1. Are you registered with or have you worked for Kelly Services in the past?

No.

1. When are you available to start work?

Available but need 2 weeks notification time to current employer.

1. Are you currently authorized to work in the USA?  You will be asked to provide proper documentation upon hire

Yes, I am holding U.S. permanent residency.

1. Are you available to work on a full-time, long-term basis?

Yes

1. Please state your salary requirements. Negotiable is not an appropriate response.

$90k

1. Please state why you are seeking employment and/or leaving your current position at this time

I used to work at NIEHS where I learned a lot about the program and all those cutting edge research projects, and I enjoyed working in this environment very much. Since I left NIEHS, I spent time at UNC then Duke University where I gained intensive experiences in Next Generation Sequencing research, parallel computing and using the cluster computing resources. I believe that I can bring back my new knowledge and skills to the research in the government research institute for the public benefit.

1. This position will be located at **NIH/NIEHS at 111 T.W. Alexander Drive, Research Triangle Park, NC**.  We are not able to provide interview or relocation expenses.

I am local and I am okay with this.

1. Please state highest degree earned (including area of study)

Master of Science in Food Microbiology

Master of Bioinformatics

1. Please summarize your background in the field of bioinformatics and/or functional genomics

I received formal training in bioinformatics from NCSU, which is one of the first few program in the States. Then, I went on worked in the bioinformatics research field since January 2003 at government research institute and renown universities. My experiences had been primarily focused on genome informatics, for toxicogenetics/toxicogenomics, cancer biology and human genome variation. My role was to manage huge genomics data, i.e. microarray, build novel statistics model and development analytical methodology for various biological research topics. I have also been responsible for interacting with researchers to help them with any bioinformatics need and provide solution/consultation promptly.

1. Please describe any experience working with and analyzing NextGen sequencing data

Since fall 2008, I entered Next Generation Sequencing field. Initially, I was able to extend my experiences with microarray and genome profiling into it counterpart in NGS – RNAseq project. I was an actively player at UNC Lineberger Cancer Center to involving developing the inhouse RNAseq analytical pipeline. On that errand, I was the main developer on the inHouse QC modules for RNAseq experiment/analytical pipeline. Recently, I obtained experience in human whole genome/exome NGS project at Duke University, Center for Human Genome Variation. I participated in maintaining and developing inhouse variant calling pipeline, also I built an in-house MySQL database keeping track of the variant calling project progress, including three major components (GWAS experiment, Illumina sequencing and variant calling).

1. Please describe any direct experience working with very large biological data

As I explained in the item 9&10, my primary experiences are handling genomics informatics project, which mostly involving huge dataset, from microarray experiment to NGS study. At this capacity, I became very experienced working in Linux/Unix environment with shell scripting. Also, I became experienced levering/using supercomputing resource, from previous LSF to recent Oracle Grid Engine (SGE). I am experienced and comfortable working with cluster computing resource and paralleling the repetitive computing jobs.

12.  Please indicate your level of proficiency with the following and make sure that these skills appear on your updated resume

1.    Java/C++: proficient

2.    MATLAB: not experienced by willing to learn if needed

3.    R: highly proficient

4.    Perl: highly proficient

5.    Python: Minimal

6.    SQL: proficient

7.    UNIX/Linux: highly proficient

8.    Windows & Macintosh: proficient with windows minimal with Mac.

13.  Please list any additional programming languages, scripting languages, or statistical/mathematical packages that you are proficient in

SAS

PHP

14.  There are multiple openings for a bioinformatics scientist with Kelly Government Solutions in Research Triangle Park, NC to work with NIEHS.  Please let me know if you are aware of additional qualified candidates that may also be interested in learning about this opportunity.

Will be glad to.