

Postdoctoral positions in Computational Genomics at UT Southwestern Medical Center

The laboratory of [Daehwan Kim](http://profiles.utsouthwestern.edu/profile/175443/daehwan-kim.html) (<http://profiles.utsouthwestern.edu/profile/175443/daehwan-kim.html>) in the Bioinformatics Department of UT Southwestern Medical Center is a highly interactive team conducting cutting-edge research in computational biology. We are developing computational and statistical methods for analyzing sequencing data from a variety of next generation sequencing experiments to further our understanding of the causes of diseases. Bioinformatics software developed in the lab includes widely used programs such as TopHat2, HISAT, TopHat-Fusion, and Centrifuge. The lab recently developed a novel indexing scheme using a graph approach that captures a wide representation of genetic variants and has low memory requirements. The lab has built a new alignment system, HISAT2, which enables fast search through the index. HISAT2 is the first and only practical method available for aligning sequencing reads to a graph at the human genome scale while only requiring the small amount of memory typically available on a conventional desktop. Building off of HISAT2, we plan to develop a practical software solution that can accurately analyze an individual's genome, transcriptome, and epigenome within a few hours on a desktop computer.

In the pursuit of this research, two postdoctoral positions are available in [the Kim lab](http://kim-lab.org) (<http://kim-lab.org>). Applications are invited for a 2 to 3-year computational postdoctoral research position. The researchers will develop novel methods for analyzing large-scale DNA-seq, RNA-seq, and other human genomics data. Potential projects include developing state-of-the-art methods for discovering and cataloguing germline and somatic mutations related to cancer, and for analyzing and assembling human genes and genomes.

Ideal applicants will have:

- A Ph.D. degree in Computer Science, Computational Biology, Biostatistics, Genetics or a related field with a solid computational background.

- Strong programming and analytical skills, including experience with next-generation sequencing data and strong theoretical background in method development.
- At least two first author papers published and demonstrated written communication skills in English.

Please apply by email to Dr. Kim [Daehwan.Kim@UTSouthwestern.edu] and include your CV, statement of research accomplishments and future goals, and arrange to have two or three letters of recommendation sent to the same email address.

The Kim lab is located on the 4th floor of the E-building in the Bioinformatics Department on UT Southwestern's South Campus. We will also work closely with other research groups within Biology, Immunology, and Pathology. Kim lab members have access to considerable computational resources, including the >6,800-core cluster with >8 Petabyte of storage available through UTSW's high-performance infrastructure (BioHPC - <https://portal.biohpc.swmed.edu>). Future lab team members will have the opportunity to work on a broad range of computational and experimental aspects of computational biology on a highly interdisciplinary team, and participate in all aspects of method development, software implementation, data analysis, and experimental validation in collaboration with biologists.

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UT Southwestern Medical Center is an Affirmative Action/Equal Opportunity Employer. Women, minorities, veterans and individuals with disabilities are encouraged to apply.