

## Job description

***Do you want to be a frontrunner in the field of population genetics by using state-of-the-art single-cell technologies to better understand disease?***

We are seeking a highly motivated and ambitious postdoctoral fellow with a background in computational biology to join the research group of Lude Franke ([www.ludesign.nl/frankelab/](http://www.ludesign.nl/frankelab/)) within the Genetics department of the University Medical Center Groningen (UMCG), the Netherlands. Our group studies how genetic risk factors cause disease by correlating genetic variation with molecular data (such as gene expression, methylation, and histone modifications) in thousands of individuals.

In our previous work, we studied the cell-type-specific effects of genetic variance on expression and co-expression interactions (Nature Genetics: <https://doi.org/10.1038/s41588-018-0089-9>) and outlined how we believe scRNA-seq data can be used to make personalized gene regulatory networks for precision medicine (Genome Medicine: <https://doi.org/10.1186/s13073-018-0608-4>). In the project that you will be appointed to, you will be involved in the analysis and interpretation of a dataset of over 800,000 cells, from 120 individuals and several pathogen stimulations. You will closely collaborate with a molecular biologist and bioinformatician to study the interplay between genetics and environment, and how this affects the regulatory wiring in immune cells. Moreover, you will play a key role in our growing international collaborative effort, the single-cell eQTLGen consortium (<https://eqtngen.org/single-cell>). This endeavor will require you to work with big data, develop new algorithms and statistical approaches, and integrate multiple data layers. This postdoc position will allow you to be at the forefront of the single-cell field and meet with many of its key players.

## Requirements

The ideal candidate will have:

- A PhD in bioinformatics, computational genetics or another relevant area. Alternately, a PhD in molecular biology, immunology, etc. combined with a very strong record of high-throughput data analysis, supported by publications in this area.
- A strong academic track record.
- Expertise in management of large datasets in the area of genetics and/or gene expression analysis.
- Excellent verbal and written English skills.
- Programming skills and experience with programming languages such as Python and R.
- Experience with analyzing bulk or single-cell RNA-sequencing data is highly preferred.
- Experience with working in Linux environments is a plus.
- Experience with working on computer clusters and with job scheduling systems (e.g. Slurm) is of benefit.

**Candidates who only partially meet this profile are nonetheless strongly encouraged to apply.**

## **Conditions of employment**

- A temporary contract for three years, 36 hours a week.
- A salary in scale 10 (CAO-UMC): max. € 4.361,- gross per month at full employment (with an 8% holiday bonus and an 8.3% end-of-year bonus).
- The start date for this position is as soon as possible.

### **Further information**

For more information about this vacancy you may contact:

Prof. Dr. Lude Franke, e-mail: [l.h.franke@umcg.nl](mailto:l.h.franke@umcg.nl)