## On the identification of sets of informative peptides on antigen microarrays

## Tatjana von Rosen<sup>1</sup>, Marju Valge<sup>2</sup>, Triin Võrno<sup>2</sup> and Ene Käärik<sup>2</sup>

<sup>1</sup>University of Tartu, Stockholm University, email: Tatjana.vonRosen@stat.su.se, <sup>2</sup>University of Tartu, Estonia, email: Ene.Kaarik@ut.ee

Keywords: high-dimensional data, profile analysis, selection of variables.

Within the last decade, the development of antigen chip technology has enabled the simultaneous measurement of thousands of peptides in biological samples. Finding sets of peptides which can uniquely characterize TB patients and healthy individuals, can, for example, help to develop better diagnostic tests and to identify candidate vaccine antigens. In this work we use the procedure for variables selection which is applicable in a high-dimensional setting worked out by Läuter et al (2009) and new identification technique of control peptides that gives high mean response and low coefficient of variation across all replicates (Ngo et al, 2009).

Using profile analysis (of sets of peptides), as the next step, will facilitate the study of behavior of the immune system of vaccinated individuals over time.

## References

- [1] Läuter, J., Horn, F., Rosołowski, M., Glimm, E. (2009). High-dimensional data analysis: Selection of variables, data compression and graphics Application to gene expression. *Biometrical Journal* **51**(2), 235-251.
- [2] Ngo, Y., Advani, R., Valentini, D., Gaseitsiwe, S., Mahdavifar, S., Maeurer, M., Reilly, M. (1994). Identification and testing of control peptides for antigen microarrays. *Journal of Immunological Methods* 343(2), 68–78.