POORVI KAUSHIK

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OBJECTIVE

To improve the diagnosis and treatment of complex diseases by developing analyses, methods and insights using computational biology, process design, high-throughput experimentation and translational medicine.

SKILLS

- Comprehensive understanding of cancer biology and the translational research landscape, focused on targeted-therapy and immunotherapy.
- Experienced in experiment design, statistical data analysis and visualization, and computational analysis of cellular networks.
- SOFTWARE - R, RStudio, Python, C, MS Excel, SQL, Adobe Illustrator, HTML5
- Cell culture, targeted drug treatment protocols, protein/RNA/DNA extraction, western-blotting, flow-cytometry, PCR, high-throughput cellular imaging, protein array design and optimization

EDUCATION

- PhD. Computational Biology and Medicine, Cornell University, New York   **9/2015**
- Graduate Diploma in Bioinformatics, Institute for Bioinformatics and Applied Biotechnology, India   **7/2005**
- B.Tech Chemical Engineering, Manipal Institute of Technology, India   **7/2003**

WORK EXPERIENCE

Postdoctoral Research Scholar, Computational Biology Department   **8/2015-Present**
Sloan Kettering Institute, New York

- Investigating the mutational basis of differential response to combination therapy in glioblastoma (GBM) in a cohort of six cell lines using Illumina next-generation RNAseq sequencing.
- Identifying markers of drug response in the treatment of GBM by modeling protein networks from time-series data using functional partial correlation analysis

Graduate Research Assistant, Computational Biology Department   **9/2008-8/2015**
Sloan Kettering Institute, New York

- Identified five effective and synergistic drug combinations applied to glioblastoma (GBM) tumorsphere lines representative of three transcriptomally distinct subtypes.
- Improved signal to noise ratio by up to 40% in data representing clinically relevant drug targets in human cell line samples by developing a numerical method to correct spatial noise in protein microarrays
- Identified two novel drug combinations in GBM that display delivery time and order dependent synergy. Performed time series analysis and visualization of protein responses to discover markers of drug response.

Junior Research Fellow, Computational Neuroscience Lab   **1/2007-7/2007**
National Center for Biological Sciences, Bangalore

- Maintained and expanded the Database of Quantitative Cell Signaling (DOQCS). Work here involved model curation and front-end maintenance.

Biomodeling Scientist , Cellworks Research Pvt. Ltd, Bangalore   **3/2005-9/2006**

- Created predictive kinetic models of cellular and neuronal signaling in Parkinsons disease
- Led a team of four associate scientists in the development of computational models of neurodegenerative disease including Parkinsons, Alzheimers and Huntingtons.

Graduate Intern, R&D, Biocon, Bangalore   **11/2004-2/2005**

- Optimized a high throughput robotic assay for automation by a Tecan digital dispenser.
- Assisted in the miniaturization of enzyme assays in food-processing applications.

PUBLICATIONS

Sequential targeting of signaling proteins modulates cellular response to lapatinib and obatoclax in glioblastoma, **Kaushik P**, Molinelli E, Bemis D, Korkut A, Wang W, Brennan C, Sander C. In preparation

Spatial normalization of reverse phase protein array data. **Kaushik P**, Molinelli EJ, Miller ML, Wang W, Korkut A, Liu W, Ju Z, Lu Y, Mills G, Sander C. PLoS One. 2014 Dec 12;9(12):e97213. doi: 10.1371/journal.pone.0097213.

Perturbation biology: infelrring signaling networks in cellular systems. Molinelli EJ, Korkut A, Wang W, Miller ML, Gauthier NP, Jing X, **Kaushik P**, He Q, Mills G, Solit DB, Pratilas CA, Weigt M, Braunstein A, Pagnani A, Zecchina R, Sander C. PLoS Comput Biol. 2013;9(12):e1003290

Integrative genomic profiling of human prostate cancer. Taylor BS, Schultz N, Hieronymus H, Gopalan A, Xiao Y, Carver BS, Arora VK, **Kaushik P**, Cerami E, Reva B, Antipin Y, Mitsiades N, Landers T, Dolgalev I, Major JE, Wilson M, Socci ND, Lash AE, Heguy A, Eastham JA, Scher HI, Reuter VE, Scardino PT, Sander C, Sawyers CL, Gerald WL. Cancer Cell. 2010 Jul 13;18(1):11-22.

Analysis of the molecular networks in androgen dependent and independent prostate cancer revealed fragile and robust subsystems. Tasseff R, Nayak S, Salim S, **Kaushik P**, Rizvi N, Varner JD. PLoS One. 2010 Jan 28;5(1):e8864. doi: 10.1371/journal.pone.0008864.

Dynamics of tyrosine hydroxylase mediated regulation of dopamine synthesis **Kaushik P**, Gorin F, Vali S. J Comput Neurosci. 2007 Apr;22(2):147-60.

REFERENCES (contact details available upon request)

Dr. Chris Sander, Chair of the Computational Biology program at Memorial Sloan Kettering Cancer Center
Dr. Cameron Brennan, M.D, Neurosurgeon and Scientist in the Human Oncology and Pathogenesis Program
Dr. Upinder Bhalla, National Center for Biological Sciences, Bangalore India
Dr. Shireen Vali, Cellworks Group, Bangalore, India