SCIENTIA FELLOWS

Statistical learning for personalised cancer therapy

Modelling and prediction in pharmacogenomic cell line screens

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This postdoc will develop innovative methods in statistics and machine learning for personalised cancer therapy. This research is part of the lively UiO:LifeScience research environment PERCATHE (https://www.uio.no/english/research/strategic-research-areas/life-science/research/convergence-environments/percathe) with research groups at both the University of Oslo and the Oslo University Hospital. Our collaboration includes the groups of Arnoldo Frigessi (https://www.med.uio.no/imb/english/people/aca/frigessi/), Eivind Hovig (https://ous-research.no/home/hovig), Jorrit Enserink (https://www.ous-research.no/enserink) and Kjetil Tasken (https://www.med.uio.no/klinmed/english/people/aca/ktasken).

Project description:
We are running a large project on drug sensitivity and drug synergy estimation and prediction in *in vitro* pharmacogenomic screens. The aim is to be able to guide the selection of cancer therapy based on the statistical prediction of how drugs will behave for the individual patient, each drug on its own and in combination, by modelling synergistic effects. We develop new multivariate (multi-task) penalized and Bayesian methods to improve prediction of drug sensitivity or synergistic effects in drug combinations in large-scale screening experiments based on molecular characterization of cancer cell lines and patient samples as well as properties of the drugs. One particular challenge is the integration of multiple heterogeneous data sources, for example via multiple kernel learning. The focus of this project could be on one of many different aspects of this problem, including design of experiments (predicting the most promising drug combination experiments based on existing data), feature selection (e.g., in multiple kernel learning, which kernels – and within kernels, which original features – provide most predictive value), or bi-clustering (given a new tumour sample with certain molecular characteristics, to which group of samples in the database is it most similar and which therapy options are most promising for this tumour).

Eligibility:
- A PhD degree (at the latest by 1 July 2020) in statistics, biostatistics, mathematics, computer science or other related disciplines with a documented competence in statistics, biostatistics or mathematics and advanced computational skills.
- You have not been resident in Norway for more than 12 months in the last 3 years.

Benefits: The fellow will be employed at the University of Oslo (UiO) for three years. The gross salary of a Fellow will amount to 515 200 Norwegian kroner/year (approximately 56,000 US Dollars). UiO will cover full health insurance and pay towards your pension with the Norwegian pension fund. As an employee in Norway the fellow has additional welfare benefits. UiO will also support research costs (laptop, travel, courses etc) with 54 600 NOK per year

References:
- Ickstadt K, Schäfer M, Zucknick M (2018). Toward Integrative Bayesian Analysis in Molecular Biology. Annual Review of Statistics and Its Application. 5:141-167.
- Menden MP et al. (2019). Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature communications, 10(1), 1-17.