Transcriptome analysis of primary and metastatic tumours

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# Introduction

Prostate cancer remains to be one of the leading causes of cancer death in men. The metastasis of prostate cancer into other sites remains an important indicator for patient outcome. Deeper insights in the pathways that cause a primary tumour to metastasize into other sites would be clinically significant towards improving patient outcomes. This STAT540 project investigates differences in the transcriptome between primary tumours and metastatic tumours and investigates biological pathways that could cause primary tumours to metastasize.

# Project scope

A data set of 60 tumour samples (Grasso et al., 2012) originating from a variety of sites (ranging from prostate, brain to bone marrow) will be used to investigate the transcriptome differences in primary and metastatic tumours. The first step will require pre-processing of the raw data using various R modules and packages. The next step will be to analyze the high-dimensional data using statistical techniques such as clustering. Publicly available algorithms (Dao et al., 2011) will be used to determine genes of interest that differentiate the primary tumours from the metastatic tumours. Finally, the genes of interest will be manually analyzed to generate hypotheses regarding the pathways the metastatic process and potentially lead towards the discovery of biomarkers for prostate cancer metastasis.

# Works cited

Dao, P., Wang, K., Collins, C., Ester, M., Lapuk, A., & Sahinalp, S. C. (2011). Optimally discriminative subnetwork markers predict response to chemotherapy. *Bioinformatics (Oxford, England)*, *27*(13), i205–13. doi:10.1093/bioinformatics/btr245

Grasso, C. S., Wu, Y.-M., Robinson, D. R., Cao, X., Dhanasekaran, S. M., Khan, A. P., Quist, M. J., et al. (2012). The mutational landscape of lethal castration-resistant prostate cancer. *Nature*, *487*(7406), 239–43. doi:10.1038/nature11125