

Dimitri Livitz

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A motivated and hardworking scientist with an outstanding publication and academic record, cross-functional teamwork and hands on research experience, as well as excellent analytical skills.

Education

University of Massachusetts – Amherst

Bachelor of Science in Chemical Engineering, **GPA: 3.80/4.0**

- Integrated Concentration in Science
- Commonwealth Honors College

May 2015

Experience

Broad Institute Associate Computational Biologist II 2017-Present Associate Computational Biologist 2015-2017	PhylogicNDT - Clonal Evolution	<ul style="list-style-type: none">• Implemented the Dirichlet Process to identify tumor subclones from genomic data in Python/Cython and developed a module to quantify the growth dynamics of disease.• Analyzed a cohort of chronic lymphocytic leukemia patients to study how the transition from indolent disease occurs through clonal analysis. Quantified the growth advantage of mutations and showed that the progression of is influenced by variants already present in the earliest stages. (Gruber et al. 2017, co-first author)• Analyzed a cohort of ALK fusion driven lung cancer patients and identified several distinct clonal evolution patterns following kinase inhibitor treatment influenced by specific mutational processes such as the APOBEC enzyme. Reconstructed the complex clonal structure of these tumors. (Manuscript in preparation, co-first author)• Demonstrated that clonal shifts observed during early treatment lead to adverse clinical outcome in a cohort of CLL patients over the course of targeted therapy. (D. Landau et al. 2017)• Identified highly recurrent events across both the primary and metastatic tumors in a cohort of glioblastoma patients. (Brastianos et al. 2017)	
	International Cancer Genome Consortium - Pan-Cancer Analysis of Whole Genomes	<ul style="list-style-type: none">• Created a tool for filtering false-positive mutation calls resulting from misalignment, which was accepted by the working group and applied to the entire dataset. Filtered the results additionally to remove mutations caused by strand orientation specific oxidative damage during sequencing. (Whalley et al. 2017)• Studied the evolutionary history of the patients in the whole genome cohort through analysis of mutation multiplicities and identified common trajectories in cancer evolution. (Gerstung et al. 2017)• Analyzed purity and clonal structure of all samples, and developed a power correction of the inferred cancer cell fraction due to limited sequencing depth.	
3M Company	Bench Scale Processing Line Development	<ul style="list-style-type: none">• Designed an experiment to develop a gas sparging assembly.• Tested several design candidates and quantitated the results with Octave and C++.• Drafted the design in Siemens NX CAD and produced sketches of the model.• Design was manufactured and installed in the line.	Summer 2014
	Specialty Monomer Synthesis and Modeling	<ul style="list-style-type: none">• Designed and executed experiments to gather kinetic rate data.• Worked with analytical lab to build a GC/MS method to quantitate products.• Built predictive model in MATLAB to assist with scale up of both continuous reaction systems.	Summer 2013
UMass	Zeolites with Wei Fan's Group	<ul style="list-style-type: none">• Synthesized uniform silica nanoparticles from 13nm to 35nm and grew a pore-size controlled 3D carbon framework using the silica as a template.• Worked on mesoporous zeolite beta synthesis through hard templating and template free methods.• Completed honors thesis on efficient synthesis of zeolite beta through steam assisted conversion.	2011 - 2015
Tufts	GC/MS and Mathematical Modeling with Robbat Group	<ul style="list-style-type: none">• Using GC/MS measured DB17 retention indices of twenty compounds, not available in literature.• Modeled partitioning properties of coal tar from literature and measured indices.• Created MATLAB tools for the research group to use built on these models. (Antle et al. 2014)	Summer 2012

Computer Skills

Strong proficiency with Python/Cython and MATLAB. Experience with C++, R and Fortran. System level experience with Windows, Linux and Mac OS.

Technical Skills

Proficient at GC/MS and HPLC. Experience with UV-Vis, XRD, physisorption, and SEM analysis.

Elective Courses Include: Molecular Biology, Numerical Algorithms, Nanomaterial Chemistry and Engineering

Interests and Hobbies: Photography, DIY Electronics

Foreign Languages Spoken: Russian

Accepted Publications

- Antle, Patrick M, Christian D Zeigler, Dimitri G Livitz, and Albert Robbat. “Two-dimensional gas chromatography/mass spectrometry, physical property modeling and automated production of component maps to assess the weathering of pollutants”. In: *Journal of Chromatography A* 1364 (2014), pp. 223–233.
- Adalsteinsson, Viktor A*, Gavin Ha*, Samuel S Freeman*, Atish D Choudhury, Daniel G Stover, Heather A Parsons, Gregory Gydush, Sarah C Reed, Denisse Rotem, Justin Rhoades, et al. “Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors”. In: *Nature Communications* 8.1 (2017), p. 1324.
- Brastianos, Priscilla K*, Naema Nayyar*, Daniel Rosebrock*, Ignaty Leshchiner*, Corey M Gill, Dimitri Livitz, Mia S Bertalan, Megan D’Andrea, Kaitlin Hoang, Elisa Aquilanti, et al. “Resolving the phylogenetic origin of glioblastoma via multifocal genomic analysis of pre-treatment and treatment-resistant autopsy specimens”. In: *npj Precision Oncology* 1.1 (2017), p. 33.
- Landau, Dan*, Clare Sun*, Daniel Rosebrock*, Sarah Herman*, Joshua Fein, Mariela Sivina, Chingiz Underbayev, Delong Liu, Julia Hoellenriegel, Sarangan Ravichandran, Mohammed Farooqui, Wandu Zhang, Carrie Cibulskis, Asaf Zviran, Donna Neuberger, Dimitri Livitz, Ivana Bozic, Ignaty Leshchiner, Gad Getz, Jan Burger, et al. “The evolutionary landscape of chronic lymphocytic leukemia treated with ibrutinib targeted therapy”. In: *Nature Communications* Accepted (2017).
- Polak, Paz*, Jaegil Kim*, Lior Z Braunstein*, Rosa Karlic, Nicholas J Haradhavala, Grace Tiao, Daniel Rosebrock, Dimitri Livitz, Kirsten Kübler, Kent W Mouw, et al. “A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer”. In: *Nature genetics* 49.10 (2017), pp. 1476–1486.
- Raphael, Benjamin J, Ralph H Hruban, Andrew J Aguirre, Richard A Moffitt, Jen Jen Yeh, Chip Stewart, A Gordon Robertson, Andrew D Cherniack, Manaswi Gupta, Gad Getz, et al. “Integrated genomic characterization of pancreatic ductal adenocarcinoma”. In: *Cancer Cell* 32.2 (2017), pp. 185–203.
- Sade-Feldman, Moshe*, Yunxin J Jiao*, Jonathan H Chen, Michael S Rooney, Michal Barzily-Rokni, Jean-Pierre Eliane, Stacey L Bjorgaard, Marc R Hammond, Hans Vitzthum, Shauna M Blackmon, et al. “Resistance to checkpoint blockade therapy through inactivation of antigen presentation”. In: *Nature Communications* 8.1 (2017), p. 1136.

Publications In Review

- Chapuy, Bjoern*, Chip Stewart*, Andrew Dunford*, Jaegil Kim, Atanas Kamburov, Robert Redd, Michael Lawrence S, Margaretha Roemer, Amy Li, Marita Ziepert, Annette Staiger, Jeremiah Wala, Matthew Ducar, Ignaty Leshchiner, Esther Rheinbay, Amaro Taylor-Weiner, Caroline Coughlin, Julian Hess, Chandra Pedamallu, Dimitri Livitz, et al. “Molecular subtypes of Diffuse Large B-cell Lymphoma are associated with distinct pathogenic mechanisms and outcomes”. In: (2017).
- Gerstung*, Moritz, Clemency Jolly*, Ignaty Leshchiner*, Stefan C Dentro*, Santiago Gonzalez, Thomas J Mitchell, Yulia Rubanova, Pavana Anur, Daniel Rosebrock, Kaixan Yu, et al. “The evolutionary history of 2,658 cancers”. In: *bioRxiv* (2017), p. 161562.
- Gruber, Michaela*, Ivana Bozic*, Ignaty Leshchiner*, Dimitri Livitz*, Kristen Stevenson, Laura Rassenti, Daniel Rosebrock, Oriol Olive, Reaha Goyette, Stacey Fernandes, Jing Sun, Chip Stewart, Carrie Cibulskis, Wandu Zhang, Johannes Reiter, Jeffrey Gerold, John Gribben, Kanti Rai, Michael Keating, Jennifer Brown, et al. “Growth dynamics in naturally progressing chronic lymphocytic leukaemia”. In: (2017).
- Haradhavala, Nicholas*, Jaegil Kim*, Yosef Maruvka*, Paz Polak, Daniel Rosebrock, Dimitri Livitz, Ignaty Leshchiner, Kent Mouw, Michael Lawrence, Julian Hess, Atanis Kamburov, and Gad Getz. “Distinct mutational signatures characterize concurrent loss of polymerase proofreading and mismatch repair”. In: (2017).
- Whalley, Justin P, Ivo Buchhalter, Esther Rheinbay, Keiran M Raine, Kortine Kleinheinz, Miranda D Stobbe, Johannes Werner, Sergi Beltran, Marta Gut, Daniel Huebschmann, et al. “Framework For Quality Assessment Of Whole Genome, Cancer Sequences”. In: *bioRxiv* (2017), p. 140921.
- Yizhak, Keren, Francois Aguet, Jaegil Kim, Julian Hess, Kirsten Kübler, Hailei Zhang, Nicholas Haradhavala, Daniel Rosebrock, Dimitri Livitz, Xiao Li, Eila Arich-Landkof, Noam Shoshani, Chip Stewart, Ayellet Segré, Philip Branton, Paz Polak, Kristin Ardlie, Jonna Grimsby, Ruslana Frazer, and Gad Getz. “A comprehensive analysis of RNA sequences reveals somatic clonal expansion across multiple normal tissues”. In: (2017).

Abstracts

- Adalsteinsson, Viktor A, Gavin Ha, Sam Freeman, Atish D Choudhury, Daniel G Stover, Heather A Parsons, Gregory Gydush, Sarah Reed, Denis Loginov, Dimitri Livitz, et al. *Abstract LB-136: High concordance of whole-exome sequencing of cell-free DNA and matched biopsies enables genomic discovery in metastatic cancer.* 2016.
- Landau, Dan A, Clare Sun, Daniel Rosebrock, Mariela Campbell, Sarah EM Herman, Julia Hoellenriegel, Mohammed Farooqui, Wandu Zhang, Donna S Neuberger, Dimitri Livitz, et al. *The landscape of dynamic genetic changes in ibrutinib-treated CLL.* 2016.
- Yizhak, Keren, Jaegil Kim, Francois Aguet, Julian Hess, Hailei Zhang, Eila Arich-Landkof, Noam Shoshani, Ayelet Segre, Chip Stewart, Daniel Rosebrock, et al. *Abstract LB-231: Identifying cancer-related processes in normal tissues via RNA-seq.* 2017.