

Identifying circRNAs in Neuroblastoma

Recently, circular RNAs (circRNAs) have been found to make up a relevant proportion of spliced transcripts from coding and non-coding genes (see Szabo *et al.* for a review). Certain circRNAs, such as CiRS-7, have been shown to have a functional role as a “sponge” for microRNAs with important regulatory roles. However, the function of the vast majority of circRNAs is still unclear.

In the Schulte lab at Charité, we use genomics and wet-lab experiments to gain new insights into neuroblastoma, the most common extracranial solid tumour in childhood. The group consists of physicians, molecular biologists and bioinformaticians working together towards an increased understanding of tumour development. As neuroblastoma is marked by extremely few coding mutations, compared with, say, lung cancer or breast cancer, other defects in the regulatory program of cell proliferation and cell differentiation can be suspected.

We are looking for a dedicated bioinformatics master student, who wants to take part in a planned study that investigates the role of circRNAs in neuroblastoma. CircRNAs are to be identified from custom RNA-Seq data, therefore a strong interest in and some familiarity with next-generation sequencing data analysis and non-coding RNAs are required.

The master student will be based at the Charité Virchow campus and mainly supervised by Dr. Joern Toedling. The thesis will be reviewed by Professor Schulte (Charité) and Professor Vingron (MPI for Molecular Genetics). In case the methods developed by the master student or any of her/his findings are going to be used in a later publication, the student will, of course, be a co-author on that publication. The project is a collaboration between our group at the Charité and Professor Nikolaus Rajewsky (MDC).

Please send applications for this position, as well as informal requests, to joern.toedling@charite.de.