

**MATEMAATIKA-LOODUSTEADUSKOND
INTEGREERITUD SÜSTEEMIDE BIOLOOGIA KESKUSE
TEADUS- JA ARENDUSTEGEVUSE AASTAARUANNE 2013**

1. Struktuur

Struktuuriüksuse nimetus eesti ja inglise keeles, direktori /juhataja nimi

Integreeritud Süsteemide Bioloogia Keskus/Centre for Biology of Integrated Systems, Acting head: Anu Aaspõllu

- struktuuriüksuse koosseisu kuuluvate õppetoolide, lektoraatide, laboratooriumide, osakondade või muu üksuse loetelu eesti ja inglise keeles ning nende juhatajate nimed

2. Teadus- ja arendustegevuse (edaspidi T&A) iseloomustus

2.1 Struktuuriüksusesse kuuluvad uurimisgrupid (*kõik uurimisgrupid näidatakse aruandes eraldi, järgides alltoodud ülesehitust*).

Uurimisgrupi nimetus (eesti ja inglise keeles) ja juhi nimi

- uurimisgrupi teadustöö kirjeldus (*inglise keeles*);
- uurimisgrupi aruandeaastal saadud tähtsamad teadustulemused (*inglise keeles*);
- uurimisgrupi kuni 5 olulisemat publikatsiooni aruandeaastal.

In 2013 the research was focused on several directions:

1) Forensic soil analysis for development tools for data management and database handling. We found that 18S marker results at metagenome level could be used to create and run a filtered database that is computationally much more efficient and flexible. Results of the study were presented also at the International Society for Forensic Genetics (ISFG) Congress.

2) Metagenomic research for differential bacterial communities. With colleagues we published study on marine bacteria in Finnish gulf. The analyses consist of ten samples. We identified 609 OTUs (operational taxonomic units), most abundant OTUs of the dataset were identified as *Sulfurimonas* and *Pelagibacter*.

3) In the first study related to human reproductive topics we studied human vaginal microflora in healthy women in reproductive age. Our study was the first of its kind to analyze the mycobiome that colonizes the healthy vaginal environment using barcoded pyrosequencing technology. We observed 196 fungal operational taxonomic units (OTUs), including 16 OTUs of *Candida* spp., which is more diverse than previously recognized.

4) In the second study related to human reproductive topics we studied granulosa cells using sequencing of small RNAs, which revealed miRNA in FSHR and aromatase genes.

5) In the third study related to human reproductive topics we studied in 102 patients the degree to which total peroxide content and antioxidant status influence infertility and pregnancy outcome. We found a significantly higher oxidative stress environment in the ovary when compared with blood plasma. The elevated oxidative stress levels were correlated to a higher number of oocytes that could be obtained via the procedure and to a lower amount of FSH needed to mature the oocytes, suggesting that oxidative stress, to some degree, is favourable for hormone stimulation outcome. A high level of lipid peroxidation products in the urine, another marker of oxidative stress, was

observed in smokers and this marker was elevated in patients with embryos that had lower developmental potential. A higher overall antioxidant status in blood plasma was advantageous for achieving pregnancy.

6) In the fourth study related to human reproductive (cancer) topics we detected significant changes in gene expression by the Ishikawa cell line after treatments with E2, P4, TAM, and RU486. These transcriptome data provide valuable insight into potential biomarkers related to endometrial receptivity, and also facilitate an understanding of the molecular changes that take place in the endometrium in the early stages of breast cancer treatment and contraception usage.

7) We were involved in development of scalable multi-task learning methods, where we developed a new approach for ensemble of trees method called MT-ExtraTrees. Published in NIPS 2013 workshop.

8) We developed PCR analysis for determination of *Castor* species to distinguish samples as native *Castor fiber* species or as invasive *Castor canadensis* species in Estonia.

Year 2013 was relatively productive: several publications published and submitted, participated in numerous international meetings with presentations.

2013 tähtsamad teadustulemused on kokku võetud järgnevas publikatsioonides:

Drell, T.; Lillsaar, T.; Tummeleht, L.; Simm, J.; Aaspõllu, A.; Väin, E.; Saarma, I.; Salumets, A.; Donders, G.G.G.; Metsis, M. (2013). Characterization of the Vaginal Micro- and Mycobiome in Asymptomatic Reproductive-Age Estonian Women. PLoS ONE, 8(1), e54379.

Laas, P.; Simm, J.; Lips, I.; Metsis, M. (2013) Spatial variability of winter bacterioplankton community composition in the Gulf of Finland (the Baltic Sea). Journal of Marine Systems. Volume 129, January 2014, Pages 127–134.

Lilje, L.; Lillsaar, T.; Rätsep, R.; Simm, J.; Aaspõllu, A. (2013). Soil sample metagenome NGS data management for forensic investigation. Forensic Science International: Genetics Supplement Series (35 - 36).Elsevier.

Tamm-Rosenstein K, Simm J, Suhorutshenko M, Salumets A, Metsis M. (2013). Changes in the transcriptome of the human endometrial Ishikawa cancer cell line induced by estrogen, progesterone, tamoxifen, and mifepristone (RU486) as detected by RNA-sequencing. PLoS One. 16;8(7):e68907.

Velthut-Meikas A, Simm J, Tuuri T, Tapanainen JS, Metsis M, Salumets A. (2013). Research resource: small RNA-seq of human granulosa cells reveals miRNAs in FSHR and aromatase genes. Mol Endocrinol. 27(7):1128-41.

Velthut A, Zilmer M, Zilmer K, Kaart T, Karro H, Salumets A. (2013). Elevated blood plasma antioxidant status is favourable for achieving IVF/ICSI pregnancy. Reprod Biomed Online. 26(4):345-52.