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Applicants should possess Ph.D. degree in computational biology, systems biology or relevant areas (e.g., statistics, mathematical biology, statistical bioinformatics, computer science, discrete mathematics, biophysics) and a notable publication record. You should have strong research skills and publications’ record, especially in the areas of genome & transcriptome data analysis, systems biology and computational cancer genomics. Good programming experience (e.g. C/C++, R, S-plus, SQL, Java, Oracle, website and database experience) and experience in experimental studies is a plus.

Possible projects might be focus on microarray and NGS data analysis, DNA-RNA-protein interactions, modelling and prediction of complex interaction networks, ncRNA structures and functions, non-canonical nuclear acid structures, identification and validation of biomarkers associations with cellular phenotypes and human diseases (specifically cancers), and relevant statistical, computational, systems biology algorithms development.

We are looking for a candidate who is independent-minded, can work well in a team environment, and willing to collaborate with experimental laboratories, clinicians and industry.

The job scope includes:

- Genome sequence and expression profile analyses relevant to basic biological or/and clinical problems with the goal of elucidating genome-phenotype relationships and the mechanisms linking the two.
- Recruit and lead a research group.
- Education of PhD students and, to a minor degree, of MSc students.

The position provides a three-year renewable contract with competitive benefits. Interested applicants should send your CV, statement of research interests and the names and addresses of three references to Dr. Vladimir Kuznetsov (vladimirk@BII.a-star.edu.sg).

Don't forget to mention Naturejobs when applying.