





ANATOLY BUCHIN, PhD


Computational Biology | Machine Learning | Drug Discovery


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EDUCATION

- PhD in Computational Neuroscience, École Normale Supérieure, Paris
2012 – 2015
- Master of Physics, Peter the Great Polytechnic University, St Petersburg
2010 – 2011
- Master of Biomedical Research, Descartes University, Paris
2009 – 2010
- Bachelor of Physics, Peter the Great Polytechnic University, St Petersburg
2005 – 2009

TECHNICAL SKILLS

- Machine Learning & AI
Deep learning, Large Language Models (LLMs), Generative models, Bayesian inference, Statistical learning, Representation learning
- Computational Biology & Bioinformatics
Single-cell & bulk RNA-seq, Omics, Sequence analysis, Genomic alignment
- Model development
MLOps, CI/CD, data pipelines
- Big Data & Cloud Computing
AWS (S3, EC2, Lambda), Distributed computing, Parallel processing, High-performance computing (HPC).
- DevOps & Infrastructure
- Unix/Linux & DevOps
Shell scripting, Docker, GitHub, workflow automation
- Distributed and cloud computing
AWS Cloud, SageMaker, Google Cloud, HPC, GPU
- Programming languages
Python, R, Matlab, Bash
- Database management
SQLalchemy, Athena, PostgreSQL

PROFILE

Computational Bioinformatics Scientist with a PhD in Computational Neuroscience and 10+ years of experience in developing computational and AI/ML models for biological data. Specialized in generative modeling, single-cell and transcriptomics analysis, and large-scale data integration for drug discovery applications. Proven track record in leading cross-functional teams, managing cloud-based infrastructures, and contributing to high-impact publications. Ability to lead interdisciplinary teams, curating high-quality biological datasets, and push models from prototype to production using cloud-native tools. Passionate about reshaping biomedical research through applied AI.

INDUSTRIES: Drug discovery, Biotechnology, GenAI

SENIOR COMPUTATIONAL BIOLOGIST - AI/ML for Computational Biology

Synthesize Bio | Seattle | August 2024 - June 2025

- Co-developed foundational AI models to generate synthetic single-cell and bulk transcriptomics data, achieving >0.63 correlation with observed expression across diverse human tissues.
- Built scalable transcriptomics data pipelines to process over 80M single-cell samples using AWS, S3, EC2 and Athena.
- Developed scalable benchmarking framework (100M cells) to ensure model generalization across drug, cell line, and tissue contexts.
- Collaborated with biologists, engineers, and software teams to deploy models on website (<https://product.synthesize.bio/>).

SENIOR SCIENTIST - Computational Biology and Drug Discovery

Cajal Neuroscience | Seattle | May 2021 - June 2024

- Led the development of machine learning models to predict cellular states based on gene expression patterns, achieving an 83% classification accuracy, supporting key target validation program.
- Created data pipelines for 20+ internally generated RNA-seq datasets (bulk and single-cell), reducing preprocessing time by 13%.
- Integrated over 6TB genomics, transcriptomics and proteomics data to support target discovery in Alzheimer's and Parkinson's disease programs.
- Developed a pseudotime inference algorithm to map disease-specific gene expression changes, achieving r=0.34 correlation with disease progression. Presented at ADPD2022, ADPD2023

SCIENTIST I - Data Science & Computational Modeling

Allen Institute for Brain Science | Seattle | April 2017 - March 2021

- Developed novel computational models for biological neurons using high-dimensional biological data, contributed to 4 high-impact publications (*Nature*, *Cell Reports*, *Neuron*).
- Designed high-throughput data analysis pipelines for neuronal morphology and transcriptomic data for over 100 reconstructed neurons.
- Developed novel deep learning and classical ML models for cell type prediction achieving over 90% accuracy.
- Scaled model parameter optimizations across HPC clusters, improving compute efficiency by 3x.

Computational tools

Data visualizations
Pyplot, Matplotlib, Seaborn

Machine learning frameworks
PyTorch, TensorFlow, Keras, scikit-learn, scvi-tools

Development tools
VS Code, Cursor, Anaconda

Containers and workflow managers
Docker, Singularity, Snakemake, Nextflow

AWARDS

2017 Assistant professor in neuroscience (France)

2016 NSF Travel grant

2016 Swartz Foundation fellowship

2014 Foundation of Medical Research grant

2011 Labex doctorate fellowship

2009 Foundation Bettencourt Shueller fellowship

LANGUAGES

ENGLISH – Full proficiency

FRENCH – Proficient

GERMAN – Proficient

RUSSIAN – Native speaker

MENTORSHIP

2024, Jayasree Peri, Cedars-Sinai Medical Center, Master student

2022, Temitope Adeoye, University of South Florida, PhD student

2021, Sasha Batoukova, Tesla high school student

REFERENCES

Ben Logsdon
Cajal Neuroscience

Costas Anastassiou
Cedars-Sinai Medical Center

Adrienne Fairhall
University of Washington

Boris Gutkin
École Normale Supérieure

POST-DOCTORAL RESEARCHER - Mathematical modeling & Data analysis

University of Washington, | Seattle | February 2016 - April 2017

- Analyzed time series electrical recordings from epileptic human brain slices using computational modeling and non-linear dynamics. Contributed to 1 high-impact publication (**eNeuro**).
- Developed novel neural network model to simulate animal behavior of *Hydra vulgaris*.
- Implemented data analysis pipelines for in vivo calcium imaging data and applied motion tracking algorithms for video behavioral data.

DOCTORAL RESEARCHER - Computational Neuroscience

École Normale Supérieure, | Paris | January 2012 - November 2015

- Developed biophysical computational models for single neurons and neural networks in human temporal lobe.
- Applied dynamical systems theory to explain brain dynamics in human epilepsy and rodent motor systems. Contributed to 2 high-impact publications (**Journal of Neuroscience**, **PLOS Computational Biology**).
- Developed a multi-scale model combining reaction-diffusion dynamics with biologically realistic neural network to explain chloride imbalance in human epilepsy.

RESEARCH ASSISTANT - Computational Science

Ioffe Institute of Physics, | St Petersburg | September 2009 - January 2012

- Developed novel computational models of neural populations using statistical physics. Contributed to 2 scientific publications (**Biophysics**, **Optical Memory and Neural Networks**).
- Developed novel theoretical framework to explain neuron properties in cat visual cortex.
- Presented research results at the national **Neuroinformatics** conference.

SELECTED PUBLICATIONS

Buchin A., et al. (2022). Multi-modal characterization and simulation of human epileptic circuitry. *Cell Reports*. (**Paper** | **Code** | **Web product**)

Wei Y., **Buchin A.**, et al. (2023). Associations between in vitro, in vivo and in silico cell classes in mouse primary visual cortex. *Nature communications*. (**Paper** | **Code**)

Nandi A., **Buchin A.** et al. (2022). Single-neuron models linking electrophysiology, morphology and transcriptomics across cortical cell types. *Cell Reports*. (**Paper** | **Code** | **Web Product**)

Berg, J., **Buchin A.** et al. (2021). Human cortical expansion involves diversification and specialization of supragranular intratelencephalic-projecting neurons. *Nature*. (**Paper** | **Code**)

Kalmbach K. E., **Buchin A.** et al. (2018). H-channels contribute to divergent electrophysiological properties of supragranular pyramidal neurons in human versus mouse cerebral cortex. *Neuron*. (**Paper** | **Code**)

Buchin A., et al. (2018). Adaptation and inhibition control pathological synchronization in a model of focal epileptic seizure. *eNeuro*, 0019-18.2018. (**Paper** | **Code**)

Buchin A. et al. (2016). Reduced Efficacy of the KCC2 Cotransporter promotes epileptic oscillations in a subiculum network model. *Journal of Neuroscience*. (**Paper** | **Code**)

Buchin A. et al. (2016). Inverse stochastic resonance in cerebellar Purkinje cells. *PLOS Computational Biology*. (**Paper** | **Code**)

SELECTED CONFERENCE PROCEEDINGS

Buchin A., et al. (2023). Lineage tracing and differential expression analysis of single nuclei RNA-seq data from human neocortex identifies novel genes and pathways involved into progression of Alzheimer's disease. *Alzheimer's and Parkinson's disease conference*. Gothenburg, Sweden.

Buchin A., et al. (2022). Lineage tracing and differential expression analysis of single cell RNA-sequencing data from human midbrain identifies novel genes affected by idiopathic Parkinson's disease. *Alzheimer's and Parkinson's disease conference*. Barcelona, Spain.

Buchin A., et al. (2019). Conserved and divergent electrophysiological and morphological properties of mouse and human transcriptomically-defined cell types. *Chicago, United States*.

Buchin A., et al. (2018). Morpho-electric properties and computational simulation of human dentate gyrus granule cells from the epileptogenic hippocampus. *Society for Neuroscience*. San Diego, United States.