

CONTACT INFORMATION	<p>E-mail : sumana.srivatsa@bsse.ethz.ch</p> <p>Website : https://anamus90.github.io/</p> <p>LinkedIn : https://www.linkedin.com/in/sumana-srivatsa</p>
RESEARCH INTERESTS	Computational biology, Probabilistic graphical models, Causal inference, Computational statistics, Machine learning
EDUCATION	<p>Eidgenössische Technische Hochschule, Zürich, Switzerland</p> <p>Ph.D. Student, Computational Biology Group <i>Feb 2016 - present</i></p> <ul style="list-style-type: none"> • Advisor : Prof. Niko Beerenwinkel • Focus : Computational biology, Perturbation screens, Statistics <p>M.Sc. in Computational Biology and Bioinformatics <i>Sep 2013 - Oct 2015</i></p> <ul style="list-style-type: none"> • Advisor : Prof. Niko Beerenwinkel • Supervisor : Dr. Fabian Schmich • Thesis : Pathway reconstruction from combinatorial gene knockdowns exploiting siRNA off-target effects <p>PES Institute of Technology, Bangalore, Karnataka, India</p> <p>B.E. in Biotechnology <i>Sep 2008 - Jun 2012</i></p> <ul style="list-style-type: none"> • Graduated with Honors
RESEARCH EXPERIENCE	<p>Eidgenössische Technische Hochschule, Zürich, Switzerland</p> <p><i>Ph.D. Student, Computational Biology Group</i> <i>Feb 2016 - present</i></p> <p>Advised by Prof. Niko Beerenwinkel</p> <p>Focus on developing statistical and computational methods for discerning various genetic interactions from high-throughput perturbation data. Previously worked on using combinatorial perturbations resulting from siRNA off-targets to improve inference of underlying causal pathways. Currently working on discovering mutation-specific synthetic lethal targets from large-scale pan-cancer perturbation screens. Additionally, ongoing collaboration with Dr. Manoj Mahimkar (ACTREC) on integrating methylation profiles and diverse molecular and clinoco-pathological data in Gingivobuccal cancers.</p> <p><i>Research Assistant, Computational Biology Group</i> <i>Feb 2015 - Oct 2015</i></p> <p>Advised by Prof. Niko Beerenwinkel and supervised by Dr. Fabian Schmich</p> <p>Explored the feasibility of pathway reconstruction from combinatorial knockdown data exploiting siRNA off-target effects.</p> <p><i>Mosaicoli - iGEM ETHZ 2014 Team</i> <i>Apr 2014 - Oct 2014</i></p> <p>Advised by Prof. Sven Panke, Prof. Jörg Stelling, and Prof. Yaakov Benenson</p> <p>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.</p> <p><i>Research Assistant, Computational Systems Biology Group</i> <i>Feb 2014 - May 2014</i></p> <p>Advised by Prof. Jörg Stelling and supervised by Dr. Mathias Ganter</p> <p>Worked on metabolic model reconstruction of <i>P. falciparum</i> and generated a refined consensus model by merging two genome-scale metabolic models for <i>P. falciparum</i> beyond the common namespace.</p>
PUBLICATIONS	<p>S. Srivatsa*, H. Montazeri*, G. Bianco, M. Coto-Llerena, S. Piscuoglio, CKY. Ng, N. Beerenwinkel, "Discovery of synthetic lethal interactions from large-scale pan-cancer perturbation screens", <i>In review</i>, Preprint bioRxiv : 10.1101/810374.</p> <p>H. Montazeri, M. Coto-Llerena, G. Bianco, E. Zangeneh, S. Taha-Mehlitz, V. Paradiso, <u>S. Srivatsa</u>, A. de Weck, G. Roma, M. Lanzafame, M. Bolli, N. Beerenwinkel, M. von Flüe, LM. Terracciano, S. Piscuoglio, CKY. Ng, "APSiC : Analysis of Perturbation Screens for the Identification of Novel Cancer Genes", <i>In submission</i>, Preprint bioRxiv : 10.1101/807248.</p>

T. Ringel, N. Frey, F. Ringnalda, S. Janjuha, S. Butz, S. Cherkaoui, S. Srivatsa, M. Pirkel, G. Russo, G. Rogler, L. Villiger, N. Beerenwinkel, N. Zamboni, T. Baubec, G. Schwank, "Genome-scale CRISPR screening in organoids identifies synergistic tumor-suppressor activities that lead to TGF- β resistance", *In review*.

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.

V. Ayyappan, A.K. Talukder, K. Sasmal, S. Srivatsa, K. Melmaiee, P. Achuthrao, B. Kingham, Z. Liu, V. Kalavacharla, "Chromatin Immunoprecipitation-Sequencing (ChIP-Seq) to understand the genome-wide hierarchy of H4K12ac and H3K9me2 acquisition in common bean (*Phaseolus vulgaris* L.) and mung bean (*Vigna mungo* L.).

*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.

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.

TEACHING AND SUPERVISION

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.

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

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.

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