The Helmholtz Institute for RNA-based Infection Research (HIRI) in Würzburg is seeking a

Data scientist / Bioinformatician "functional genomics in infection biology"

HIRI was established in May 2017 as a joint venture between the Helmholtz Centre for Infection Research (HZI) in Braunschweig and the Julius Maximilian University of Würzburg (JMU). It is the first research institution worldwide to exclusively address the role of ribonucleic acids (RNA) in infection processes. Based on novel findings, innovative therapeutic approaches are developed in an integrated research approach and made clinically usable through the development of pharmaceutical forms of application. For more information, please visit www.helmholtz-hiri.de.

Project description:

The HIRI is recruiting an interdisciplinary computational researcher to develop methods and platforms to integrate, analyze, and visualize large-scale bacterial RNA-related datasets. We have established a wide range of high-throughput sequencing-based functional genomics assays for RNA and infection biology [1], including RNA-seq [2], RIP-seq [3] and CLIP-seq [4], transposon insertion sequencing [5], and RNA modification detection. The successful applicant will work with experienced bioinformaticians and experimentalists to develop integrated analyses and interactive visualization platforms that will generate new biological insights from the large data sets produced by these technologies. The applicant will have ample opportunities to work with experimentalists to validate and address resulting findings; collaboration within the institute and beyond will be encouraged. The successful applicant will work in the dynamic environment of the HIRI in Würzburg, which is part of the Helmholtz Centre for Infection Research.

Further reading:

[1] Barquist and Vogel (2015) Ann Rev Genet 49:367-394.
[2] Holmqvist et al. (2018) Mol. Cell 5(7):971-982.
[3] Michaux et al. (2017) PNAS 114(26):6824-6829.
[4] Westermann et al. (2016) Nature 529:496-501.
[5] Barquist et al. (2016) Bioinformatics 32(7):1109-1111.

Qualifications

- Masters or PhD degree in computer science, bioinformatics, physics, or a related data intensive, computational field
- Experience with least one mathematical or statistical programming language (e.g. Python, Perl, R)
- Experience in handling large data sets in a Linux environment
- Basic (undergraduate-level) knowledge of probability and statistics
- Strong written and spoken English language communications skills
- Strong interest to learn about infection biology, microbiology, or RNA biology

Desired (non-essential) skills

- Experience with high-throughput sequencing data, particularly transcriptomics or other functional genomics techniques
- Experience working in a high-performance computing environment (e.g. Sun Grid Engine, parallel computing)
- Background in machine learning or Bayesian statistical techniques
- Experience with data visualization or web development

Applications should include a short cover letter, CV without a picture, publication list, copies of relevant documents and contact information for academic references as a single PDF file to info@helmholtz-hiri.de

For more details regarding the position, please contact lars.barquist@helmholtz-hiri.de

www.helmholtz-hiri.de

AN INSTITUTION OF
HZI HELMHOLTZ
Centre for Infection Research

IN COOPERATION WITH
Julius-Maximilians-
UNIVERSITÄT
WÜRZBURG