative publications:

- **Models of cancer regulation via Boolean networks.** *Fitting Boolean networks from steady state perturbation data.* ([link](#)) For the supporting R package see [ternarynet](https://github.com/almudevar/ternarynet).
- **Biomarker** development and validation. *Micro RNA expression profiles as adjunctive data to assess the risk of hepatocellular carcinoma recurrence after liver transplantation.* ([link](#))
- **Psychometrics and outcomes measurement.** *Screening for adolescent depression: Comparison of the Kutcher Adolescent Depression Scale with the Beck Depression Inventory.* ([link](#)) [227 citations]
- **Predictive models for workers compensation claims.** Includes **neural net-based prediction of time loss using NWISP injury code standards.** *Using artificial neural networks to predict claim duration in a work injury compensation environment.* ([preprint](#))
- **Analysis of -omics data.** *On non-detects in qPCR data.* ([link](#)) [207 citations]
- **Stochastic control.** Foundational work in **stochastic control** and **reinforcement learning**. Much of this work is published in Almudevar, A. (2014) *Approximate Iterative Algorithms*, CRC Press.
- **Bayesian networks and causal modeling.** Numerous projects involving models of biological networks (pedigrees from natural populations and gene regulatory networks) and methods of formal inference *A hypothesis test for equality of Bayesian network models.* ([link](#))
- **Smart home support.** Signal processing methods for trajectory reconstruction of human subjects in a Smart Home environment. *Home monitoring using wearable radio frequency transmitters.* ([link](#))

- **Immunology and vaccine modeling.** *Statistical projection of post-vaccination antibody kinetics between dosing schedules.* ([link](#)) *A model for the regulation of follicular dendritic cells predicts invariant reciprocal-time decay of post-vaccine antibody response.* ([link](#))

Daiichi-Sankyo Inc; Biostatistician [Contract Completed]; (2021-2022)

- Experienced in creating and reviewing TLFs, SAPs and ADaM and SDTM datasets.

Statistician, Workers' Compensation Board, Halifax, Nova Scotia, Canada (1998-1999)

- Data analysis in a worker's compensation environment.

Software Developer, ACOM Computer Systems, Montreal, Quebec, Canada (1984-1992)

- Hotel back-office software development and training.

SKILLS

- I have experience in all main areas of **statistical and machine learning methodology**, including predictive modeling; multivariate methods; outcomes research; propensity score analysis; survival analysis; classification; a wide range of supervised and unsupervised learning methods, including KNN; random forests; LASSO; PCA and other dimension reduction techniques.
- I am also experienced in multiple **computing platforms**, including R (creation of R packages with C++ support; Shiny apps, ggplot), SAS, JMP, SPSS, Stata and Python (including deep learning and reinforcement learning applications using TensorFlow and TORCH). I also have experience with high-performance and cloud computing (AWS).
- Throughout my career I have acquired experience in many **computational biology** applications, including the analysis of microarrays; transcriptomic, proteomic and microbiomic data; NGS; sc-RNAseq, perturb-Seq, using a variety of platforms (limma, Cell Ranger, Seurat). In addition, I am familiar with currently used pathway curation resources, with experience interrogating and analyzing large multi-omic publicly available data sets.
- I have 30 years of **teaching experience** at the undergraduate and graduate level, including statistics and probability; machine learning; calculus and operations research. For a complete list of courses taught see <https://www.linkedin.com/in/anthony-almudevar-37108994>.
- I have extensive experience in **biostatistics**, from **primary research to human subject studies**:
 - Design of observational and experimental studies; creation of SAPs and data management plans. Experience harvesting public database compendiums. Thorough literature reviews.
 - Rigorous power analysis and sample size estimation (adhering to NIH good practices).
 - Expert knowledge of a wide range of analysis methods, ANOVA; hypothesis testing; design of experiments (DOE); linear/nonlinear regression; GLMs; longitudinal models (GEE, mixed models); survival analysis; psychometrics; outcomes research; analysis of claims data; propensity score analysis; causal inference.
 - Experience writing and submitting research funding grants (as PI and biostatistician).
 - Excellent scientific writing skills (LaTeX and WORD).
 - Data management, cleaning and quality control; documentation and metadata control; rigorous missing data procedures. Familiar with REDCap data collection support.
 - Excellent consulting and mentoring skills. I expect to be the go-to person for any questions regarding statistical practices.

PUBLICATIONS

Approximately 100 peer-reviewed publications and two textbooks ([Approximate Iterative Algorithms](#) and [Theory of Statistical Inference](#), see also [JASA review](#)). A complete list can be found at scholar.google.com.

EDUCATION

- **Doctor of Philosophy** Department of Statistics, University of Toronto, Toronto, Canada
- **Master's Degree** Department of Statistics, University of Toronto, Toronto, Canada
- **Bachelor of Science** Department of Mathematics, Concordia University, Montreal, Canada