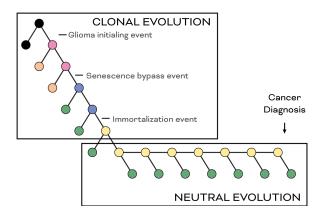


Postdoctoral Fellow (Tumor Evolution)

The Barthel laboratory is focused on unraveling the role of telomere dysfunction in glioma development and evolution. We employ computational biology, evolutionary genetics, functional genomics and molecular biology to map the ramifications of dysfunctional telomeres on glioma genomes. We are looking for a talented, passionate and highly motivated individual to enrich our team and study tumor evolution.

Position Summary

This project aims to reconstruct evolutionary and developmental lineages of gliomagenesis. The successful applicant will employ next-generation



genomic analysis (deep DNA sequencing, epigenome profiling, single-cell RNA sequencing) across multiple image-mapped samples per tumor to reconstruct tumor phylogenies and evolutionary trajectories in space and time. They will collaborate with other dry lab scientists in the lab to detect telomere dysfunction and determine the natural order and evolution of genomic variation driven by damaged telomeres. They will be involved in data analysis, interpretation and write manuscripts to describe their findings. They will lead their own project but will be a part of a team and help on other projects as well.

Career Development

We value our trainee's personal development and strive to unlock their full potential. Trainees are provided with ample opportunities for additional training in computational and cancer biology. Successful applicants are encouraged to attend scientific meetings and the lab will provide support for at least one scientific conference per year. While this position is not contingent upon securing additional funding, successful candidates will be supported and encouraged to apply for outside sources of funding. Candidates are welcomed to explore their own scientific interests into areas of research that fall within the general scope of the lab.

Education and Preferred Qualifications

The ideal candidate will have a PhD in a relevant field and have experienced analyzing next-generation sequencing data. A track record of peer reviewed publications in (tumor) evolution is preferred. An understanding of cancer biology and genomics is a plus. The candidate should have experience with a statistical programming language such as Python or R and have a good understanding of statistical theory, phylogenetics and evolution. Experience in Unix-based computing environments is a plus. Candidates from all backgrounds will be considered.

Location

We are located at the Translational Genomics Institute (TGen) set to the backdrop of the stunning Sonoran Desert. The successful candidate will be a part of the Cancer and Cell Biology Division at TGen and will have numerous opportunities to work with our partners at the Neurosurgery Department of the Amsterdam UMC in The Netherlands and the Department of Computational and Quantitative Medicine (DCQM) at City of Hope (COH).

Application

Please direct all questions to barthel AT barthel-lab.com. Application via our HR management system at https://recruiting.paylocity.com/Recruiting/Jobs/Details/543317. Attach a letter describing your research interests and motivation to join our group. Include an academic CV detailing your past research experience, publication track record and (conference) presentations. We will start reviewing applications immediately and until the position is filled.

For additional information, please see www.barthel-lab.com