

Laura Adam, PhD

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Education

Ph.D. in Computational Biology, Bioinformatics and Genetics; Graduate Certificate in the Politics and Policy Studies of Science and Technology | 2013 | Virginia Polytechnic Institute and State University

M.Eng. in Computer Science and Applied Mathematics | 2010 | Ecole Nationale Supérieure d'Informatique et de Mathématiques Appliquées de Grenoble (ENSIMAG)

Skills & Abilities

PROGRAMMING

- Languages: Python, R, MATLAB, Javascript, HTML, Java, C++, Prolog
- Databases: graph database (Neo4j), relational database (SQL), document database (CouchDB)
- Other: Git, Docker, Open Source Projects, Full-stack, Linux

DATA SCIENCE

- Strong math background & recent coursework on predictive analytics (machine learning, optimization, big data)
- ETL, analysis and visualization of various experimental data (e.g. flow cytometry (high-dimensional), microscopy (images)) and public data (genetic databases, web scraping)
- Practical experience making predictions of biological systems using diverse modeling approaches; data analysis using nonlinear curve fitting, dimensionality reduction, clustering

SCIENTIFIC COMMUNICATION

- [Peer-review publications](#) (Nature Biotechnology, PLoS computational biology, Bioinformatics, Elife), conference talks (6), International Genetically Engineered Machine judge (6y), biosecurity panel member, reviewer (4 journals), grant writing
- French (native), English (fluent), Spanish

Experience

Co-founder & Head of Technology | EBIOSEC, Inc. | From 2017

- I designed, implemented and deployed [EBIO-OME](#), a 'github' for molecular biology experiments: interactive data visualizations, integrative management of sequences, samples, and experimental data – a spin-off supported by fellowships from CoMotion at the University of Washington.
 - Technologies used: Python (Flask), graph database (neo4j), docker, git, JavaScript, HTML. Central concept is a knowledge graph.
- I am surveying bioengineering around the world using twitter data, image classifier and natural language processing tools.
 - Technologies used: CouchDB, Flask and HTML/JavaScript. It includes interactive data visualization.

Consultant | Rancho BioSciences, Pacific Northwest Research Institute, Biocellion | From 2017

- I design and implement full-stack scientific software. Projects include design and implementation of GUI image analysis pipeline, design and project management of an interactive bio simulation software demo.
- I conduct biomedical bespoke data curation, compiling relevant information from a variety of sources.

Postdoctoral Researcher | University of Washington | 2014-2017

- To study yeast growth modulated by genetic engineering, I performed experimental design, data collection and analysis using a variety of lab instruments.
- I devised a model for inducible yeast colony growth arrest and extended it to make predictions for a yeast coculture diagnostic system.

- I created a domain-specific language to model (attributed graph grammars) and simulate (2D physics) engineered yeast spatiotemporal development.

Postdoctoral Researcher | James Martin Center for Nonproliferation Studies | 2013-2014

- I investigated the emerging concept of digital biothreats. At a cross between science policy and technology, I worked on several technical proposals and engaged with numerous shareholders. Since then, several publications have been discussing 'cyberbiosecurity' compiled on the website I curate information-biosecurity.org.

Graduate Research Assistant | Virginia Bioinformatics Institute | 2009-2013

- I conceptualized the use and design of languages to create novel DNA constructs and implemented the backend and data management system of a computer-aided design, modeling and predictive modeling of genetic systems, [GenoCAD](#).
 - Technologies used: Java, Prolog (logic programming), Copasi and SQL. My work relied on formal language theory and dynamical systems theory.
- I took a science policy guidance and turned it into an algorithm; I supervised a team that implemented a sequence screening for Select Agent and Toxin using parallel sequence alignments against large public databases and I performed the testing and performance characterization. Work was recognized by FBI and other federal agencies.
 - The software is written in java and uses blast. We used parallel computing principles.