

Postdoc Bioinformatics - mRNA translation in cancer

Function Description

In the research group of Reuven Agami at the division of Oncogenomics at the Netherlands Cancer Institute in Amsterdam, we are interested in identifying novel cellular vulnerabilities that can be exploited for cancer therapies. For this purpose, we develop innovative genomic and functional genetic tools and combine biochemical and bioinformatics tools to understand the underlying mechanisms. In recent years, the Agami lab used ribosome profiling (Ribo-seq) and CRISPR screens to study the impact of various amino acid shortages on mRNA translation (Loayza-Puch et al., Nature 2016; Slobodin et al., Cell 2017; Sun et al., EMBO 2020). This research line led us to uncover a surprising effect of amino acid shortages on protein production. We showed that these treatments stimulate cancer cells to produce aberrant proteins by ribosomal frameshifting and codon reassignments (Bartok et al., Nature 2021; Champagne et al., Mol. Cel. 2022; Pataskar et al., Nature 2022). These defective proteins can be processed and presented as neoepitopes at the surface of cancer cells, potentially activating immune cells. Currently, our lab is actively expanding the outreach of such vulnerabilities to be tested in clinical settings. These projects involve novel research questions and comprise several computational challenges. The lab is well-equipped with computational resources, including five high-performance servers and a computational resource from the Dutch government.

Responsibilities:

We are looking for a candidate to establish an independent research line studying cancer, diet, and immune cells. In this context, the applicant will be responsible for the analysis and further development of bioinformatics pipelines to examine large datasets of Ribo-seq, DNaseq, RNA-seq, and mass spectrometry. In addition, the applicant will analyze functional genetic screenings and biochemical experiments. Apart from this, the applicant can incorporate in-house and external resources to develop predictive models of defective protein production. We expect the successful applicant to have direct interactions with other computational and experimental researchers, to supervise PhD and undergraduate students, and finally to be involved in the writing of scientific papers, project reports, and grant applications.

Job Requirements

The Agami lab seeks to recruit an ambitious bioinformatics Postdoc with a strong background in large-scale data analysis and a strong commitment to science.

In particular, we seek candidates with the following computational skills;

1. Experience with analyzing proteomics datasets (protein expression, phosphoproteomics etc) is an advantage.
2. Experience with analyzing genomics (RNA-seq, Ribo-seq, CRISPR-screening) datasets.
3. Proficient in R, and at least one of the following programming languages; PERL and Python.
4. Experience with high-performance computing and proficiency in UNIX and BASH scripting.
5. Experience with cancer datasets (TCGA, CPTAC etc.), will be beneficial.
6. Experience with proteogenomics pipelines is a big plus.
7. Experience with machine learning and statistical modeling is a plus.

Furthermore, general knowledge of cancer biology and functional genetics tools is advantageous. We expect the candidate to be highly motivated, creative, and able to work in a team. Apart from being a true team player, we expect the candidate to exhibit a high degree of independence, have a problem-solving attitude, and have strong analytical and technical abilities in addition to excellent communication and presentation skills.

Interested?

For further information and addresses, visit our website (<https://www.nki.nl/divisions/oncogenomics/agami-r-group/>) or contact Reuven Agami at r.agami@nki.nl.