





## **Bioinformatics Master's Project in Cancer Research**

The labs of Johannes Zuber and Anna Obenauf at the Research Institute of Molecular Pathology (IMP) / Campus Vienna Biocenter (VBC) are recruiting a **Bioinformatics Master student** for a computational project focused on the integrative analyses of genome-wide CRISPR/Cas9 screening datasets, which provide a transformative approach to decipher genetic drivers and dependencies in cancer and discover new targets for therapy development (reviewed in *Housden & Muhar et al., Nature Reviews Genetics*). Beyond probing essential genes, which have meanwhile been annotated in hundreds of cancer cell lines (e.g. see https://depmap.org/), the Zuber/Obenauf labs (in collaboration with Boehringer Ingelheim) have devised optimized sgRNA libraries, screening assays and data analysis pipelines to investigate regulators of major oncogenes and genetic modifiers of available cancer therapeutics.

The main objectives of this Master's project will be to (1) perform analyses of recently completed and currently ongoing CRISPR/Cas9 screens and develop an interface for data browsing and integration, (2) investigate features impacting the technical screen performance (which will guide the design of third-generation sgRNA libraries), (3) integrate screening results with existing functional-genetic, genome and transcriptome profiling data to discover and evaluate genetic interactions in defined cancer contexts. To accomplish these goals, we are seeking Master student who shares our enthusiasm about cutting-edge functional genomics, is excited to join a vibrant and very collaborative research team, and highly motivated to learn how to handle and deeply investigate large NGS datasets in cancer research.

## As Bioinformatics Master student in our team you will

- 1. work embedded in a group of experienced bioinformaticians and computational biologists with complementary expertise (affiliated with different research groups at IMP), who will provide constant support and training
- 2. work closely together with an experienced bioinformatician (Tobias Neumann), who has profound expertise in all relevant computational methods and will train and supervise the student
- 3. gain knowledge and experience in the primary analysis and integration of diverse NGS datasets (using state-of-the-art and newly developed bioinformatic analysis tools and pipelines)
- 4. develop a customized interface that will be routinely used for data browsing and integration
- 5. join the design of third-generation CRISPR/Cas9 screening reagents and contribute to ongoing screening projects and planned publications

## Successful candidates should have

- 1. proficient experience with UNIX-like operating systems
- 2. programming skills in R/Bioconductor and be confident to acquire knowledge in R's Tidyverse and Shiny
- 3. a sound understanding of NGS data analysis principles
- 4. basic experience with relational databases
- 5. interest and basic knowledge in machine learning, artificial intelligence, and statistical methods
- 6. excellent communication skills in English and an ability to translate and communicate results

Applications, including a letter of motivation describing your past research experiences and your particular interest in this position, a CV, and the names and contact details of referees should be sent to <a href="mailto:tobias.neumann@imp.ac.at">tobias.neumann@imp.ac.at</a>. The application deadline is **February 1, 2019**.

Further information: <a href="https://www.imp.ac.at/groups/johannes-zuber/">https://www.imp.ac.at/groups/johannes-zuber/</a>
<a href="https://www.imp.ac.at/groups/johannes-zuber/">https://www.imp.ac.at/groups/johannes-zuber/</a>