

Bioinformatic modelling of molecular processes altered in the ovaries of infertile women

Summary

Infertility affects about every 6th couple worldwide, but its aetiologies vary greatly. Ovarian dysfunction may lead to anovulation, inadequate steroid biosynthesis as well as problems with oocyte meiotic and cytoplasmic maturation causing female infertility. By studying the ovarian somatic cells of in vitro fertilization patients and their treatment outcomes, we can pinpoint the variable molecular aspects of ovarian infertility that in the future lead to better medical options for these women.

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| Research field: | Biomedicine and health technology |
| Supervisor: | Agne Velthut-Meikas |
| Availability: | This position is available. |
| Offered by: | School of Science Department of Chemistry and Biotechnology |
| Application deadline: | Applications are accepted between January 01, 2025 00:00 and January 24, 2025 23:59 (Europe/Zurich) |

Description

The PhD project aims to understand the molecular communication between the cells in the ovarian follicle to better understand ovarian function and the reasons for its dysfunction. The work involves generating and the computational analysis of short (miRNAs and piRNAs), long (PacBio data), single-cell and standard short-read sequencing data from ovarian somatic cells obtained from in vitro fertilization patients. Promising results will be functionally validated in cell culture experiments.

The work is carried out during fully funded 4 years at the Reproductive Biology Research group: <https://taltech.ee/en/reproductive-biology-research-group>.

We are a vibrant team engaging students from all levels of education, collaborating with infertility clinics and international research groups. We are proud of carrying out interdisciplinary research combining computational and molecular biology methods with biomedicine. We regularly present our research results at international conferences in high impact research journals.

We expect the candidate to possess the following minimum qualities:

- Previous experience in statistical or bioinformatic data analysis. Ability to use R packages and standard linux environment are considered as bonus.
- Laboratory work experience with nucleic acids (preferably RNA) and/or
- Laboratory work experience involving mammalian cell cultures.
- Interest to learn advanced level computational data analysis methods for genome-wide transcriptomic data.
- Excellent English oral, reading and writing skills (C1 level or higher education obtained in English language).
- Ability to work both independently and in a team.
- Willingness to be engaged in teaching and supervision activities.
- MSc degree in a relevant field (molecular or cell biology, bioinformatics, biomedicine etc)

The advantageous but not compulsory qualities include:

- Previous experience with generating and analysing RNA sequencing data
- Experience with RT-PCR, immunohistochemistry or immunocytochemistry, fluorescent microscopy, FACS, ELISA.



- Experience with primary cell cultures.



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