



Genome Institute  
of Singapore

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## Postdoctoral Fellow: Bioinformatics/Computational Genomics

The Genome Institute of Singapore (GIS) is looking for an enthusiastic bioinformatics postdoctoral fellow to work in the area of computational genomics and cell identity. The candidate will analyse large scale genomic and transcriptomic data sets to study control of cell fate in pluripotent stem cells (differentiation, reprogramming, embryonic development). The project will also involve approaches for single cell genomics/epigenomics. Candidates with a background in mathematics/computer science/statistics that are interested to work with cutting-edge technologies and exciting cell models to advance high throughput biology are highly welcome to apply. The successful candidate will join the team of GIS Fellow Jonathan Goke.

### Requirements

Candidates should have a PhD in a mathematical discipline (or related), a solid understanding of probability and statistics, programming experience (R is a plus), and experience in one or more of the following areas: machine learning, SVMs, string kernels, regulatory genomics, transcriptome analysis, DNA sequence analysis. A strong interest in molecular biology and good communication skills are required as the successful candidate is expected to closely interact with experimental groups.

### Contact

For inquiries or to apply, please email your CV to Jonathan Goke ([gokej@gis.a-star.edu.sg](mailto:gokej@gis.a-star.edu.sg)).

### Relevant Publications

Chan, YS.\*, Göke, J.\*, Ng JH.\*, Lu X., Gonzales K., Tan C-P., ... & Ng HH. (2013) Induction of a Human Pluripotent State with Distinct Regulatory Circuitry that Resembles Preimplantation Epiblast. *Cell Stem Cell*, 13(6), 663-675

Lu, X.\*, Göke, J.\*, Sachs, F., Jacques, PE., Liang, H., Feng, B., ... & Ng, HH. (2013). SON connects the splicing-regulatory network with pluripotency in human embryonic stem cells. *Nature cell biology*, 15(10) : 1141-5

Göke, J., Chan, YS., Yan, J., Vingron, M., & Ng, HH. (2013). Genome-wide Kinase-Chromatin Interactions Reveal the Regulatory Network of ERK Signaling in Human Embryonic Stem Cells. *Molecular Cell*, 50(6), 844-855

Göke, J., Schulz, MH., Lasserre, J., & Vingron, M. (2012). Estimation of pairwise sequence similarity of mammalian enhancers with word neighbourhood counts. *Bioinformatics*, 28(5), 656-663.