Sumana Srivatsa

CONTACT
INFORMATION

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RESEARCH
INTERESTS

Public health policy, causal inference, computational statistics, machine learning

EDUCATION

Eidgenössische Technische Hochschule, Zürich, Switzerland

Ph.D. Student, Computational Biology Group   *Feb 2016 - Mar 2020*
- Advisor : Prof. Niko Beerenwinkel
- Committee : Prof. Peter Bühlmann, Prof. Randall Platt, and Prof. Rainer Spang
- Thesis : Discerning interactions from high-throughput perturbation data

M.Sc. in Computational Biology and Bioinformatics   *Sep 2013 - Oct 2015*
- Advisor : Prof. Niko Beerenwinkel
- Supervisor : Dr. Fabian Schmich
- Thesis : Pathway reconstruction from combinatorial gene knockdowns exploiting siRNA off-target effects

PES Institute of Technology, Bangalore, Karnataka, India

B.E. in Biotechnology   *Sep 2008 - Jun 2012*
- Graduated with Honors

RESEARCH
EXPERIENCE

Eidgenössische Technische Hochschule, Zürich, Switzerland

Scientific Assistant & Postdoctoral researcher, Computational Biology Group   *Apr 2020 - Aug 2020*
Advised by Prof. Niko Beerenwinkel
Worked on extending the application of our rank-based statistical method to DepMap data to identify synthetic lethal interactions from CRISPR data.

Ph.D. Student, Computational Biology Group   *Feb 2016 - Mar 2020*
Advised by Prof. Niko Beerenwinkel
Developed statistical and computational methods for discerning various interactions from large-scale perturbation data. Improved inference of underlying causal pathways using combinatorial perturbations resulting from siRNA off-target effects. Subsequently, developed a rank-based statistical method for discovering mutation-specific synthetic lethal interactions from large-scale pan-cancer perturbation screens. Further, identified clinically relevant markers in Gingivobuccal cancers through the multi-omics integrative analyses, in collaboration with Dr. Manoj Mahimkar (ACTREC, India).

Research Assistant, Computational Biology Group   *Feb 2015 - Oct 2015*
Advised by Prof. Niko Beerenwinkel and supervised by Dr. Fabian Schmich
Explored the feasibility of pathway reconstruction from combinatorial knockdown data exploiting siRNA off-target effects.

Mosaicoli - iGEM ETHZ 2014 Team   *Apr 2014 - Oct 2014*
Advised by Prof. Sven Panke, Prof. Jörg Stelling, and Prof. Yaakov Benenson
Won best model award among graduate teams. Developed mass action kinetics based multi-module whole cell model. Estimated and fitted parameters to experimental data which furthered development of a diffusion model, which was validated experimentally.

Research Assistant, Computational Systems Biology Group   *Feb 2014 - May 2014*
Advised by Prof. Jörg Stelling and supervised by Dr. Mathias Ganter
Worked on metabolic model reconstruction of *P. falciparum* and generated a refined consensus model by merging two genome-scale metabolic models for *P. falciparum* beyond the common namespace.

PATENTS

MDM2 inhibitor response prediction method and use of MDM2 inhibitors. 2019. *Patent Pending.*

PUBLICATIONS   S. Srivatsa*, H. Montazeri*, G. Bianco, M. Coto-Llerena, S. Piscuoglio, C.K.Y. Ng, N. Beerenwinkel, "Discovery of synthetic lethal interactions from large-scale pan-cancer perturbation screens", *In revision*, Preprint bioRxiv : 10.1101/810374.

G. Bianco, M. Coto-Llerena, J. Gallon, S. Taha-Mehlitz, V. Kancherla, M. Konantz, S. Srivatsa, H. Montazeri, M. De Menna, V. Paradiso, C. Ercan, N. Beerenwinkel, M. Kruithof-de Julio, L.M. Terracciano, C. Lengerke, R.M. Jeselsohn, C.K.Y. Ng, S. Piscuoglio, "GATA3 and MDM2 are synthetic lethal in estrogen receptor-positive breast cancers", *In revision*, Preprint bioRxiv : 10.1101/2020.05.18.-101998.

H. Montazeri, M. Coto-Llerena, G. Bianco, E. Zangeneh, S. Taha-Mehlitz, V. Paradiso, S. Srivatsa, A. de Weck, G. Roma, M. Lanzafame, M. Bolli, N. Beerenwinkel, M. von Flüe, L.M. Terracciano, S. Piscuoglio, C.K.Y. Ng, "Systematic Identification of Novel Cancer Genes through Analysis of Deep shRNA Perturbation Screens", *In revision*, Preprint bioRxiv : 10.1101/807248.

T. Ringel, N. Frey, F. Ringnalda, S. Janjuha, S. Butz, S. Cherkaoui, S. Srivatsa, M. Pirkl, G. Russo, G. Rogler, L. Villiger, N. Beerenwinkel, N. Zamboni, T. Baubec, G. Schwank, "Genome-scale CRISPR screening in human intestinal organoids identifies drivers of TGF-β resistance", Cell Stem Cell (2020), doi : 10.1016/j.stem.2020.02.007.

S. Srivatsa, J. Kuipers, F. Schmich, S. Eicher, M. Emmenlauer, C. Dehio, N. Beerenwinkel, "Improved pathway reconstruction from RNA interference screens by exploiting off-target effects", Bioinformatics (2018), doi : 10.1093/bioinformatics/bty240.

C. Wang, F. Schmich, S. Srivatsa, J. Weidner, N. Beerenwinkel, A. Spang, "Context-dependent deposition and regulation of mRNAs in P-bodies", eLife (2018), doi : 10.7554/eLife.29815.

*Equal contribution

PRESENTATIONS   S. Srivatsa, J. Kuipers, F. Schmich, S. Eicher, M. Emmenlauer, C. Dehio, N. Beerenwinkel, "Improved pathway reconstruction from RNA interference screens by exploiting off-target effects", Oral presentation at ISMB 2018, Chicago, USA.

S. Srivatsa, J. Kuipers, F. Schmich, N. Beerenwinkel, "Improved pathway reconstruction from RNA interference screens by exploiting off-target effects", Poster presentation at BC2 2017, Basel, Switzerland.

S. Srivatsa, F. Schmich, J. Kuipers, N. Beerenwinkel, "Pathway reconstruction from combinatorial gene knockdowns exploiting siRNA off-target effects", Poster presentation at RECOMB 2016, Santa Monica, USA.

S. Srivatsa, M. Ganter, R. Van Heck, J. Stelling, "Metabolic model reconstruction and evaluation of *Plasmodium falciparum*", Poster presentation at 4th Conference on Constraint-Based Reconstruction and Analysis 2015, Heidelberg, Germany.

TEACHING AND SUPERVISION   Supervised and mentored two graduate students during their lab rotations in the Computational Biology Group, ETHZ.

Teaching assistant for Statistical Models in Computational Biology (636-0702-00L), ETH Zürich
Taught by Prof. Niko Beerenwinkel
Developed exercises and performed academic tutoring for three semesters. Also presented lectures on Nested effects models and Statistical Phylogenetics.

Teaching assistant for sophomore Linear Algebra, PES Institute of Technology
Taught by Asst. Prof. Renna Sultana
Developed study material including solutions for exercises from Introduction to Linear Algebra by Gilbert Strang.

PROFESSIONAL EXPERIENCE	**InterpretOmics**, Bangalore, India *Jul 2012 - Dec 2012*

PROFESSIONAL EXPERIENCE

InterpretOmics, Bangalore, India   *Jul 2012 - Dec 2012*
Bioinformatics Analyst
Designed and built a detailed pipeline for analysis of histone modified ChIP-Seq data. Analysed ChIP-Seq data focussing on H4K12ac and H3K9me2 in common bean and mung bean.

GVN Institute of Oncology, Trichy, India,   *Jan 2012 - Jun 2012*
Research Intern
Analyzed time series imaging data from 13 live patients from a hospital in South India with various liver diseases. Designed an effective system to characterize various liver disorders based on model parameters.

Philips Research, Bangalore, India,   *Aug 2011 - Dec 2011*
Research Intern
Designed a two compartment model describing the transport of amino acids across the blood-brain barrier in Phenylketonuria patients.

HONORS AND AWARDS

SystemX travel grant for ISMB 2018   *Jul 2018*

Scholarship for International students, ETH Zürich   *2014 - 2015*

Prof. MRD Scholarship, PES Institute of Technology   *2012*
- for securing rank 2/95 in Dept. of Biotechnology

Distinction Award, PES Institute of Technology   *2008 - 2012*
- for excellence in Undergraduate Studies for all 8 semesters

State level Bio-Quiz, Runner up, Bangalore, Karnataka   *May 2011*

Intel CBSE Science Exhibition, National Level Finalist, Delhi, India   *Aug 2006*

COMPUTER SKILLS

- Current programming languages : R, Python
- Previous experience : MATLAB, Perl, C, MySQL, Shell scripting
- Tools : Git, Travis, Vim, LaTeX

RELEVANT COURSES

- Machine Learning
- Data mining
- Multivariate statistics
- Introduction to causality
- Computational Systems Biology
- Cell Biology and Genetics
- Advanced computational statistics
- Introduction to Mathematical Optimization
- Applied Regression
- Biostatistics
- Biochemistry
- Molecular Biology