SCIENTIA FELLOWS

Scalable Bayesian Methods for Cancer Subtyping and Biomarker Discovery in Genomic Data Integration

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Project Description: The project focuses on the development of scalable statistical methods for the analysis of genomic data from different sources. Applications will include cancer subtyping and signature/biomarker discovery. Bayesian methods are a key tool in quantifying variability and incorporating biological understanding in such contexts, and the project aims to leverage a Bayesian framework. Possible project directions include, but are not limited to, building on two existing and complementary Bayesian approaches: first, we propose the generalization of a Bayesian Mallows model for ranks[1], which is intrinsically suited to the purpose of horizontal genomic data integration and handles missing data and uncertainty quantification. Second, we plan incorporation of more flexible prior distributions into a Bayesian two-way latent structure model for integrative clustering[2] in order to better assess genomic heterogeneity within disease subtype clusters. For both approaches, development goals also include variable selection and cluster parsimony tuning.

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.
- 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

1. Vitelli, V., Sørensen, Ø., Crispino, M., Frigessi, A., and Arjas, E., "Probabilistic preference learning with the Mallows rank model", *Journal of Machine Learning Research*, 18(158), 1-49, 2018
2. Swanson, D., Lien, T., Bergholtz, H., Sorlie, T., Frigessi, A., "A Bayesian Two-Way Latent Structure Model for Genomic Data Integration Reveals Few Pan-Genomic Cluster Subtypes in a Breast Cancer Cohort", *Bioinformatics*, May 2019