

**RESEARCH SUMMARY** My two research programs interface cancer immunology with Artificial Intelligence and probabilistic approaches. **First**, my cancer-immunology program identifies drugs with dual anticancer potential through novel AI/statistical methods. It has identified a new class of drugs called bipotent drugs, for which I was awarded the prestigious Michelson Prize by Human Vaccines Project and was also selected among the "40 most promising young Cancer Immunology scientists" by Irving Foundation. **Second**, my single-cell research program, funded through K99 pathway to independence award, develops probabilistic approaches for single-cell and spatial genomics data. My lab will extend these programs to precision medicine and antibody design.

**ACADEMIC POSITION** **University of Colorado Anschutz Medical Campus** 2022-  
Asst. Clinical Professor, Department of Obstetrics and Gynecology

**Broad Institute** 2018-2022  
Human Vaccine Project Fellow, Data Science  
Adviser: Prof. X. Shirley Liu, Prof. Rafael Irizarry, Prof. Keith T Flaherty

**ACADEMIC AWARDS**

NCI K99 Pathway to Independence Career Award

- National Cancer Institute K99 Career Award, 2020.

Arthur L. Irving Family Foundation Cancer Immunology

- 40 promising young scientists in Cancer Immunology , 2020.

Michelson Medical Research Foundation and Human Vaccines Project

- Michelson Prize, 2019.

Quantitative Challenges in Cancer Immunology and Immunotherapy

- Stellar Research Award, 2019.

National Institute of Minority Health and Health Disparities fellowship

- Health Disparity Research Fellowship, 2016-2017.

Invention of the year, UMD, 2016

- Harnessing Synthetic Rescues to Assess and Counteract Resistance to Treatment in Cancer, University of Maryland, 2016 Invention of the year.

National Institute of Health GPP research fellowship

- Graduate Partnership Program Fellowship, 2012.

Max-Planck-Institut für Informatik fellowship

- Summer research German Govt. fellowship, 2012.

Dean fellowship, University of Maryland

- Dean Fellowship, 2011.

## EDIC fellowship

- EDIC Swiss Doctoral Fellowship, 2011.

## MSc Research Scholar

- MSc Research Scholar Fellowship, EPFL 2010.

## Indian Statistical Institute Calcutta Entrance Exam

- All India Rank 2, Indian Statistical Institute Entrance exam, 2003.

EXTERNAL  
RESEARCH  
SUPPORT**K99/R00 Career Development Award**

2020 – 2025

Identifying drug synergistic with cancer immunotherapy.  
*NIH/NCI K99CA248953*  
 PI (\$971,726)

**Michelson Med Res Foundation, Young Investigator Award**

2019 – 2022

AI-predictor to identify immunomodulatory drugs.  
*MP19-02-190-Sahu-A*

PENDING  
RESEARCH  
SUPPORT**Novartis Drug Discovery and Translational Research Program** Pending

Developing AI-based precision oncology by targeting inter-lesion and intra-tumor heterogeneity in highly resistant patients.  
**Selected for final round**  
 PI: Sahu & Juric

## EDUCATION

**University of Maryland, College Park,**

PhD., Computer Science(2016),  
 Adviser: Prof. Eytan Ruppin, Prof. Sridhar Hannenhalli  
 Thesis : Data driven approaches to identify determinants of heart disease and cancer resistance.

**École Polytechnic Fédérale de Lausanne, Switzerland (and University of Washington, Seattle)**

M.S, Genome Science, Computer Science (2011)  
 Adviser: Prof. Bernard Moret , Prof. William Stafford Noble  
 Master Thesis: *ENCODE: Unsupervised Segmentation of ENCODE data*

**National Institute of Technology, Trichy, India,**

B.Tech.(2007), Electronics and Communication Engineering NIT  
 Bachelor Thesis: *Hiding audio in video with optimized source and channel coding*  
 Adviser: Dr. P. Palaniswamy

ADVISEES/Co-  
ADVISEES

*Mentoring role, Research area, Accomplishments, Institution*

**Postdoctoral trainees:**

- Nishanth U. Nair, Ph.D. 2015-2017  
Research co-advisor  
Big data and Oncology  
First-authored scholarship of mentored research  
University of Maryland
- Songpeng Zu, Ph.D. 2020-2021  
Research co-advisor  
Probablistic modelling  
First-authored scholarship under preparation  
Harvard University

**Ph.D. and MS students:**

- Xiaoman Wang 2018-2020  
Research co-advisor  
Statistical methods  
Co-first authored publication of mentored research and PhD thesis  
Peking Union Medical College; Visiting student at DFCI
- Phillip Nicol 2020-  
Ph.D. co-advisor  
Probablistic modelling  
First authored publication in submission  
Harvard School of Public Health
- Gege Qian 2020-2021  
Master thesis supervisor  
Single cell analysis  
Completed MS thesis on Exploit Immunological Information through Single-cell Sequence Analysis and Image Assay  
Harvard Medical School
- Peter Shen 2018  
MS supervisor  
AI  
Completed MS thesis on AI-predictor of immunotherapy response using transfer learning  
Harvard Medical School
- Ya Han 2018  
Research co-advisor  
AI  
Tonji University
- Sailing Shi 2018  
Research co-advisor  
Tonji University
- Tong Han 2018  
Research co-advisor  
Tonji University
- Binbin Wang 2019

Research co-advisor  
Epigenetics  
Tonji University

- Ben Kompa  
Summer rotation supervisor  
AI  
Harvard Medical School

- **UG students:**

- Chongming Ni 2018  
Research supervisor  
AI and Immuno-oncology
- Sanna Madan 2017  
Research supervisor  
Big data  
University of Maryland
- Danielle Paulson 2019 (Summer student) High school RSI Research supervisor  
Single cell analysis  
Harvard University

## SOFTWARE

- **BTAS:** AI predictor of immunotherapy response.  
<https://rconnect.dfc.harvard.edu/BTAS/>
- **bipotentR:** Method to identify gene targets that kill tumor by two mechanisms concurrently.  
<http://bipotentr.dfc.harvard.edu/>
- **MSSC:** Bayesian model for robustly identifying differentially expressed genes in single cell data.  
<https://github.com/JunLiuLab/mssc>
- **CellPhen:** Probabilistic model to map immune populations to biological phenotypes such as patient survival or immunotherapy response through bulk tumor transcriptomes.  
<https://github.com/vinash85/CellPhen>
- **scDiffPop:** Single cell probabilistic inference of cell populations (e.g. immune cells) perturbed by biological conditions such as disease or perturbation experiments.  
<https://github.com/vinash85/scdiffpop/tree/phil>
- **DeepImmune:** AI-predictor of immunomodulatory drugs through perturbation model of tumor immune microenvironment.  
<https://github.com/vinash85/deepImmune>
- **TRIM:** Statistical approach to identify Transcription Regulator of Immune-Metabolism (TRIM).  
<https://github.com/vinash85/TRIM>
- **INCISOR:** Identification of synthetic rescue interactions. The genetic interactions determine resistance to cancer targeted and immunotherapy. (Patented)  
<https://github.com/vinash85/INCISOR>

- **GOAL** : Bayesian tool to find causal expression regulatory polymorphisms by integration of genetic and epigenetic data .  
<https://www.cbcb.umd.edu/software/goal>
- **ISLE**: Identification of clinically relevant synthetic lethal interactions.  
<https://github.com/jooslee/ISLE>
- Hirdaya: SVM predictor of driver genes in idiopathic dilated Image result for cardiomyopathy.
- CellToPhenotype: Machine learning predictor of migration and proliferation potential  
<https://github.com/nishanth83/CellToPhenotype>
- ChIPnorm: A statistical method for identifying interesting regions in histone modification libraries.  
<http://lcb. epfl. ch/ software. html>

TEACHING  
EXPERIENCE

Course	Role	Institution & level	Responsibilities
Big data statistics in genomic and genetic research, 2020	Teaching Assistant	Harvard Grad	Create/presented a lecture.
Introduction to Computational Biology and Bioinformatics, 2019	Teaching Assistant	Harvard UG	Create/presented a lecture & grade a exercise.
Big data and systems biology, 2017	Assistant Instructor	UMD Grad	Grade exercises and class projects. Create/present 4 lectures: TCGA data analysis, Flux balance analysis, and Identify synthetic lethal and synthetic rescue interactions.
Introduction to Artificial Intelligence, 2011	Teaching Assistant	UMD UG	Homework lectures, Teaching hour assistance, grade weekly exercises.
Systems biology & genomics, 2018	Guest lecturer	DNA Damage Workshop	
Field Programmable Gate Arrays programming, 2006	Guest lecturer		

INVITED  
SPEAKER

Broad institute, Single cell meeting, Cambridge, MA.	2022
Cancer Center Symposium and Retreat. University of Colorado	2022
Seven Bridge and Harvard Center of Mathematical Science and Applications, Cambridge, MA.	2019
Dana-Farber Cancer Institute Center Genomic meetup(CFCE), Boston, MA.	2018
Immunotherapy response & resistance	Weill Cornell Medical College 2017

Synthetic rescue and immunotherapy resistance	Tango Therapeutics	2017
Personalized medicine	Weizmann Institute	2016
Personalized medicine	Metabomed Inc. Israel	2015
Cardiovascular diseases	Center for Bioinformatics and Computational Biology Seminar	2015
Personalized medicine	Tel Aviv University	2015
Epigenetics	Center for Bioinformatics and Computational Biology Seminar	2013
Enhancers associated with hypertension	National human genome research Inst.	2012
Hierarchical and multipass segmentation	University of Washington, Seattle	2012
Normalization of ChIP-Seq data	Pacific Science Biocomputing	2012

## CONSULTING

- [Lead Pharma](#)(Ongoing)
- [Checkmate Pharmaceuticals](#) (Ongoing)
- [C-Reveal Therapeutics](#)(Ongoing)
- [Metabomed](#)
- [Pangea Therapeutics](#)

ADDITIONAL  
PROFESSIONAL  
EXPERIENCE

**STMicroelectronics, Imaging Dept**, Grenoble, France

*Design Architect*

**May 2007 to August 2009**

Responsibilities (Optical image stabilizations, JPEG, Video stabilization):

- Formulation of Architecture & specification of an IP.

PROFESSIONAL  
MEMBERSHIPS

- Society for Immunotherapy of Cancer (STIC) since 2020
- International Society for Computational Biology (ISCB) since 2010
- American Association for Cancer Research (AACR) since 2015
- Swiss Institute of Bioinformatics (SIB) since 2010

PROFESSIONAL  
SERVICES

- Ad hoc reviewer for journals:
  - Nature
  - Nature Biotechnology
  - Cell
  - Nature Method
  - Bioinformatics
  - Nature Medicine
  - Nature Communications
  - Genome Research
  - Nucleic Acids Research
  - BMC Bioinformatics
  - IEEE/ACM Transactions on Computational Biology and Bioinformatics

## PUBLICATIONS

\*Co-corresponding Author,(Reverse chronological)

Appear as "Avinash Das" or "Avinash Sahu" due to a name change

**Journal**

Avinash D.\*, Xiaoman W., ..., Keith F., Data-driven discovery of targets for bipotent anticancer drugs identifies Estrogen Related Receptor Alpha. *Cancer Discovery*. (In press) <https://www.biorxiv.org/content/10.1101/2021.10.25.465724v1>

Mike M, ..., Avinash D, ..., Benjamin V. A Community Challenge to Predict Clinical Outcomes After Immune Checkpoint Blockade in Non-Small Cell Lung Cancer. *Journal of Clinical Oncology*. <https://doi.org/10.1101/2022.12.05.518667>. 2022.

Xiaoman W., ..., Avinash D.\*, INCISOR: An algorithm to identify synthetic rescue mediators of resistance to targeted and immunotherapy. Springer, *Methods in Molecular Biology*; 2021.

Elise A., ..., Avinash D., ..., Roberta Z., Supporting the next generation of scientists to lead cancer immunology research. *Cancer Immunology Research*, 2021.

David L., ..., Avinash D., ..., Genevieve B., Evolution of Resistance to Immunotherapy in a Melanoma Exceptional Responder. *Nature Medicine*; 2021.

Shengqing G., ..., Avinash D., ..., X. Shirley L., Therapeutically increasing MHC-I expression potentiates immune checkpoint blockade. *Cancer Discovery*. 2021.

Bernard P., Cristopher C., ..., Avinash D., ..., Dejan J., Cell-free DNA captures tumor heterogeneity and driver alterations in rapid autopsies with pre-treated metastatic cancer. *Nature Communication*. 2021 May 27

Zexian Z., ..., Avinash D., ..., X. Shirley L., Cross-site concordance evaluation of tumor DNA and RNA sequencing platforms for the CIMAC-CIDC network. *Clinical Cancer Research*. 2020

Shengqing G., ..., Avinash D., ..., X. Shirley L., Clonal tracing reveals diverse patterns of response to immune checkpoint blockade. *Genome Biology*. 2020

Jian Z., ..., Avinash D., ..., X. Shirley L. Immune receptor repertoires in pediatric and adult acute myeloid leukemia. *Genome Medicine*. 2020

Ziyi L., ..., Avinash D., ..., X. Shirley L. CRISPR Screens Identify Essential Cell Growth Mediators in BRAF Inhibitor-resistant Melanoma. *Genomics, Proteomics & Bioinformatics*. 2020

Gaurav P., ..., Avinash D., ..., Zeev Ronai, Translational Reprogramming Marks Adaptation to Asparagine Restriction in Cancer. *Nature Cell Biology*. 2019

Alicia H., ..., Avinash D. ..., Sridhar H. Allele-specific enhancers mediate associations between LCAT and ABCA1 polymorphisms and HDL metabolism. *PLoS one*. 2019.

Cristopher C., Avinash D., ..., Dejan J., Plasma sequencing demonstrates that breast cancer patients have a higher prevalence of clonal and multiple PIK3CA mutations than other solid tumor patients. *CANCER RESEARCH*.

Yan L., ..., Avinash D., ..., Zeev R., Gut microbiota dependent anti-tumor immunity restricts melanoma growth in Rnf5-null mice. *Nature Comm*. 2019.

Joo Sang L., Avinash D., ..., Eytan R. Harnessing synthetic lethality to predict clinical outcomes of cancer treatment. *Nature Communication*, 2019.

- Avinash D\*, ...,Eytan R\* Genome-wide prediction of synthetic rescue mediators of resistance to immunotherapy. *Molecular Sys. Bio.*, 2019. \*Corresponding author
- Assaf M, Avinash D., ..., Sridhar H. Charting the landscape of pairwise gene expression states associated with survival in cancer. *Cell Reports*, 2019.
- Avinash D., Joo S.L, Eytan Rupp. Computer System And Methods For Harnessing Synthetic Rescues And Applications Thereof. 2019
- Peng J., ..., Avinash D., .., X. Shirley L., Signatures of T-cell dysfunction and exclusion predict cancer immunotherapy response. *Nature Medicine*. 2018
- Nishanth N., Avinash D., ..., Eytan R., Cell migration is a stronger predictor of patient survival in breast cancer than cell proliferation. *Scientific Report*. 2018
- Nishanth N., Avinash D., .., Sridhar Hannehalli, Putative functional genes in idiopathic dilated cardiomyopathy. *Scientific Reports*, 2018
- Gaurav P.,... Avinash D., ..., Zeev R. Targeting the Warburg Effect via LDHA inhibition engages ATF4 signaling for cancer cell survival. *The EMBO*, 2018.
- David L., ...,Avinash D., .., Genevieve B., Phylogenetic analysis of longitudinal melanoma samples to reveal convergent evolution and markers of immunotherapy resistance. *Journal of Clinical Oncology*, 2018.
- Kun W, ..., Avinash D., ..., Sridhar H., Comprehensive map of age-associated splicing changes across human tissues and their contributions to age-associated diseases. *Scientific reports*, 2018
- Shrutii S, Avinash D., ..., Sridhar H. Distal CpG islands can serve as alternative promoters to transcribe genes with silenced proximal-promoters. *Genome Research*, 2017.
- Uri Amit, ..., Avinash D., ..., Jonathan L., A New Role for Interleukin-13 Receptor in Myocardial Homeostasis and Heart Failure. *Journal of the American Heart Association*, 2016.
- P Cardo,..., Avinash D.,..., Euan A., A community overlap strategy reveals central genes and networks in heart failure. <https://doi.org/10.1101/038174>, *BioArxiv*.
- Mahashweta Basu, ..., Avinash D., Sridhar Hannehalli. Prediction and Subtyping of Hypertension from pan-tissue transcriptomic and genetic analyses. *Genetics*, 2016.
- Kun W., Avinash D., ..., Sridhar H. "Phenotype-dependent coexpression gene clusters: application to normal and premature ageing." *Computational Biology and Bioinformatics, IEEE/ACM Transactions on* 12, no. 1 (2015): 30-39.
- Nishanth N., ..., Avinash D., ..., Bernard M, Study of cell differentiation by phylogenetic analysis using histone modification data. *BMC bioinformatics*. 2014



Avinash D\*, M Morley, Moravec CS, Tang WHW, Hakonarson H, Margulies KB et al. Bayesian integration of genetics and epigenetics detects causal regulatory SNPs underlying expression variability. *Nature Communications*. 2016 Oct 12;6. 8555.

Avinash D.,..., Sridhar H., Epigenomic model of cardiac enhancers with application to Genome wide association studies. *PSB*, 2013.

Kun W., Avinash D., ... Sridhar H.: Identification of gene clusters with phenotype-dependent expression with application to normal and premature ageing. *ACM BCB*, 2013.

Nishanth N., Avinash D., ..., Bernard Moret. ChIPnorm: A statistical method for identifying interesting regions in histone modification libraries. *PLoS ONE* 2012.

ENCODE Project Consortium. Integrative analysis of the human genome by the ENCODE Project. *Nature*, 2012.

#### **Non-peer reviewed Conferences**

Gaurav P., ..., Avinash D., ..., Zeev R., Co-targeting MAPK signaling and asparagine metabolism in pancreatic cancer, *Gastroenterology*, 2020.

Avinash D., Xiaoman W, ..., X. Shirley L. Identification of drugs that synergize with immunotherapy. *AACR Annual Meeting*, 2020.

Genome-wide prediction of synthetic rescue mediators of resistance to targeted and immunotherapy. *Cancer Research* 2019.

Signatures of T-cell dysfunction and exclusion predict cancer immunotherapy response. *Cancer Immunology Research* 2019.

Harnessing genetic interactions to advance whole-exome precision cancer treatment. *ISMB* 2019.

Genome-wide prediction of synthetic rescue mediators of resistance to targeted and immunotherapy. *AACR Annual Meeting* 2019.

Harnessing genetic interactions to advance whole-exome precision cancer treatment. *AACR Annual Meeting* 2019.

Avinash D., Data-driven approach to detecting novel gene interactions in cancer with applications to drug response prediction and cancer stratification. *Cancer Research* 2017.

Harnessing synthetic lethality to predict clinical outcomes of cancer treatment. *Molecular Cancer Therapeutics* 2017.

Cell migration is a stronger predictor of patient survival in breast cancer than cell proliferation. *Molecular Targets Conference* 2017.

Avinash D., et al. "Genome-wide identification of gene determinant of cancer resistance" *AACR Annual Meeting* (2017).

Avinash D., et al. "Tracing synthetic rescue reprogramming to counteract cancer resistance." *Molecular Cancer Therapeutics* 14.12 Supplement 2 (2015): B56-B56.

Assaf M., Avinash D., Sridhar H., Data-driven approach to detecting novel gene interactions in cancer with applications to drug response prediction and cancer stratification. *Cancer Research*, 2017

- Avinash D., Eytan R., Harnessing synthetic rescues to evaluate and mitigate resistance to cancer therapy. 2017, Cancer Research.
- Y Li, ..., Avinash D., ..., Zeev R., Coordinated regulation of gut microbiota and immune checkpoint activity by the ubiquitin ligase RNF5 controls melanoma growth. *FEBS JOURNAL*, 2017.
- Paula D, ..., Avinash D., ..., Raya A., Co-expression of immune checkpoint mRNAs and miR-15a and miR-15b in bladder cancer—highlighting potential novel targets and approaches for immunotherapy. 2017.
- Avinash D., Sridhar H.. Dirichlet process model for joint haplotype inference and GWAS. *BMC Bioinformatics*. 2012
- Manish P., Avinash D., Mohammed H., Graph Balancing: A special case of scheduling on unrelated machines. *UMD Annals*. 2012
- Avinash Sahu, Sridhar Hannenhalli. Bayesian integration of genetics and epigenetics detects causal regulatory SNPs underlying the cardiac failure. *Gordon Research Conference. Human Nucleotide Polymorphism and Diseases*. 2014 Aug.
- Avinash D. Sahu, Ludovic Chotard. Architecture and hardware implementation of Relative Motion Vector estimation of the image. *IP based Electronic System Conference & Exhibition*. Grenoble 2008.

### Manuscript in preparations

\*Corresponding Author

- Phillip Nicol., ..., Rafael I\*, Aviansh D.\*. Robust cell prioritization method for single-cell transcriptome revealed role of LEF1+ T helper cells in anti-PD1 response (In revision, Nature Biotech, available upon request).
- Murad M., Avinash D.,..., Alexander M., Genome-wide CRISPR screens reveal metabolic and transcriptional regulation of butyrophilin 3A and susceptibility to V $\gamma$ 9V $\delta$ 2 T cell targeting. (In review Nature)
- Nishant N., ..., Avinash D., ..., Cyri B., A landscape of synergistic drug combinations in non-small-cell lung cancer. (In revision Nature Cancer ).  
<https://www.biorxiv.org/content/10.1101/2021.06.03.447011v1>.
- Avinash D.\*, Songpeng Zu, ..., X. Shirley L., Probablistic inference of functional role of immune populations in patient prognosis reveals  $\gamma\delta$  T cells essential for healthy immune system.

### Patents

- Avinash D., Joo Sang L., Eytan R. Computer system and methods for harnessing synthetic rescues and applications thereof. 2016
- Avinash D., Ludovic C. Architecture and hardware implementation of Relative Motion Vector estimation of the image.