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Curriculum vitae: Peter LoVerso
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Biography

I am a bioinformatician with passions for cancer biology, next-generation sequencing, RNA-seq, computer security, and big data processing. I enjoy spending my time learning about new technologies and techniques and applying them to learn more about the world around me, and proactively try to indulge my curiosities and excitements about learning. I have worked both alone and in groups on the creation of novel bioinformatics algorighms, led the development of pipelines to streamline workflows to ensure speed and consistency, and led the exploration and implementation of new technologies into existing workflows.

Education

Master of Science, Bioinformatics
Rochester Institute of Technology, graduated May 2015, final GPA: 3.81 (out of 4)
Bachelor of Science, Molecular Bioscience and Biotechnology
Rochester Institute of Technology, graduated May 2013, final GPA: 3.47 (out of 4)

Publications

Wood, D. E., et al. "A machine learning approach for somatic mutation discovery." *Science translational medicine* 10.457 (2018).

Grossman, R. L., et al. "Collaborating to compete: Blood Profiling Atlas in Cancer (BloodPAC) Consortium." *Clinical Pharmacology & Therapeutics* 101.5 (2017): 589-592.

Bao, F., LoVerso, P. R., Fisk, J. N., Zhurkin, V. B., & Cui, F. (2017). p53 binding sites in normal and cancer cells are characterized by distinct chromatin context. *Cell Cycle*, *16*(21), 2073-2085.

LoVerso, P. R., & Cui, F. (2016). Cell type-specific transcriptome profiling in mammalian brains. *Frontiers in bioscience (Landmark edition)*, *21*, 973.

LoVerso, Peter R., and Cui, Feng. "A computational pipeline for cross-species analysis of RNA-seq data using R and Bioconductor." *Bioinformatics and Biology insights* 9 (2015): 165.

LoVerso, Peter R., Wachter, Christopher M., and Cui, Feng. "Cross-species transcriptomic comparison of in vitro and in vivo mammalian neural cells." *Bioinformatics and biology insights* 9 (2015): 153.

LoVerso, Peter R., Zhurkin, Victor B., and Cui, Feng. "Nucleosome organization and accessibility of p53 response elements in the chromatin context." *Cancer Research* 75.15 Supplement (2015): 4780-4780.

Cui, Feng, et al. "Prediction of nucleosome rotational positioning in yeast and human genomes based on sequence-dependent DNA anisotropy." *BMC bioinformatics* 15.1 (2014): 1.

AACR Abstracts

Nesselbush, M., Angiuoli, S., Diaz, L.A., Georgiadis, A., Glynn, S., Jones, S., Keefer, L., LoVerso, P., Murphy, D., Parpart-Li, S. and Riley, D., 2017. Clinical validation of a cell-free DNA liquid biopsy approach for noninvasive molecular profiling.

Novak, M., Angiuoli, S., Diaz, L.A., Georgiadis, A., Jones, S., Loverso, P.R., Parpart-Li, S., Sevdali, M., Velculescu, V.E., Verner, E.L. and White, J., 2017. Accurate identification and prioritization of candidate neoantigens from integrated cancer exome and transcriptome sequencing of FFPE samples.

Cui, F., LoVerso, P. and Bao, F., 2016. Distinctive chromatin organization of p53 binding sites in normal and cancer cells.

LoVerso, P.R., Zhurkin, V.B. and Cui, F., 2015. Nucleosome organization and accessibility of p53 response elements in the chromatin context.

Thesis

<u>Trans-species Transcriptomic Comparison of in vitro and in vivo Neural Cells</u>

The transcriptomes of *in vitro* neurons, astrocytes, and glial progenitor cells were sequenced for *R. norvegicus*, and the transcriptomes of *in vitro* neurons and astrocytes were sequenced for *H. sapiens*. These transcriptomes were analyzed and compared to one another, both within and across species, and were compared to published literature transcriptomes for these cell types, within and across species, with the purpose of comparing our *in vitro* data to published *in vitro* and *in vivo* RNA-seq datasets to quantify the differences between *in vitro* and *in vivo* lineages. A pipeline was developed to trivially allow the comparison of gene expression data across arbitrary species.

Work experience

Personal Genome Diagnostics

Principal Software Engineer	07/2020 – Present
Bioinformatics Software Engineer II	11/2017 – 07/2020
Bioinformatics Software Engineer I	6/2015 – 11/2017

This position involves writing software to process cancer tissue and plasma samples to identify mutations, immunotherapy targets, and other relevant information to generate a clinical report which can be used to inform patient treatment. Duties include scaling existing processes and developing new processes and data management techniques that enabled processing throughput to increase by several orders of magnitude, development of new software to identify novel types of variants or otherwise improve data processing by developing methods for which off-the-shelf software is not available. Other responsibilities include development of variant calling pipelines and custom analysis tasks as requested.

Skills

Fluent in Perl, R, and bash. Proficient in D, Java, and Python. Capable of working with C and C++. Fluent with UNIX-like systems- 6 years experience using Linux as primary operating system for both personal computing and personal hosted services (Arch, Debian, Ubuntu, CentOS). Proficient with Git. Familiar with Ansible, Bamboo, Foreman, and AWS.

Very experienced with NGS data, both genomic and transcriptomic. Knowledgable about details of demultiplexing, alignment, variant calling, consensus collapse, and quality control metrics for NGS data. Familiar with the codebases of Picard, cutadapt, bcl2fastq, and others.

Research and Projects

Researcher, Grant-funded Research   2/2013 – 05/2015

> Wrote programs in R, Java, and Python to analyze hundreds of response elements for p53. These programs would use a provided script to calculate nucleosome positioning scores at various places in the sequence, and would then analyze these scores to determine whether the p53 binding site was exposed or buried. Graphs would be generated, and grouped by response element type. Paid position under the supervision of PI Dr. Feng Cui.

Researcher, Independent Research   11/2012 – 5/2013

> Constructed, proposed, and carried out an examination into the cytoskeletal dynamics of *Pyrocystis fusiformis* and the mechanism by which it moves organelles internally. A presentation of the research findings will be presented to the RIT College of Science. Under the supehttps://repositive.io/about/rvision of Dr. Hyla Sweet during independent research.

Student Researcher, Class Project   11/2012 – 2/2013

> Carried out a characterization of Arabidopsis gene AT1G75750, including isolation of DNA from the plant, transformation using pNED193, and sequence analysis. The gene expression as it relates to drought stress was particularly focused upon. Under the

supervision of Dr. Dawn Carter during the Plant Molecular Biology course.

Student, Class Project   8/2012 – 11/2012

Carried out a characterization of T4rII mutant bacteriophage. The assays conducted include growth curves, multiplicity reactivations, transductions, and complementation tests. The mutant had an unknown mutation in its rII region, the location and nature of which was identified. A poster was made and the findings were presented to the class. Under the supervision of Dr. Jean Douthwright during the Viral and Microbial Genetics course.

Project Leader, ImagineRIT Project   5/2011 and 5/2012

Led a small team of students to plan and construct a simple transverse-wave simulator for RIT's ImagineRIT festival. The project was presented to thousands of guests. The project was carried out for each of two different festivals.

Teaching Experience

Graduate TA: Introduction to Bioinformatics   Spring 2015

Designed and taught a series of 10 labs designed to teach undergraduate and graduate Bioinformatics students to use the R programming language and its assorted features in a manner.

Graduate TA: Molecular Biology   Fall 2014

Supervised a molecular biology lab and taught and assisted the students in learning the principles of transforming bacteria and proper laboratory technique. Assisted the students in designing and carrying out their own experiment involving transformed *E. coli*.

Teacher, MIT ESP   3/2012, 11/2012, 11/2013, 11/2014, 11/2015, 11/2017

Volunteered to teach multiple different in-depth classes, each several hours long to several hundred high-school students on a variety of topics, including: Ethics discussions on genetics; the current state of the art in biotechnology and gene sequencing; and the life cycle, genomics, symbiotes, and points of interest of a variety of species of parasitic wasp.

Speaker, RIT BarCamp   10/2011 and 4/2013

Gave a half hour talk to all interested BarCamp patrons on the life cycle, genomics, symbiotes, and points of interest of a variety of species of parasitic wasp.

Awards

MS Honorable Mention Award – Rochester Institute of Technology   October 2017

Eagle Scout – Boy Scouts of America   August 2009

Memberships

Free Software Foundation

Electronic Frontier Foundation