



## Postdoc Program between the Freie Universität Berlin (FUB) and the China Scholarship Council (CSC)

### Open Postdoc position at FUB for CSC scholarship candidates 2017

*Please note: the postdoc position is only offered to Chinese who graduated with a PhD degree from a Chinese university.*

<b><u>Department/Institute:</u></b>	Mathematics and Computer Science
<b><u>Subject area:</u></b>	Medical Bioinformatics
<b><u>Professor / Research Group:</u></b>	Prof. Dr. Rosario M. PIRO (Mr.)
<b><u>Number of open Postdoc positions:</u></b>	1
<b><u>Project title:</u></b>	Identification of mutation-induced aberrant transcript structures from next-generation DNA- and RNA-sequencing data

#### **Postdoc Project description:**

Next-generation sequencing has provided a wealth of data for computational biology, e.g. to identify mutations (such as single nucleotide variants or small insertions and deletions) or genomic alterations (such as copy number changes, rearrangements, etc.) in sporadic cancers as well as in various hereditary diseases.

Yet, much of the data remains unexplored because most analyses concentrate on specific contents of the provided information (e.g. exonic mutations) while often ignoring other aspects (e.g. intronic non-coding mutations in whole genome sequencing data).

In this project we will apply state-of-the-art bioinformatics techniques and develop novel methods in order to analyze the potential impact of non-coding mutations (both germline mutations in hereditary disorders and somatic mutations in cancer) on gene transcript structure in order to identify mutational events that significantly alter expressed transcripts, e.g. by causing aberrant splicing or premature polyadenylation.

The project will aim at integrating data from different sources (e.g. whole genome sequencing data and RNA-seq data) and relating them to disease phenotypes in order to discern which of the identified events (mutations, structural aberrations of transcripts, etc.) are likely to be disease-relevant driver events rather than mere „passengers“.

#### **Language requirements:**

Very good knowledge in English is required (ELTS 6,5 or TOEFL 95 ibt). German is helpful, but no requirement.

#### **Academic requirements:**

Applicants should have a PhD in bioinformatics/computational biology or highly related field. Alternatively, candidates from mathematics, computer science or physics might be considered, if they have sufficient knowledge in programming languages and a previous familiarity with applications to biological research topics (including knowledge about the underlying molecular biology/genetics).

Familiarity with Next-Generation Sequencing data analysis is required.

#### **Information of the professor or research group leader:**

Rosario M. Piro is an assistant professor (Juniorprofessor) in bioinformatics and principal investigator at the Institute of Bioinformatics and the Institute of Computer Science at FU Berlin. At the same time he is a member of the Institute of Human Genetics and Medical Genetics at the Charité University Hospital. His research concentrates on computational neuropathology (i.e. computational approaches to study neurological disorders and neuropathologies, including brain tumors) and computational oncology in general (including the development and evolution of cancers in other organs or tissues). Website: <http://rmpiro.net>

#### **Please note:**

In a first step the complete application should be submitted to the Beijing Office for evaluation by November 6, 2016. Please don't contact the professor before. He/She will get in contact with you after having received the complete application.