

# Positions in Computational Cancer Genomics in Skandlab@GIS

*Interested in computational biology, medical genomics, cancer, and/or non-coding DNA?*

Postdoc and PhD positions available, read more below. We also have excellent project/internship opportunities for current Master's students (see [here](#), and contact me for more information).

## Background

[The Skanderup lab](#) is a newly started combinational biology group at Genome Institute of Singapore (GIS). Our focus is on developing integrated clinical, experimental, and computational approaches to solve important challenges in medical genomics, especially cancer diagnosis and treatment. We accomplish this in close collaboration with excellent experimental and clinical groups at GIS and in Singapore. We are particularly interested developing computational approaches to decipher the influence of non-coding elements and transcripts in cancer (previous work: [Weinhold, Jacobsen et al. 2014, Nature Genetics](#); [Jacobsen et al. 2013, Nature Structural & Molecular Biology](#)).

## Projects

The successful candidates will primarily work on projects relating to, 1) computational methods for discovery and characterization of non-coding

driver elements from large-scale cancer whole-genome sequencing data, 2) computational analysis of non-coding RNAs in cancer, 3) computational methods for discovery of cancer vulnerabilities in large functional screens. All projects will use both in-house generated data as well as large datasets from international cancer consortia (TCGA and ICGC).

## Qualifications

The successful candidate must have documented skills in analyzing large-scale biological datasets and must have a solid computational/statistical background. The candidate must have a strong interest in (or be motivated to learn) cancer biology and genomics.

### **PostDoc, required qualifications:**

1. PhD in Bioinformatics or related field with strong emphasis on quantitative data analysis
2. Strong and documented programming and quantitative data-analysis skills
3. Proven excellence in research (e.g. publication in established journals)
4. Fluent written and spoken english

### **PhD, required qualifications:**

1. Bachelor or Masters degree in Bioinformatics, Computer Science, Statistics, Physics or related field with strong emphasis on quantitative data analysis.
2. Documented programming and data-analysis skills
3. Fluent written and spoken english
4. Note: Successful applicants will receive a [SINGA fellowship](#) and will

be enrolled at National University of Singapore. **Deadline for August 2016 intake is Jan 1, 2016.** Contact Anders Jacobsen Skanderup ([skanderupamj@gis.a-star.edu.sg](mailto:skanderupamj@gis.a-star.edu.sg)) for more information.

**Additional beneficial qualifications for all candidates:**

- Experience with analysis of *raw* high-throughput sequence data
- Experience with analysis of non-coding RNAs
- Experience with analysis of ChIP/RIP-seq data
- Flexible programming skills (ideally multiple programming languages)
- Experience with statistical programming in R
- Experience with statistical/machine learning

## **Application**

Applications should consist of the following:

1. Cover letter (**Max 1 page**): previous experience and results, describe your motivation for working on the above-mentioned problems.
2. CV (**Max 2 pages**): include publication list and contact information for 3 references
3. 2–3 reference letters (can be submitted later)

Please contact or send applications directly to Anders Jacobsen Skanderup ([skanderupamj@gis.a-star.edu.sg](mailto:skanderupamj@gis.a-star.edu.sg)).