
EDUCATION	<p>Brown University, Providence, RI Sc. M., Ph.D., Physics (2007)</p> <p>Sharif University of Technology, Tehran, Iran Sc. B., Physics (2001)</p>
INTERESTS	<ul style="list-style-type: none">• Cancer genomics, Evolutionary dynamics of clonal populations, Molecular epidemiology of infectious diseases, Bioinformatics for precision medicine• In my past life: Observational cosmology, Gravitational lensing
APPOINTMENTS	<p>Assistant Professor (2015 – present) Rutgers University, Rutgers Cancer Institute of New Jersey Rutgers Robert Wood Johnson Medical School, Department of Pathology</p> <p>Associate Research Scientist (2013 – 2015) Columbia University, Departments of Biomedical Informatics & Systems Biology</p> <p>Postdoctoral Research Scientist (2008 – 2012) Columbia University, Center for Computational Biology and Bioinformatics</p> <p>Postdoctoral Research Associate (2007 – 2008) Brown University, Department of Physics</p> <p>Graduate Teaching Assistant and Research Fellow (2001 – 2007) Brown University, Department of Physics</p> <p>Undergraduate Research Fellow (1997 – 1999) Institute for Research in Fundamental Sciences (IPM), School of Physics</p>
PEER-REVIEWED PUBLICATIONS	<ol style="list-style-type: none">1 Severson EA, Riedlinger GM, Connelly CF, Vergilio J, Goldfinger M, Ramkissoon S, Frampton GM, Ross JS, Fratella-Calabrese A, Gay L, Ali S, Miller V, Elvin J, Hadigol M, Hirshfield KM, Rodriguez-Rodriguez L, Ganesan S [✉], Khiabanian H [✉]. Detection of Clonal Hematopoiesis of Indeterminate Potential in Clinical Sequencing of Solid Tumor Specimens. <i>Blood</i>. 2018 April 20. <u>Contribution</u>: Designed the study, interpreted data, and wrote the manuscript2 Khiabanian H ^{†✉}, Hirshfield KM [†], Goldfinger M, Bird S, Stein M, Aisner J, Toppmeyer D, Wong S, Chan N, Dhar K, Gheeya J, Vig H, Hadigol M, Pavlick D, Ansari S, Ali S, Xia B, Rodriguez-Rodriguez L, Ganesan S [✉]. Inference of germline mutational status and evaluation of loss of heterozygosity in high-depth tumor-only sequencing data. <i>JCO Precis Oncol</i>. 2018 Jan 19. <u>Contribution</u>: Designed the study, interpreted data, and wrote the manuscript3 Tzoneva G, Dieck CL, Oshima K, Ambesi-Impiombato A, Sánchez-Martín M, Madubata CH, Khiabanian H, Yu J, Waanders S, Iacobucci I, Sulis ML, Kato M, Koh K, Paganin M, Basso G, Gastier-Foster JM, Loh ML, Kirschner-Schwabe R, Mullighan CG, Rabadan R, Ferrando AA. Clonal evolution mechanisms in <i>NT5C2</i>-mutant relapsed acute lymphoblastic leukemia. <i>Nature</i>. 2018 Jan 25;553(7689):511-514. <u>Contribution</u>: Performed deep sequencing analysis and interpreted data4 Marsilio S, Khiabanian H, Fabbri G, Vergani S, Scuoppo C, Montserrat E, Shpall EJ, Hadigol M, Marin P, Rai KR, Rabadan R, Devereux S, Pasqualucci L, Chiorazzi N. Somatic CLL mutations occur at multiple distinct hematopoietic maturation stages: documentation and cautionary note regarding cell fraction purity. <i>Leukemia</i>. 2018 Apr;32(4):1041-1044. <u>Contribution</u>: Designed computational pipeline, interpreted data, and wrote the manuscript5 Snider EJ, Compres G, Freedberg DE, Giddins MJ, Khiabanian H, Lightdale CJ, Nobel YR, Toussaint NC, Uhlemann AC, Abrams JA. Barrett's Esophagus is associated with a distinct oral microbiome. <i>Clin Transl Gastroenterol</i>. 2018 Feb 20;9(3):135. <u>Contribution</u>: Performed 16S sequencing analysis and interpreted data6 Rabadan R, Bhanot G, Marsilio S, Chiorazzi N, Pasqualucci L, Khiabanian H [✉]. On statistical modeling of sequencing noise in high depth data to assess tumor evolution. <i>J Stat Phys</i>. 2017 Dec 21. <u>Contribution</u>: Designed the study, interpreted data, and wrote the manuscript7 Gorshein E, Wei C, Ambrosy S, Budney S, Vivas J, Shenkerman A, Manago J, McGrath MK, Tyno A,

[†] Equal contribution

[✉] Corresponding author

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- Lin Y, Patel V, Gharibo M, Schaar D, Jenq RR, **Khiabani H**[†], Strair R[†]. *Lactobacillus rhamnosus GG* probiotic enteric regimen does not provide protection against GVHD after allogeneic hematopoietic stem cell transplantation. *Clin Transplant*. 2017 May;31(5).
Contribution: Designed 16S sequencing analyses, interpreted data, and wrote the manuscript
- 8 Morgan KM, Fischer BS, Lee FY, Shah JJ, Bertino JR, Rosenfeld J, Singh A, **Khiabani H**, Pine S. Gamma secretase inhibition by BMS-906024 enhances efficacy of paclitaxel in lung adenocarcinoma. *Mol Cancer Ther*. 2017 Dec;16(12):2759-2769.
Contribution: Interpreted data and wrote the manuscript
- 9 Uhlemann AC, McAdam PR, Sullivan SB, Knox JR, **Khiabani H**, Rabadan R, Davies PR, Fitzgerald JR, Lowy FD. Evolutionary Dynamics of Pandemic Methicillin-Sensitive *S. aureus* ST398 and Its International Spread via Routes of Human Migration. *MBio*. 2017 Jan 17;8(1).
Contribution: Performed molecular evolution analyses
- 10 Abate F, da Silva-Almeida AC, Zairis S, Robles-Valero J, Couronne L, **Khiabani H**, Quinn SA, Kim MY, Laginestra MA, Kim C, Fiore D, Bhagat G, Piris MA, Campo E, Lossos IS, Bernard OA, Inghirami G, Pileri S, Bustelo XR, Rabadan R, Ferrando AA, Palomero T. Activating mutations and translocations in the guanine exchange factor *VAV1* in peripheral T-cell lymphomas. *Proc Natl Acad Sci U S A*. 2017 Jan 24;114(4):764-769.
Contribution: Interpreted sequencing data
- 11 Oshima K[†], **Khiabani H**[†], da Silva-Almeida AC, Tzoneva G, Abate F, Ambesi-Impiombato A, Sanchez-Martin M, Carpenter Z, Penson A, Perez-Garcia A, Eckert C, Nicolas C, Balbin M, Sulis ML, Kato M, Koh K, Paganin M, Basso G, Gastier-Foster JM, Devidas M, Loh ML, Kirschner-Schwabe R, Palomero T, Rabadan R, Ferrando AA. Mutational landscape, clonal evolution patterns and role of RAS mutations in relapsed acute lymphoblastic leukemia. *Proc Natl Acad Sci U S A*. 2016 Oct 4;113(40):11306-11311
Contribution: Designed computational pipeline, interpreted data, and wrote the manuscript
- 12 Spina V[†], **Khiabani H**[†], Messina M, Monti S, Cascione L, Brusca A, Spaccarotella E, Holmes AB, Arcaini L, Lucioni M, Tabbò F, Zairis S, Diop F, Cerri M, Chiaretti S, Marasca R, Ponzoni M, Deaglio S, Ramponi A, Tiacci E, Pasqualucci L, Paulli M, Falini B, Inghirami G, Bertoni F, Foà R, Rabadan R, Gaidano G, Rossi D. The Genetics of Nodal Marginal Zone Lymphoma. *Blood*. 2016 Sep 8;128(10):1362-73.
Contribution: Performed sequence data analysis, interpreted data, and wrote the manuscript
- 13 Rasi S[†], **Khiabani H**[†], Ciardullo C, Terzi-di-Bergamo L, Monti S, Spina V, Brusca A, Cerri M, Deambrogi C, Martuscelli L, Biasi A, Spaccarotella E, De Paoli L, Gattei V, Foà R, Rabadan R, Gaidano G, Rossi D. Clinical impact of small subclones harboring *NOTCH1*, *SF3B1*, or *BIRC3* mutations in chronic lymphocytic leukemia. *Haematologica*. 2016 Apr;101(4):e135-8.
Contribution: Designed computational pipeline, interpreted data, and wrote the manuscript
- 14 Paganin M, Buldini B, Germano G, Segnanfreddo E, Meglio Ad, Magrin E, Grillo F, Pigazzi M, Rizzari C, Cazzaniga G, **Khiabani H**, Palomero T, Rabadan R, Ferrando AA, Basso G. A Case of T-cell Acute Lymphoblastic Leukemia Relapsed As Myeloid Acute Leukemia. *Pediatr Blood Cancer*. 2016 Sep;63(9):1660-3.
Contribution: Interpreted sequencing data
- 15 Almeida da Silva A[†], Abate F[†], **Khiabani H**, Martinez-Escala E, Guitart J, Tensen CP, Vermeer MH, Rabadan R, Ferrando A, Palomero T. The mutational landscape of cutaneous T cell lymphoma and Sézary syndrome. *Nature Genet*. 2015 Dec;47(12):1465-70.
Contribution: Interpreted data and wrote the manuscript
- 16 Emmett K, Lee A, **Khiabani H**[✉], Rabadan R[✉]. High-resolution genomic surveillance of 2014 ebolavirus using shared subclonal variants. *PLoS Curr*. 2015 Feb 9;7.
Contribution: Designed the study, interpreted data, and wrote the manuscript
- 17 Lee A, Kulcsar K, Elliott O, **Khiabani H**, Nagle ER, Jones ME, Amman BR, Sanchez-Lockhart M, Towner JS, Palacios G, Rabadan R. Transcriptome Reconstruction and Annotation of the Egyptian Roussette Bat. *BMC Genomics*. 2015 Dec 7;16:1033.
Contribution: Interpreted data and wrote the manuscript
- 18 Rossi D[†], **Khiabani H**[†], Spina V, Ciardullo C, Brusca A, Famà R, Rasi S, Monti S, Deambrogi C, De Paoli L, Wang J, Gattei V, Guarini A, Foà R, Rabadan R, Gaidano G. Clinical impact of small *TP53* mutated subclones in chronic lymphocytic leukemia. *Blood*. 2014 Apr 3;123(14):2139.
Contribution: Designed the study, interpreted data, and wrote the manuscript (Plenary paper)
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- 19 Palomero T[†], Couronné L[†], **Khiabani H**[†], Kim MY, Ambesi-Impiombato A, Perez-Garcia A, Carpenter Z, Abate F, Allegretta M, Haydu JE, Jiang X, Lossos IS, Nicolas C, Balbin M, Bastard C, Bhagat G, Piris MA, Campo E, Bernard OA, Rabadan R, Ferrando AA. Recurrent mutations in epigenetic regulators, *RHOA* and *FYN* kinase in peripheral T cell lymphomas. *Nature Genet.* 2014 Feb;46(2):166-70.
Contribution: Performed sequencing analyses, interpreted data, and wrote the manuscript
- 20 Wang J[†], **Khiabani H**[†], Rossi D[†], Fabbri G, Gattei V, Forconi F, Laurenti L, Marasca R, Del Poeta G, Foà R, Pasqualucci L, Gaidano G, Rabadan R. Tumor Evolutionary Directed Graphs and the History of Chronic Lymphocytic Leukemia. *eLife.* 2014 Dec 11;3.
Contribution: Developed statistical tools, interpreted data, and wrote the manuscript
- 21 **Khiabani H**[✉], Carpenter Z, Kugelman J, Chan J, Trifonov V, Nagle E, Warren T, Iversen P, Bavari S, Palacios G, Rabadan R. Viral diversity and clonal evolution from unphased genomic data. *BMC Genomics.* 2014;15 Suppl 6:S17.
Contribution: Designed the study, developed mathematical tools, and wrote the manuscript
- 22 Lee A[†], **Khiabani H**[†], Kugelman J, Elliott O, Nagle E, Yu GY, Warren T, Palacios G, Rabadan R. Transcriptome Reconstruction and Annotation of Cynomolgus and African Green Monkey. *BMC Genomics.* 2014 Oct 3;15:846.
Contribution: Designed computational pipeline, interpreted data, and wrote the manuscript
- 23 Zairis S, **Khiabani H**, Blumberg A, Rabadan R. Moduli spaces of phylogenetic trees describing tumor evolutionary patterns. *Lecture Notes in Computer Science.* 2014; 8609:528-539.
Contribution: Interpreted data and wrote the manuscript
- 24 Pasqualucci L, **Khiabani H**, Fangazio M, Vasishtha M, Messina M, Holmes AB, Ouillette P, Trifonov V, Rossi D, Tabbò F, Ponzoni M, Chadburn A, Murty VV, Bhagat G, Gaidano G, Inghirami G, Malek SN, Rabadan R, Dalla-Favera R. Genetics of follicular lymphoma transformation. *Cell Rep.* 2014 Jan 16;6(1):130-40.
Contribution: Developed bioinformatics tools for sequencing analysis and wrote the manuscript
- 25 Melamed R, **Khiabani H**, Rabadan R. Data-driven discovery of seasonally linked diseases from an Electronic Health Records system. *BMC Bioinformatics.* 2014;15 Suppl 6:S3.
Contribution: Developed statistical tools and interpreted data
- 26 Messina M, Del Giudice I, **Khiabani H**, Rossi D, Chiaretti S, Rasi S, Spina V, Holmes AB, Marinelli M, Fabbri G, Picocchi A, Mauro FR, Guarini A, Gaidano G, Dalla-Favera R, Pasqualucci L, Rabadan R, Foà R. Genetic lesions associated with chronic lymphocytic leukemia chemo-refractoriness. *Blood.* 2014 Apr 10;123(15):2378-88.
Contribution: Performed sequencing analysis, developed statistical tools, and interpreted data
- 27 Kode A, Manavalan JS, Mosialou I, Bhagat G, Rathinam CV, Luo N, **Khiabani H**, Lee A, Murty VV, Friedman R, Brum A, Park D, Galili N, Mukherjee S, Teruya-Feldstein J, Raza A, Rabadan R, Berman E, Kousteni S. Leukemogenesis induced by an activating β -catenin in osteoblasts. *Nature.* 2014 Feb 13;506(7487):240-4.
Contribution: Performed mouse sequencing analysis and interpreted data
- 28 Fabbri G[†], **Khiabani H**[†], Holmes AB, Wang J, Messina M, Mullighan CG, Pasqualucci L, Rabadan R, Dalla-Favera R. Genetic lesions associated with chronic lymphocytic leukemia transformation to Richter syndrome. *J Exp Med.* 2013 Oct 21;210(11):2273-88.
Contribution: Designed computational pipeline, interpreted data, and wrote the manuscript
- 29 Tzoneva G[†], Perez Garcia A[†], Carpenter Z[†], **Khiabani H**, Tosello V, Allegretta M, Paietta E, Racevskis J, Rowe JM, Tallman MS, Paganin M, Basso G, Hof J, Kirschner-Schwabe R, Palomero T, Rabadan R, Ferrando A. Activating mutations in the *NT5C2* gene drive chemotherapy resistance in relapsed ALL. *Nature Med.* 2013 Mar;19(3):368-71.
Contribution: Performed sequencing analysis and interpreted data
- 30 Blair DR, Lyttle CS, Mortensen JM, Bearden CF, Jensen AB, **Khiabani H**, Melamed R, Rabadan R, Bernstam EV, Brunak S, Jensen LJ, Nicolae D, Shah NH, Grossman RL, Cox NJ, White KP, Rzhetsky A. A nondegenerate code of deleterious variants in mendelian Loci contributes to complex disease risk. *Cell.* 2013 Sep 26;155(1):70-80.
Contribution: Contributed data to the study
- 31 Rossi D, Rasi S, Spina V, Brusca A, Monti S, Ciardullo C, Deambrogi C, **Khiabani H**, Serra R, Bertoni F, Forconi F, Laurenti L, Marasca R, Dal-Bo M, Rossi FM, Bulian P, Nomdedeu J, Del Poeta G, Gattei V, Pasqualucci L, Rabadan R, Foà R, Dalla-Favera R, Gaidano G. Integrated Mutational and
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- Cytogenetic Analysis Identifies New Prognostics Subgroups in CLL. *Blood*. 2013 Feb 21;121(8):1403.
Contribution: Interpreted data for the study
- 32 Dapito DH, Mencin A, Gwak GY, Pradere JP, Jang MK, Mederacke I, Caviglia JM, **Khiabani H**, Adeyemi A, Bataller R, Lefkowitz JH, Bower M, Friedman R, Sartor RB, Rabadan R, Schwabe RF. Promotion of hepatocellular carcinoma by the intestinal microbiota and TLR4. *Cancer Cell*. 2012 Apr 17;21(4):504
Contribution: Performed 16S sequencing analysis and interpreted data
- 33 Holmes A, Hawson A, Liu F, Friedman C, **Khiabani H**[✉], Rabadan R[✉]. Discovering Disease Associations Integrating Electronic Clinical Data and Medical Literature. *PLoS One*. 2011;6(6):e212.
Contribution: Designed the study, interpreted data, and wrote the manuscript
- 34 Rossi D, Brusca A, Spina V, Rasi S, **Khiabani H**, Messina M, Fangazio M, Vaisitti T, Monti S, Chiaretti S, Guarini A, Del Giudice I, Cerri M, Cresta S, Deambrogi C, Gargiulo E, Gattei V, Forconi F, Bertoni F, Deaglio S, Rabadan R, Pasqualucci L, Foà R, Dalla-Favera R, Gaidano G. Mutations of the *SF3B1* splicing factor in chronic lymphocytic leukemia: association with progression and fludarabine-refractoriness. *Blood*. 2011 Dec 22;118(26):6904-8.
Contribution: Performed sequencing analysis
- 35 Fabbri G, Rasi S, Rossi D, Trifonov V, **Khiabani H**, Ma J, Grunn A, Fangazio M, Capello D, Monti S, Cresta S, Gargiulo E, Forconi F, Guarini A, Arcaini L, Paulli M, Laurenti L, Larocca LM, Marasca R, Gattei V, Oscier D, Bertoni F, Mullighan CG, Foà R, Pasqualucci L, Rabadan R, Dalla-Favera R, Gaidano G. Analysis of the Chronic Lymphocytic Leukemia Coding Genome: Role of *NOTCH1* Mutational Activation. *J Exp Med*. 2011 Jul 4;208(7):1389-401.
Contribution: Developed bioinformatics tools and performed deep-sequencing analysis
- 36 Van Vlierberghe P[†], Palomero T[†], **Khiabani H**, Van der Meulen J, Castillo M, Van Roy N, De Moerloose B, Philippé J, González-García S, Toribio ML, Taghon T, Zuurbier L, Cauwelier B, Harrison CJ, Schwab C, Pisecker M, Strehl S, Langerak AW, Gecz J, Sonneveld E, Pieters R, Paietta E, Rowe JM, Wiernik PH, Benoit Y, Soulier J, Poppe B, Yao X, Cordon-Cardo C, Meijerink J, Rabadan R, Speleman F, Ferrando A. *PHF6* mutations in T-cell acute lymphoblastic leukemia. *Nature Genet*. 2010 Apr;42(4):338-42.
Contribution: Developed bioinformatics tools and performed sequencing analysis
- 37 **Khiabani H**[✉], Holmes AB, Kelly BJ, Gururaj M, Hripcsak G, Rabadan R. Signs of the 2009 Influenza Pandemic in the New York-Presbyterian Hospital Electronic Health Records. *PLoS One*. 2010 Sep 9;5(9).
Contribution: Designed the study, interpreted data, and wrote the manuscript
- 38 **Khiabani H**[✉], Van Vlierberghe P, Palomero T, Ferrando AA, Rabadan R. ParMap, an algorithm for the identification of small genomic insertions and deletions in nextgen sequencing data. *BMC Res Notes*. 2010 May 27;3:147.
Contribution: Designed computational tools, interpreted data, and wrote the manuscript
- 39 **Khiabani H**[✉], Trifonov V., Rabadan R. Reassortment Patterns in Swine Influenza Viruses. *PLoS One*. 2009 Oct 7;4(10):e7366.
Contribution: Designed the study, interpreted data, and wrote the manuscript
- 40 **Khiabani H**[✉], Farrell GM, St George K, Rabadan R. Differences in Patient Age Distribution between Influenza A Subtypes. *PLoS One*. 2009 Aug 31;4(8):e6832.
Contribution: Designed the study, interpreted data, and wrote the manuscript
- 41 Trifonov V, **Khiabani H**, Rabadan R. Geographic Dependence, Surveillance and the Origins of the 2009 Influenza A (H1N1) Virus. *New Engl J Med*. 2009 Jul 9;361(2):115-9.
Contribution: Performed sequencing analysis, interpreted data, and wrote the manuscript
- 42 Trifonov V, **Khiabani H**, Greenbaum B, Rabadan R. The origin of the recent swine influenza A (H1N1) virus infecting humans. *Euro Surveill*. 2009 Apr 30;14(17).
Contribution: Performed sequencing analysis, interpreted data, and wrote the manuscript
- 43 Kubo J, **Khiabani H**, Dell'Antonio I, Wittman D, Tyson J. Dark Matter Halos in the Deep Lens Survey. *Astrophys J*. 2009; 702(2):980.
Contribution: Designed the study, interpreted data, and wrote the manuscript
- 44 **Khiabani H**, Dell'Antonio I. A Multi-Resolution Weak Lensing Reconstruction Method. *Astrophys J*. 2008; 684(2):794.
Contribution: Designed the study, developed mathematical tools, and wrote the manuscript
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	<p>45 Kubo J, Stebbins A, Annis J, Dell'Antonio I, Lin H, Khiabani H, Frieman J. The Mass of Coma Cluster from Weak Lensing in SDSS. <i>Astrophys J</i>. 2007; 671(2):1466. <u>Contribution</u>: Contributed statistical tools and interpreted data</p>
REVIEWS, BOOK CHAPTERS	<p>46 Paratala B, Dolfi SC, Khiabani H, Rodriguez-Rodriguez L, Ganesan S, Hirshfield KM. Emerging role of genomic rearrangements in breast cancer: applying knowledge from other cancers. <i>Biomark Cancer</i>. 2016 Feb 11;8(Suppl 1):1-14. <u>Contribution</u>: Interpreted data for the review</p> <p>47 Greenbaum B, Trifonov V, Khiabani H, Levine A, Rabadan R. The Emergence of 2009 H1N1 Pandemic Influenza. In: G. Del Giudice and R. Rappuoli (eds.). <i>Influenza Vaccines for the Future</i>. 2nd edition 2010 <u>Contribution</u>: Interpreted data and wrote the book chapter</p>
THESES, PRE-PRINTS	<p>1 Singh A, Bhanot, G, Khiabani H [✉]. TuBA: Tunable Biclustering Algorithm reveals clinically relevant tumor transcriptional profiles in breast cancer. <i>bioRxiv</i> 2018 <u>Contribution</u>: Designed the study, interpreted data, and wrote the manuscript</p> <p>2 Hadigol M, Khiabani H [✉]. MERIT: a Mutation Error Rate Identification Toolkit for Ultra-deep Sequencing Applications. <i>bioRxiv</i> 2017 <u>Contribution</u>: Designed the study, interpreted data, and wrote the manuscript</p> <p>3 Zairis S, Khiabani H, Blumberg A, Rabadan R. Genomic data analysis in tree spaces. <i>arXiv</i> 2016 <u>Contribution</u>: Performed genomic analysis, interpreted data, and wrote the manuscript</p> <p>4 Hernandez C, Chan J, Khiabani H, Rabadan R. Understanding the Origins of a Pandemic Virus. <i>arXiv</i> 2011 <u>Contribution</u>: Interpreted data and wrote the manuscript</p> <p>5 Khiabani H. A Maximum-Likelihood Multi-Resolution Weak Lensing Mass Reconstruction Method. Doctoral Dissertation. Brown University 2008 <u>Contribution</u>: Designed the study, interpreted data, and wrote the thesis</p>
PROFESSIONAL ACTIVITIES	<ul style="list-style-type: none"> Assistant Professor of Pathology in Medical Informatics, tenure-track, Rutgers Robert Wood Johnson Medical School (2015 – present) Resident Member at Rutgers Cancer Institute of New Jersey, Center for Systems and Computational Biology, the Genome Instability and Cancer Genetics Program (2015 – present) Member of the graduate faculty in the Department of Physics and Astronomy (2016 – present), the Institute for Quantitative Biomedicine (2016 – present), Microbiology and Molecular Genetics, Molecular Biosciences Program (2017 – present) at Rutgers University Scientific Coordinator in Education and Outreach in the Center for Topology of Cancer Evolution and Heterogeneity, Columbia University (2015 – 2017) Member of the faculty in the Department of Biomedical Informatics at Columbia University College of Physicians and Surgeons (2013 – 2015) Academic editor: PeerJ (2017 – present) Proposal review panelist: National Science Foundation (2017) Participant: NIH Early Career Reviewer (ECR) program (2017) Professional membership: American Society of Hematology, International Society for Computational Biology, American Association for Cancer Research <i>Ad Hoc</i> Reviewer: JCO Precision Oncology, Nature Communications, PLoS Pathogens, PLoS Computational Biology, Scientific Reports, PLoS One, Bioinformatics, Journal of Virology, Virology, BMC Evolutionary Biology, BMC Bioinformatics, BMC Genomics, AMIA, ISMB etc.
TEACHING EXPERIENCE	<ul style="list-style-type: none"> Faculty Mentor. DIMACS Research Experience for Undergraduates Program, Rutgers University (Summer 2017, 2018) Lecturer (<i>Introduction to Systems and Computational Biology</i>). Introduction to Molecular Medicine. Rutgers University (Fall 2017) Organizer and Lecturer. Workshop on Quantitative Methods in Cancer Genomics. Center for Systems and Computational Biology, Rutgers Cancer Institute of New Jersey (September 2016) Faculty Moderator. Molecular Medicine Seminar, Rutgers Cancer Institute (Fall 2015 – 2016)

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- Lecturer (*Intro. to Molecular Epidemiology: Dynamics of Clonal Evolution*). Introduction to Biomedical Informatics, Columbia University (Fall 2014)
 - Lecturer (*Clonal Expansions & Introduction to DNA Sequencing Methods*). Quantitative and Computational Aspects of Infectious Diseases, Columbia University (Spring 2011 – 2013)
 - Lecturer (*Introduction to Computational Biology and Genomics*). Advanced Seminar on Modeling for Public Health and Clinical Research, Columbia University (Spring 2013)
 - Instructor (*Introduction to Bioinformatics Tools*). Quantitative Approaches to Biological Problems, International Centre for Theoretical Physics, Trieste, Italy (October 2011)
 - Teaching Assistant. Experiments in Modern Physics, Brown University (Spring 2002)
 - Teaching Assistant. Introduction to Astronomy, Brown University (Fall 2001)
 - Course grader and Tutor. Introductory undergraduate courses in Physics, Astrophysics, and Cosmology, Brown University, 2002 – 2007.
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ADVISING

- Postdoctoral fellow: Mohammad Hadigol (NJCCR Fellow, 2016 – present)
 - Doctoral students: Amartya Singh (Physics, 2016 – present), Jui Wan Loh (Molecular Biosciences, 2017 – present)
 - Undergraduate students: Anthony Calabrese (Biochemistry, 2016 – 2017), Simon Bird (DIMACS fellow, 2017), Srinivas Rajagopalan (Biomathematics, 2018), Caitlin Guccione (DIMACS fellow, 2018)
 - Doctoral thesis committee membership: Manasi Pethe (Chemistry, Rutgers), Albert Lee (Bioinformatics, Columbia), Anshuman Panda (Physics, Rutgers)
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PRESENTATIONS

Invited Talks and Oral Presentations

- Dynamics of Clonal Evolution in Leukemia Development and Progression
Cancer Genomics Retreat, Princeton University, Princeton, NJ, March 2017
 - Genomic data analysis and dimensionality reduction in tree spaces
Center for Quantitative Biology, Rutgers University, Piscataway, NJ, January 2017
 - Clonal Evolution and Relapse in Leukemia Institute for research in fundamental Sciences (IPM), Tehran, Iran, December 2016
 - Statistical Inference and dimensionality reduction in evolutionary tree spaces
Schloss Dagstuhl Seminar, Leibniz Center for Informatics, Wadern, Germany, June 2016
 - Clonal Dynamics in Cancer Evolution
The Feinstein Institute for Medical Research, Manhasset, NY, April 2016
 - High-resolution surveillance of viral clonal evolution
Institute for Quantitative Biomedicine, Rutgers University, Piscataway, NJ, February 2016
 - Intra-host evolution and high-resolution genomic surveillance of filoviruses
Columbia University Systems Biology Retreat, Tarrytown, NY, June 2015
 - Dynamics of Clonal Evolution in Leukemia
Rutgers Cancer Institute of New Jersey, New Brunswick, NJ, January 2015
 - Dynamics of Clonal Evolution in Leukemia
Department of Pathology, Weill Cornell Medical College, New York, NY, December 2014
 - Moduli Spaces of Phylogenetic Trees Describing Tumor Evolutionary Patterns
The 5th Beyond the Genome Conference, Harvard Medical School, Boston, MA, October 2014
 - Viral Diversity and Clonal Evolution from Unphased Genomic Data
The 12th Recomb-CG Meeting, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, October 2014
 - Intra-host Evolution and Subclonal Diversity in Acute Infections using Unphased Genomic Data
AMIA Joint Summits on Translational Science, San Francisco, CA, April 2014
 - Data Mining Electronic Health Records at New York Presbyterian Hospital
The Conte Center 1st Annual Meeting, The University of Chicago, Chicago, IL, March 2012
 - Tracking the Evolution of Influenza Viruses
The 2nd Systems Biology and New Sequencing Meeting, ICTP, Trieste, Italy, November 2011
 - Emergence of a Pandemic Virus
University of Bologna, Bologna, Italy, October 2011
 - Data Mining Electronic Health Records
Columbia University Center for Infection and Immunity, New York, NY, June 2011
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- Fancy Counting in Large Biological Datasets
Department of Physics, Sharif University of Technology, Tehran, Iran, April 2011
 - Reassortment Patterns in Influenza Viruses
The Simons Center for Systems Biology, IAS, Princeton, NJ, March 2011
 - Influenza Virus and its Evolution
Sharif University of Technology, Tehran, Iran, April 2010
 - Statistics of Dark Matter Halos via Maximum-Likelihood Weak Lensing Mass Reconstruction
The BioMaPS Institute, Rutgers University, Piscataway, NJ, May 2008

Selected Peer-reviewed Abstracts

- Hirshfield KM, Goldfinger M, Bird S, Hadigol M, Ansari S, Rodriguez-Rodriguez L, Ganesan S, **Khiabani H**[✉]. Inference of germline mutational status and evaluation of loss of heterozygosity in high-depth tumor-only sequencing data. RECOMB-CCB, Paris, France, April 2018
- Severson EA, ... Ganesan S[†], **Khiabani H**^{†✉}. Detection of Clonal Hematopoiesis of Indeterminate Potential in Solid Tumors: Implications for Interpretation of Molecular Testing. AACR Molecular Targets and Cancer Therapeutics Conference, Philadelphia, PA, Oct. 2017
- Oshima K[†], **Khiabani H**[†], et al. Mutational landscape, clonal evolution patterns and role of RAS mutations in relapsed ALL. 58th ASH Annual Meeting, San Diego, CA, Dec. 2016
- Zairis S, **Khiabani H**[✉], Blumberg A, Rabadan R. Machine learning and statistical inference in evolutionary moduli spaces. Keystone Conference on the Cancer Genome, Banff, Alberta, Feb. 2016
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