

The Barski laboratory at Cincinnati Children's Hospital is developing software for analysis of Next-Generation Sequencing data for use in bioinformatics/ epigenomics/ transcriptomics research.

We are looking for a software developer who has experience or interest in bioinformatics software development with a focus on designing, developing and maintaining production software systems in data-intensive scientific settings. The developer must be able to adapt to changing specifications and priorities, be willing to take initiative and ownership of their work, and learn.

The ideal candidate should have experience in at least some of the following areas:

- Bioinformatics
  - o Analysis of ChIP-Seq and similar data
  - o Analysis of RNA-Seq and similar data
  - o Gene ontology/pathways/networks analysis

- o Statistical procedures using R
  
  
  
  
  
  
  
  
  
  
- Programming:
  - o Python or similar scripting language
  
  
  
  - o Working on server-side components (including clusters and/or clouds) or client-side (web UI) components,
  
  
  
  - o Server side JavaScript (e.g. Node.JS) and modern JavaScript UI frameworks such as AngularJS or ExtJS
  
  
  
  - o SQL or NoSQL databases (e.g. MongoDB)

The successful candidate will be working on enhancement of existing software (see <http://biowardrobe.com>) under a guidance of an experienced developer and analysis of experimental data related to epigenomic regulation of immune response and other biological problems. The position is available as either staff or postdoctoral fellow. Combined wet lab/computational position is also possible.

Opportunities for Master's or PhD thesis research are available.

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25.10.2015 10:25 -

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For additional information, please contact Artem Barski barskilab@cchmc.org

<http://www.cincinnatichildrens.org/bio/b/artem-barski/>

More about Cincinnati Children's: <http://www.cincinnatichildrens.org/research/default/>