

Patrick V. Phaneuf

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Curriculum Vitae

Bioinformatics and Systems Biology
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EDUCATION AND TRAINING

Ph.D. Bioinformatics and Systems Biology, 2016–2021, University of California, San Diego, CA
M.Sc. Computer Science, 2014–2016, University of California, San Diego, CA
Software and Firmware Engineer, 2010–2014, Thermo Fisher Scientific, Eugene, OR
B.Sc. Computer Engineering, *cum laude*, 2004–2009, Mercer University, Macon, GA

RESEARCH, TECHNICAL, AND PROFESSIONAL EXPERIENCE

Systems Biology Research Group (SBRG), Postdoc advised by Prof. Bernhard Palsson, 2021 – present,
Ph.D. and M.Sc. candidate advised by Dr. Adam Feist, 2014 – 2021

- **Data-driven strain design using aggregated ALE data**, 2019 – present
Designing application-focused sequence changes to the *E. coli* K-12 genome using a novel multi-dimensional adaptive laboratory evolution dataset, a multi-scale graph-based genome annotation engine, and structural biology tools. [10.1021/acssynbio.1c00337](https://doi.org/10.1021/acssynbio.1c00337)
- **Graph-based genome annotation engine and mutation enrichment**, 2018 – present
Applying enrichment methods to mutations described by a novel multi-scale annotation framework and a consolidated set of experimental evolution conditions to automate key mutation identification and to deconvolute mutation selection pressures. [10.1186/s12864-020-06920-4](https://doi.org/10.1186/s12864-020-06920-4)
- **ALEdb: a web-accessible experimental evolution mutation and conditions database**, 2014 – present
Developed first version of a web-accessible public database consolidating and reporting on mutations from experiments executed by researchers across the field of experimental evolution (aledb.org). Managing further development, maintenance, and growth by a team of software engineers and data curator (1–3). Major milestones include containerization, cloud-deployment, and the integration of 6000 samples (75000 unique mutations), . [10.1093/nar/gky983](https://doi.org/10.1093/nar/gky983)
- **Automated mutation calling pipeline for large-scale ALE experiments**, 2014 – present
Developed initial versions of an automated mutation calling pipeline used by the Novo Nordisk Foundation Center for Biosustainability (CfB). Managing further development and maintenance by a team of software engineers (1–3). Major milestones include automated quality control, metadata workflow, large-scale sample set auto-organization, ensemble mutation calling, containerization, and cloud-enabled parallelization.
- **ALE group software team lead**, 2016 – 2021
Managed a team of full-time software engineers (1–3) and data curator that developed and maintained 4 different products. Interfaced with multiple research, software, and informatics groups within the CfB. Lead efforts in adoption of cloud services for compute and storage within the SBRG.

Software and Firmware Engineer, Thermo Fisher Scientific, 2010 – 2014

Developed system control software and firmware for the Attune® Acoustic Focusing Cytometer and Attune® Autosampler projects. Experience the complete product life-cycle for both a software and hardware product through a combination of the first and second iteration of the Attune® and its Autosamplers.

SELECTED PUBLICATIONS

1. Patrick V Phaneuf, Daniel C Zielinski, James T Yurkovich, Josefin Johnsen, Richard Szubin, Lei Yang, Se Hyeuk Kim, Sebastian Schulz, Muyao Wu, Christopher Dalldorf, Emre Ozdemir, Rebecca M Lennen, Bernhard O Palsson, and Adam M Feist, *enEscherichia coli* Data-Driven strain design using aggregated adaptive laboratory evolution mutational data, *ACS Synth. Biol.* [10.1021/acssynbio.1c00337](https://doi.org/10.1021/acssynbio.1c00337) (2021).
2. Patrick V Phaneuf, James T Yurkovich, David Heckmann, Muyao Wu, Troy E Sandberg, Zachary A King, Justin Tan, Bernhard O Palsson, and Adam M Feist, Causal mutations from adaptive laboratory evolution are outlined by multiple scales of genome annotations and condition-specificity, *BMC Genomics* **21**, 514 (2020).

3. Patrick V Phaneuf, Dennis Gosting, Bernhard O Palsson, and Adam M Feist, ALEdb 1.0: a database of mutations from adaptive laboratory evolution experimentation, *Nucleic Acids Res.* **47**, D1164–D1171 (2019).
4. Kevin Rychel, Katherine Decker, Anand V Sastry, Patrick V Phaneuf, Saugat Poudel, and Bernhard O Palsson, iModulonDB: a knowledgebase of microbial transcriptional regulation derived from machine learning, *Nucleic Acids Res.* [10.1093/nar/gkaa810](https://doi.org/10.1093/nar/gkaa810) (2020).
5. Cameron R Lamoureux, Kumari Sonal Choudhary, Zachary A King, Troy E Sandberg, Ye Gao, Anand V Sastry, Patrick V Phaneuf, Donghui Choe, Byung-Kwan Cho, and Bernhard O Palsson, The bitome: digitized genomic features reveal fundamental genome organization, *Nucleic Acids Res.* **48**, 10157–10163 (2020).
6. Troy E Sandberg, Richard Szubin, Patrick V Phaneuf, and Bernhard O Palsson, Synthetic cross-phyla gene replacement and evolutionary assimilation of major enzymes, *Nat Ecol Evol* **4**, 1402–1409 (2020).
7. David Heckmann, Anaamika Campeau, Colton J Lloyd, Patrick V Phaneuf, Ying Hefner, Marvic Carrillo-Terrazas, Adam M Feist, David J Gonzalez, and Bernhard O Palsson, Kinetic profiling of metabolic specialists demonstrates stability and consistency of in vivo enzyme turnover numbers, *Proc. Natl. Acad. Sci. U. S. A.* [10.1073/pnas.2001562117](https://doi.org/10.1073/pnas.2001562117) (2020).
8. Bin Du, Connor A Olson, Anand V Sastry, Xin Fang, Patrick V Phaneuf, Ke Chen, Muyao Wu, Richard Szubin, Sibe Xu, Ye Gao, Ying Hefner, Adam M Feist, and Bernhard O Palsson, Adaptive laboratory evolution of escherichia coli under acid stress, *Microbiology* **166**, 141–148 (2020).
9. Amitesh Anand, Ke Chen, Laurence Yang, Anand V Sastry, Connor A Olson, Saugat Poudel, Yara Seif, Ying Hefner, Patrick V Phaneuf, Sibe Xu, Richard Szubin, Adam M Feist, and Bernhard O Palsson, Adaptive evolution reveals a tradeoff between growth rate and oxidative stress during naphthoquinone-based aerobic respiration, *Proc. Natl. Acad. Sci. U. S. A.* **116**, 25287–25292 (2019).
10. Colton J Lloyd, Zachary A King, Troy E Sandberg, Ying Hefner, Connor A Olson, Patrick V Phaneuf, Edward J O'Brien, Jon G Sanders, Rodolfo A Salido, Karenina Sanders, Caitriona Brennan, Gregory Humphrey, Rob Knight, and Adam M Feist, The genetic basis for adaptation of model-designed syntrophic co-cultures, *PLoS Comput. Biol.* **15**, e1006213 (2019).
11. Amitesh Anand, Connor A Olson, Laurence Yang, Anand V Sastry, Edward Catoiu, Kumari Sonal Choudhary, Patrick V Phaneuf, Troy E Sandberg, Sibe Xu, Ying Hefner, Richard Szubin, Adam M Feist, and Bernhard O Palsson, Pseudogene repair driven by selection pressure applied in experimental evolution, *Nat Microbiol* **4**, 386–389 (2019).
12. Gabriela I Guzmán, Connor A Olson, Ying Hefner, Patrick V Phaneuf, Edward Catoiu, Lais B Crepaldi, Lucas Goldschmidt Micas, Bernhard O Palsson, and Adam M Feist, Reframing gene essentiality in terms of adaptive flexibility, *BMC Syst. Biol.* **12**, 143 (2018).
13. Jonathan E Pekar, Patrick Phaneuf, Richard Szubin, Bernhard Palsson, Adam Feist, and Jonathan M Monk, Gapless, unambiguous genome sequence for escherichia coli c, a workhorse of industrial biology, *Microbiol Resour Announc* **7**, [10.1128/MRA.00890-18](https://doi.org/10.1128/MRA.00890-18) (2018).
14. Laurence Yang, Nathan Mih, Amitesh Anand, Joon Ho Park, Justin Tan, James T Yurkovich, Jonathan M Monk, Colton J Lloyd, Troy E Sandberg, Sang Woo Seo, Donghyuk Kim, Anand V Sastry, Patrick Phaneuf, Ye Gao, Jared T Broddrick, Ke Chen, David Heckmann, Richard Szubin, Ying Hefner, Adam M Feist, and Bernhard O Palsson, Cellular responses to reactive oxygen species are predicted from molecular mechanisms, *Proc. Natl. Acad. Sci. U. S. A.* **116**, 14368–14373 (2019).
15. Hemanshu Mundhada, Jose M Seoane, Konstantin Schneider, Anna Koza, Hanne B Christensen, Tobias Klein, Patrick V Phaneuf, Markus Herrgard, Adam M Feist, and Alex T Nielsen, Increased production of l-serine in escherichia coli through adaptive laboratory evolution, *Metab. Eng.* **39**, 141–150 (2017).