Ryan Spangler

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Summary of Qualifications

- Software engineer specializing in computational infrastructure for biological modeling and large-scale distributed simulations.

- 16 years of professional experience working in whole-cell modeling, multi-scale simulation, distributed systems, and process calculi.

- Interested in developing computational frameworks for biological discovery, model integration and synthesis, and biologically inspired algorithms.

Experience

2020–present **Machine Learning Engineer**, *Allen Institute for Cell Science*, Seattle WA.

I develop models, infrastructure, tools, and systems to explore the organization and dynamics of human cell biology. I collaborate on a number of projects around the Institute, leading multiple group coding and learning sessions on a variety of biological, mathematical, and computational topics.

Achievements:

- Lead an ongoing collaborative effort building a multi-scale simulation of actin networks using Vivarium where different levels of detail (fiber and monomer) inform and relate to one another: https://github.com/simularium/vivarium-models/tree/buckling

- Created a library for programmatically generating bigraphical simulations, with a parser and interpreter for the "big" bigraphical language: http://github.com/prismofeverything/bigraph

- Contributed to the development of cellPACK, a tool for packing 3d molecular entities into biological membranes and meshes: http://github.com/mesoscope/cellpack

- Developed a server for running distributed Vivarium simulations that communicates with a websockets based visualization front-end (Simularium)

- Released Serotiny, a library for generating configurable and reproducible machine learning workflows: http://github.com/AllenCellModeling/serotiny

2018–2020   **Software Engineer**, *Stanford Bioengineering - Covert Lab*, Stanford CA.

I coordinated the efforts of the whole-cell modeling team with graduate students, postdocs and PI's, and in collaboration with other institutions. Beyond the code, I provided computational support, design consultation, implementation strategies and pair programming mentorship. In addition, I lead a consistent and productive practice of code reviews, pull requests, continuous integration, version control and other software engineering best practices.

Achievements:

- Created a platform for distributed multi-scale modeling of whole-cell colonies in a shared molecular environment, with a websockets-based interactive visualization: http://github.com/CovertLab/vivarium

- Built a workflow and execution system on Google Cloud to run whole-cell simulations and whole-colony experiments: http://github.com/CovertLab/sisyphus

- Implemented a generalized version of the Gillespie algorithm in C to get around a critical performance bottleneck: http://github.com/CovertLab/arrow

- Worked with the experimental teams to solve challenges of computational scale and organization for imaging and microscopy data.

2016–2018   **Software Engineer**, *OHSU - Computational Biology*, Portland OR.

At OHSU I worked with scientists and engineers to build on infrastructure and analysis pipelines to support all of the different research efforts at the University. My main focus was the development of a graph database for cancer genomics to provide a means to query, analyze and visualize this data as a whole.

Achievements:

- Engineered a large graph database system that automatically transforms and integrates all incoming data into a single graph http://bmeg.io/

- Created a schema to encode queries themselves as data so they can be programmatically generated, optimized and processed.

- Created an interactive visualization for navigating and querying the live graph.

- Engineered a distributed event system to trigger pattern-discovery analyses as data streams into the system.

2014–2016   **Lead Developer**, *Little Bird Technologies*, Portland OR.

At Little Bird I took their mass of social network data and applied graph theoretical, statistical and machine learning methods to find patterns and draw conclusions from that data.

Achievements:

- Built a 3D network visualization to explore and interact with vast, interconnected data.

- Used Bayesian networks and random forest to build a classification system of user behavior.

- Released much of the infrastructure as open-source: https://github.com/littlebird

- Instituted a workshop for collaboratively improving the whole team's coding and software development skills, starting by implementing well-known graph algorithms.

2007–2014 **Senior Developer**, *Instrument*, Portland OR.
I worked with the Labs team to transform concepts through code into practical applications.
Achievements:

- Created Caribou — an open source Clojure web ecosystem for building large high-performance web applications with great alacrity: https://github.com/caribou

- Built Schmetterling — a browser-based debugger for inspecting running Clojure programs: http://github.com/prismofeverything/schmetterling

- Pioneered a weekly workshop for collaboratively learning 3D graphics programming.

2006–2007 **Programmer**, *Performance Logic*, Portland OR.
I learned the fundamentals of real world development using C++ while simplifying and modularizing a large legacy code base.
Achievements:

- Built a variety of visualization methods for generating reports from large data sets.

- Enhanced the custom scripting language with features from functional programming.

Education

2009–2012 **Master of Science, Systems Science**, *Portland State University*, Portland OR.
Computational Neuroscience, System Dynamics, Information Theory, Agent Based Systems

2002–2005 **Bachelor of the Arts**, *The Evergreen State College*, Olympia WA.
Math, Performance, Computer Science

1999–2001 **Undergraduate Study**, *Oberlin College*, Oberlin OH.
Cognitive Science, Computer Science

Publications

1. Skalnik, C.J., Agmon, E., **Spangler, R.K.**, Talman, L., Morrison, J.H., Peirce, S.M., and Covert, M.W. (in review). Whole-Colony Modeling of *Escherichia coli*. *bioRxiv*.

2. Shaikh, B., Smith, L. P., Vasilescu, D., Marupilla, G., Wilson, M., Agmon, E., **Spangler, R.K.**, [...] and Karr, J. R. (2022). BioSimulators: a central registry of simulation engines and services for recommending specific tools. *Nucleic Acids Research*: https://doi.org/10.1093/nar/gkac331

3. Agmon, E., **Spangler, R.K.**, Skalnik, C.J., Poole, W., Morrison, J.H., Peirce, S.M., and Covert, M.W. (2022). Vivarium: an interface and engine for integrative multi-scale modeling in computational biology. *Bioinformatics*, 38(7), 1972-1979.

4. Allison Creason, David Haan, Kristen Dang, Kami E. Chiotti, Matthew Inkman, Andrew Lamb, Thomas Yu, Yin Hu, Thea C. Norman, Alex Buchanan, Marijke J. van Baren, **Ryan Spangler**, [...] and Kyle Ellrott (2021). A community challenge to evaluate RNA-seq, fusion detection, and isoform quantification methods for cancer discovery. *Cell Systems*, Volume 12, Issue 8, 827-838.e5.

5. Agmon, E., and **Spangler, R.K.** (2020). A multi-scale approach to modeling *E. coli* chemotaxis. *Entropy*, 22: 1101.

6. Macklin, D.N., Ruggero, N.A., Carrera, J., Choi, H., Horst, T.A., Mason, J.C., Sun, G., Agmon, E., DeFelice, M.M., Maayan, I., Lane, K., **Spangler, R.K.**, Gillies, T.E., Paull, M.L., Akhter, S.,

Bray, S.R., Weaver, D.S., Keseler, I.M., Karp, P.D., Morrison, J.H., and Covert, M.W. (2020). Simultaneous cross-evaluation of heterogeneous *E. coli* datasets via mechanistic simulation. *Science*, 369, eaav3751.

7. Adam Struck, Brian Walsh, Alexander Buchanan, Jordan A. Lee, **Ryan Spangler**, Joshua M. Stuart, and Kyle Ellrott (2020). Exploring Integrative Analysis Using the BioMedical Evidence Graph. *JCO Clinical Cancer Informatics*, :4, 147-159.

Technology

Languages	Clojure, Python, JavaScript, C/C++, Julia, Java, Bash, SQL
Tools	Kafka, Docker, Postgresql, RabbitMQ, Mongo, Git, Unix, Emacs, GLSL
Areas	Biological Modeling, Network Science, Graph Databases, Machine Learning, Data Visualization, Generative Music

Interests

Biology	Molecular Biology, Cell Biology, Systems Biology: How does life work? How can these principles be discovered and applied to other realms?
Music	Piano Tuning, Music Theory, Performance: Exploring the space of all possible musical structures and relationships.
Games	I have designed and published an award-winning board game - Sol: Last Days of a Star. http://elephantlaboratories.com/sol