

Master thesis (MA, 30 ECTS)

Transcriptomic analysis of prostate and bladder cell lines

Description

While cell lines are integral to many experiments, they tend to drift way from the parent tumor's genomic and morphological features. This is a widely recognized limitation. Nevertheless, some cell lines will maintain substantial similarities in their transcriptomes, in particular, in the context of specific pathways, and hence, represent reasonably good models to study cancer treatment.

We are collaborating with the groups of PD Dr. Hugo Murúa-Escobar (Universitätsmedizin Rostock) and Prof. Ingo Nolte (Stiftung Tierärztliche Hochschule Hannover Klinik für Kleintiere) and have access to a number of RNA-seq libraries of canine prostate and bladder cancer samples as well as derived cell lines. The aim of this project is to comparatively analyse the transcriptomes and determine similarities at the pathway level, identifying the best model depending on the cancer type and treatment.

Relevant literature

- Taher L, Beck J, Liu W, Roof C, Soller JT, Rütgen BC, Hammer SE, Chodisetti M, Sender S, Sterenczak KA, Fuellen G, Junghans C, Brenig B, Nolte I, Schütz E, Murua Escobar H. Comparative High-Resolution Transcriptome Sequencing of Lymphoma Cell Lines and *de novo* Lymphomas Reveals Cell-Line-Specific Pathway Dysregulation. *Sci Rep*. 2018 Apr 19;8(1):6279.
- Conesa A, Madrigal P, Tarazona S, Gomez-Cabrero D, Cervera A, McPherson A, Szczesniak MW, Gaffney DJ, Elo LL, Zhang X, Mortazavi A. A survey of best practices for RNA-seq data analysis. *Genome Biol*. 2016 Jan 26;17:13.
- Current ENCODE guidelines for RNA-seq experiments (<https://www.encodeproject.org/about/experiment-guidelines/>)

Requirements

Familiarity with UNIX, bash, a scripting language (Perl or Python), and R. These skills could be acquired during the preparation of the thesis, but this would require substantial additional time and effort.

Start date

As soon as possible

Duration

Approximately six months

Contact

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