Postdoctoral Research Positions in Computational Cancer Biology and Statistical Genetics

Specific areas: Computational Cancer Biology, Genetic Epidemiology, Statistical Genetics, Molecular Genetics, Human Genetics, Cancer Genetics, Genomic Medicine, Population Sciences

Postdoctoral positions are available in the lab of Dr. Paul Scheet. Major research activities include the development and application of algorithms for the analysis of cancer genomic and human genetic data. We are particularly interested in experiments using DNA technologies, such as next-generation sequencing and SNP microarrays, to characterize tumor and germline genomic variation and relate discoveries to risk, prognosis, and outcomes of disease.

The ideal applicant will possess innate curiosity, fortitude, an ability to exude selflessness, strong computational skills and a willingness to learn from others. Opportunities abound to bring and pursue one's own agenda or plug into those around them -- and anywhere in between.

Statistical genomics and computational cancer biology. Our lab has recently developed a computational technology to interrogate subtle mixtures of inherited and aberrant genomes within a population of cells from a tissue or tissues of a single patient. Our work provides a novel window into the landscape of acquired genomic variation that may exist in a small portion of cells from various tissues in either healthy or diseased tissues. We are currently interrogating large existing and emerging public data sets, such as from the TCGA, as well as data generated in our own wet lab and funded collaborations. We consistently work with faculty pursuing translational science, such as physician-scientists, to conduct analyses of cancer genomes to identify potentially targetable mutations. Examples include studies of premalignant lesions (lung, skin, colon) and field cancerization (normal tissue adjacent to tumor). Such studies often present problems in integrating data of disparate types.

Genetic epidemiology, statistical genetics, human & cancer genetics. We have been active in developing methods and software for analysis of genome-wide association (GWA) data, including models for haplotype variation and genotype imputation. We co-lead the analysis team for a family-based GWA study of behavioral phenotypes from the Netherlands Twin Register and collaborate on studies of pharmacogenomics of treatment for childhood acute lymphoblastic leukemia. Currently we are generating a large set of sequenced germline exomes of pancreatic cancer patients for a case-control study to discover risk alleles of intermediate effects. Other projects include translating knowledge gained in genomic sciences to inform modifiable behaviors, integrating epidemiological and genomic data for enhanced early detection or risk assessment and studying the genomes of cancer patients undergoing immunotherapies to find predictors of adverse responses to therapy.

The lab is one where a trainee may develop a research program in translational and computational genomics, through access to local, national and international collaborators. We have multiple NIH- or CPRIT-funded projects and collaborations at various institutions, including Texas Children's Hospital, St. Jude Children's Research Hospital, Stanford, the VU (Amsterdam), and Moffitt Cancer Center. Lab

members have academic and real-world experience in bioinformatics, genome sequencing, computer science, and statistics.

The lab serves as a fun and supportive home with opportunities to develop skills that complement one's main research activities through the diversity of our researchers. Among current lab members and alumni, we have three recipients of the Outstanding Predoctoral Student in Cancer Prevention, multiple platform talks at ASHG and CSHL, Regents Outstanding Teaching Award, Thomas Matney award in human genetics, George Stancel Fellowship, and the Goldstein Fellowship.

MD Anderson consistently tops U.S. News & World Report's list for cancer care ("America's Best Hospitals") and is located in the Texas Medical Center (TMC), the world's largest. The proximity of the TMC to Rice University and the Museum District, light rail connections to world-class performing arts and professional sporting venues, a short drive from Galveston and the Texas coast, and a diverse population of Houston are a few features of this uniquely cosmopolitan and affordable city.

To apply, send a brief letter personalizing one's interest in the position, with information about research experience and interests, a CV, and the names and contact information for references to: pascheet@mdanderson.org.

Paul Scheet, Ph.D.
Professor and Chair, Dept. of Epidemiology
Joint: Genomic Medicine and Translational Molecular Pathology
Program Leader: Risk, Detection & Outcomes | Cancer Center Support Grant
University of Texas M. D. Anderson Cancer Center

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Borras (2016). Genomic landscape of colorectal mucosa and adenomas. *Can Prev Res*.
Golemis (2018). Molecular mechanisms of the preventable causes of cancer in the United States. *Genes Dev.*
Jakubek (2016). Genomic Landscape Established by Allelic Imbalance in the Cancerization Field of a Normal Appearing Airway. *Can Res.*
Jakubek (2018). Directional allelic imbalance profiling and visualization from multi-sample data with RECUR. *Bioinformatics..*
Liu 201(6). A meta-analytic framework for detection of genetic interactions. *Genet Epidem.*
Liu (2018). Assessing inter-component heterogeneity of biphasic uterine carcinosarcomas. *Gynecol Oncol.*
San Lucas (2014). Cancer in silico drug discovery: a systems biology tool for identifying candidate drugs to target specific molecular tumor subtypes. *Mol Cancer Ther.*
San Lucas (2016). Rapid and powerful detection of subtle allelic imbalance from exome sequencing data with hapLOHseq. *Bioinformatics.*
Sivakumar (2017). Genomic Landscape of Atypical Adenomatous Hyperplasia Reveals Divergent Modes to Lung Adenocarcinoma. *Cancer Res.*
Vattathil & Scheet (2016). Extensive Hidden Genomic Mosaicism Revealed in Normal Tissue. *Am J Hum Genet.*
Vattathil & Scheet (2013). Haplotype-based profiling of subtle allelic imbalance with SNP arrays. *Genome Res.*
Zheng (2011). A comparison of approaches to account for uncertainty in analysis of imputed genotypes. *Genet Epidem.*