Postdoctoral Position in Statistical Genetics

Center for Statistical Genetics
Baylor College of Medicine
Houston, Texas, USA

A postdoctoral position in Statistical Genetics is available at the Center for Statistical Genetics, Department of Molecular and Human Genetics, Baylor College of Medicine.

The postdoctoral fellow will develop novel statistical genetics methods in particular those used to perform association analysis of next-generation sequence and imputed data generated for population- and family-based studies. He/she will evaluate the type I error and power of these methods as well as apply them to large datasets of exome, whole-genome sequence and imputed data. The postdoctoral fellow will also write and publish manuscripts and give presentations at international meetings.

The postdoctoral fellow should have a Ph.D. or related degree in bioinformatics, statistics, physics, epidemiology, computer science or other computational field. Previous experience analyzing next-generation sequence or genotype array data is highly desirable. Must have excellent working knowledge in one or more programming languages e.g. R, Python or C.

Please email your curriculum vitae, research statement and the names and contact information for four references to Suzanne Leal statgenpositions@gmail.com with the header Statistical Genetics Postdoc.

Baylor College of Medicine is located in the Texas Medical Center (TMC) in Houston, Texas. The TMC is the largest medical complex in the world and is at the forefront of advancing life sciences. World-renowned TMC nurtures cross-institutional collaborations, creativity and innovation.

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Postdoctoral Position in Mendelian Genomics

Center for Statistical Genetics
Department of Molecular and Human Genetics
Baylor College of Medicine
Houston, Texas, USA

A postdoctoral position in Mendelian Genomics is available at the Center for Statistical Genetics, Department of Molecular and Human Genetics, Baylor College of Medicine.
The postdoctoral fellow will analyze next-generation sequence data (exome and whole-genome) generated on samples from individuals with a variety of Mendelian traits including nonsyndromic hearing impairment, eye disease, intellectual disabilities, skeletal disorders, etc. He/she will use filtering techniques, bioinformatics evaluation, and molecular modeling to identify putatively pathogenic variants. Additionally for some of the families, linkage analysis will be performed in order to map the causal variant to a specific genomic region and aid in gene identification. In addition to analyzing in-house Mendelian data, the postdoctoral fellow will analyze data generated by the Centers for Mendelian Genomics. The postdoctoral fellow will also write and publish manuscripts and give presentations at international meetings.

The postdoctoral fellow should have an M.D. or Ph.D. (or related degree) in bioinformatics, genetics, molecular biology, epidemiology, computer science or related field. Previous experience in analyzing genetic data e.g. next-generation sequence data and programming/writing scripts e.g. Python is highly desirable.

Please email your curriculum vitae, research statement and the names and contact information for four references to Suzanne Leal statgenpositions@gmail.com with the header Mendelian Genomics Postdoc.

Postdoctoral Position in Genetics of Hearing Impairment

Baylor College of Medicine

Houston, Texas, USA

A postdoctoral position in the Genetics of Hearing Impairment is available at the Center for Statistical Genetics, Department of Molecular and Human Genetics, Baylor College of Medicine.

The postdoctoral fellow will analyze next-generation sequence data (exome and whole-genome) generated on samples from individuals with nonsyndromic hearing impairment (NSHI). The postdoctoral fellow will be working on a study of over 1,000 families with NSHI that have been ascertained from Pakistan, Iran, Hungary (Roma), Switzerland, Germany, Poland, Jordan, Turkey and the USA. This study has led to the publication of a large number of NSHI genes including S1PR2, KARS and ADCY1. The postdoctoral fellow will use filtering techniques, bioinformatics evaluation, and molecular modeling to identify pathogenic variants. Additionally for some of the families linkage analysis will be performed in order to map the causal variant to a specific genomic region and aid in gene identification. The postdoctoral fellow will also oversee the work of laboratory technicians in order to follow up putatively pathogenic variants, e.g. designing primers and performing PCR for Sanger sequencing and measuring and aliquoting DNA samples. The postdoctoral fellow will also write and publish manuscripts and give presentations at international meetings.
The postdoctoral fellow should have an M.D. or Ph.D. (or related degree) in bioinformatics, genetics, molecular biology, epidemiology, or other related field. A background in genetic studies of hearing impairment and experience in designing primers and performing PCR, analyzing genetic data, e.g. next-generation sequence data and programming/writing scripts e.g. python is highly desirable.

Please email your curriculum vitae, research statement and the names and contact information for four references to Suzanne Leal statgenpositions@gmail.com with the header Postdoc in Genetics of Hearing Impairment.

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Assistant Professor in Mendelian Genomics of Hearing Impairment

Baylor College of Medicine
Houston, Texas, USA

An assistant professor (non-tenure track) in Mendelian Genomics of Hearing Impairment is available at the Center for Statistical Genetics, Department of Molecular and Human Genetics, Baylor College of Medicine.

The assistant professor will be responsible for overseeing a project on nonsyndromic hearing impairment (NSHI). This large ongoing study has over 1,000 families with NSHI that have been ascertained from Pakistan, Iran, Hungary (Roma), Switzerland, Jordan, Poland, Germany and USA. A large number of NSHI genes have been identified and published using this collection of families including S1PR2, KARS and ADCY1. The assistant professor will be responsible for overseeing all aspects of this study including evaluation of audiological data, pathogenic variant identification using next-generation sequence data (filtering, bioinformatics evaluation, and molecular modeling) and functional evaluation of pathogenic variants. The Assistant Professor will work closely with the principal investigator Suzanne Leal as well as with postdoctoral fellows and laboratory technicians. He/she will also write and publish manuscripts and give presentations at international meetings.

The Assistant Professor should have an M.D. or Ph.D. (or related degree) in otolaryngology, genetics, molecular biology, epidemiology or related field. Previous experience in genetics and hearing impairment-related studies are required. Additionally experience in designing primers and performing PCR, analyzing genetic data, e.g. next-generation sequence data and programming/writing scripts e.g. python is highly desirable.

Please email your curriculum vitae, research statement and the names and contact information for four references to Suzanne Leal statgenpositions@gmail.com with the header Assistant Professor Position.
Houston is the fourth largest city in the USA an international and diverse city with many restaurants, parks and world-class arts (fine arts, music, dance and theater) and sports (baseball, basketball, football and soccer) venues. A high standard of living can be obtained in Houston due to the low cost of living.

Read more about Houston and the TMC at http://www.visithoustontexas.com/. Also visit the BCM webpage https://www.bcm.edu/ and the Center for Statistical Genetics website https://statgen.research.bcm.edu/index.php/Main_Page to learn more about our research.